

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2005, 04:49:33 ; Search time 3552 Seconds
(without alignments)
3819.668 Million cell updates/sec

Title: US-10-015-388a-54

Perfect score: 1432

Sequence: 1 MCFUNKULLLAVLGWLFQIP.....LRAQGPBPARGRRGCSRA 280

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US10015388/runat:28032005.130453.6142/app.query.fasta_1.455
-DB=GenEmbl -QWMT=fastcap -SUFFIX=rgse -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALLIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10015388 @CGN.1.1.560 @runat:28032005.130453.6142 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sv.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1432	100.0	3580	6	AX696985 Sequence
2	1432	100.0	3580	9	AY358467 Homo sapi
3	1432	100.0	4350	9	BC066640 Homo sapi
4	1432	100.0	4354	9	BC052568 Homo sapi

5	1432	100.0	4725	9	AF525398 Homo sapi
6	1424	99.4	3212	9	BC001092
7	1424	99.4	3212	9	BC008333 Homo sapi
8	1424	99.4	3212	9	BC008334 Homo sapi
9	934	65.2	129517	2	AC016400 Homo sapi
10	934	65.2	148295	2	AC090510 Homo sapi
11	866	60.5	260033	2	AC099267
12	866	60.3	181602	10	AL935168
13	566.5	39.6	110000	2	AC106723_0
14	371.5	25.9	166294	2	BX537330
15	371.5	25.9	170138	5	BX569781
16	371.5	25.9	323764	2	BX569781
17	255	17.8	985	6	CQ729264
18	255	17.8	985	6	CQ729264
19	183.5	12.8	110000	5	BC081098
20	167.5	11.7	2192	3	AK174174
21	128	8.9	3904	6	CQ599307
22	128	8.9	3983	3	AY051770
23	128	8.9	4660	3	AF487678S2
24	128	8.9	7602	6	CQ599306
25	128	8.9	18737	6	CQ575162
26	128	8.9	30583	2	AC017314
27	128	8.9	171868	3	AC010118
28	128	8.9	257867	3	AC005557
29	128	8.9	303191	3	AE003472
30	127	8.9	4661	3	AF487675S2
31	116	8.1	223547	2	AC098514
32	114.5	8.0	177744	2	AC073954
33	113.5	7.9	92785	10	CNS07YOV
34	113.5	7.9	101777	9	AC105210
35	113.5	7.9	164959	9	AC087823
36	113.5	7.9	174906	9	AC067930
37	113.5	7.9	181075	10	CNS07YEP2
38	113.5	7.9	190784	10	AL645797
39	112	7.8	2760	10	MUSTWISTG
40	112	7.8	11894	1	AE012256
41	112	7.8	198423	2	AC148253
42	112	7.8	207636	2	AC019122
43	112	7.8	348942	1	BX572596
44	111.5	7.8	1104	6	AX663882
45	111.5	7.8	110000	1	AE000516_24
46	111.5	7.8	110000	1	AE016822_11
47	111.5	7.8	196140	2	AC084107
48	111.5	7.8	212370	10	AC122334
49	111.5	7.8	213308	2	AC079164
50	111.5	7.8	306050	1	BX248341
51	111.5	7.8	348247	1	BX842579
52	111	7.8	321250	1	SC093911
53	110.5	7.7	562	11	BV104927
54	110.5	7.7	110000	1	AE000516_26
55	110.5	7.7	232605	1	AE017222
56	110.5	7.7	233835	2	AC132778
57	110.5	7.7	306550	1	BX248342
58	110	7.7	1362	1	AY029247
59	110	7.7	4693	8	AB073881
60	110	7.7	114085	9	AC093734
61	110	7.7	307551	1	AP003015
62	109.5	7.6	34503	2	AC151612
63	109.5	7.6	139962	14	AY386264
64	109	7.6	1362	1	AY029240
65	109	7.6	1362	1	AY029244
66	109	7.6	1362	1	AY029249
67	109	7.6	1712	6	I34703
68	109	7.6	2351	1	PSEEXOS
69	109	7.6	300425	1	AP005038
70	108.5	7.6	1457	6	AX331540
71	108.5	7.6	1457	9	HSBHLH
72	108.5	7.6	39474	3	AC016024
73	108	7.5	76513	8	AE016820_14
74	108	7.5	179447	2	AC060806
75	108	7.5	180846	2	AC145151
76	108	7.5	187235	2	AC113428
77	108	7.5	223984	2	AC097915

370	97.5	6.8	246941	2	AC145215	AC145215 Homo sapi	443	96.5	6.7	110000	1	AE017283_19	Continuation (20 o
371	97.5	6.8	254633	2	CR762389	CR762389 Danio rer	444	96.5	6.7	110000	1	BS571965_05	Continuation (6 of
C 372	97.5	6.8	256584	2	AC133754	AC133754 Rattus no	C 445	96.5	6.7	110000	1	BS571966_27	Continuation (28 o
373	97.5	6.8	271708	2	AC094667	AC094667 Rattus no	C 446	96.5	6.7	112467	9	HS0505B13	Z98052 Human DNA s
374	97.5	6.8	298550	1	AP005029	AP005029 Streptomy	C 447	96.5	6.7	136367	9	AC098874	AC098874 Homo sapi
C 375	97.5	6.8	298425	1	AP005037	AP005037 Streptomy	C 448	96.5	6.7	154218	9	AC020663	AC020663 Homo sapi
376	97.5	6.8	300029	8	AE017090	AE017090 Oryza sat	C 449	96.5	6.7	155749	2	AC135345	AC135345 Homo sapi
C 377	97.5	6.8	300774	1	AE016912	AE016912 Chromobac	C 450	96.5	6.7	160842	2	AC124090	AC124090 Homo sapi
C 378	97.5	6.8	309050	1	SC0939117	SC0939117 Streptomy	C 451	96.5	6.7	177574	9	AC124086	AC124086 Homo sapi
379	97	6.8	1499	6	BD134425	BD134425 Human nuc	C 452	96.5	6.7	177613	9	AC124089	AC124089 Homo sapi
380	97	6.8	1499	6	AX017254	AX017254 Sequence	C 453	96.5	6.7	184695	2	AC145147	AC145147 Homo sapi
381	97	6.8	1499	6	AX524958	AX524958 Sequence	C 454	96.5	6.7	190289	9	AC135329	AC135329 Homo sapi
382	97	6.8	1519	9	HS0808130	HS0808130 Homo sapi	C 455	96.5	6.7	190766	14	MCU60315	U60315 Molluscum c
383	97	6.8	2898	1	AE017965	AE017965 Sequence	C 456	96.5	6.7	188289	9	AC140899	AC140899 Homo sapi
C 384	97	6.8	3120	9	HS058917	HS058917 Xanthomon	C 457	96.5	6.7	194490	9	AC135718	AC135718 Homo sapi
C 385	97	6.8	3223	6	AR034066	AR034066 Sequence	C 458	96.5	6.7	195397	2	AC135718	AC135718 Homo sapi
C 386	97	6.8	3223	6	AR097656	AR097656 Sequence	C 459	96.5	6.7	204655	2	AC142537	AC142537 Homo sapi
C 387	97	6.8	3223	6	AR097733	AR097733 Sequence	C 460	96.5	6.7	205191	2	AC145314	AC145314 Homo sapi
C 388	97	6.8	3223	6	AR102359	AR102359 Sequence	C 461	96.5	6.7	234228	2	AC125852	AC125852 Homo sapi
C 389	97	6.8	3223	6	ARI04870	ARI04870 Sequence	C 462	96.5	6.7	234903	2	AC131216	AC131216 Rattus no
C 390	97	6.8	3223	6	ARI131081	ARI131081 Sequence	C 463	96.5	6.7	304282	1	AE016910	AE016910 Chromobac
C 391	97	6.8	3223	6	ARI37603	ARI37603 Sequence	C 464	96.5	6.7	349260	1	BS572595	BS572595 Rhodospheu
C 392	97	6.8	3223	6	BD023246	BD023246 Method fo	C 465	96.5	6.7	349652	1	BS569690	BS569690 Synchococ
C 393	97	6.8	3223	6	AR453137	AR453137 Sequence	C 466	96	6.7	3999	6	E34092	E34092 Protein par
C 394	97	6.8	3223	6	BC011624	BC011624 Homo sapi	C 467	96	6.7	1362	1	AY029245	AY029245 Pseudomon
C 395	97	6.8	3223	9	BC011624	BC011624 Homo sapi	C 468	96	6.7	1813	6	AR380926	AR380926 Sequence
C 396	97	6.8	7291	12	ASPSVPFAZI	ASPSVPFAZI	C 469	96	6.7	2205	12	BT007802	BT007802 Synthetic
C 397	97	6.8	7294	12	ASPSVPFAZI	ASPSVPFAZI	C 470	96	6.7	2205	12	BT007802	BT007802 Synthetic
C 398	97	6.8	7438	6	AX116382	AX116382 Sequence	C 471	96	6.7	2401	9	BC053316	BC053316 Homo sapi
C 399	97	6.8	7573	6	AX114856	AX114856 Sequence	C 472	96	6.7	2580	9	BC007777	BC007777 Homo sapi
C 400	97	6.8	7573	6	AX114870	AX114870 Sequence	C 473	96	6.7	2580	9	AF055077	AF055077 Homo sapi
C 401	97	6.8	10000	1	AC009042	AC009042 Homo sapi	C 474	96	6.7	2678	6	AR270666	AR270666 Sequence
C 402	97	6.8	10811	1	AE012335	AE012335 Xanthomon	C 475	96	6.7	2678	6	AX335046	AX335046 Sequence
C 403	97	6.8	11196	1	AE012055	AE012055 Xanthomon	C 476	96	6.7	2678	9	HUMMZFI	HUMMZFI Human zinc
C 404	97	6.8	11461	1	AE007275	AE007275 Sinorhizo	C 477	96	6.7	2687	6	CQ731517	CQ731517 Sequence
C 405	97	6.8	15719	4	BT416457	BT416457 Bos tauru	C 478	96	6.7	2905	9	AF055078	AF055078 Homo sapi
C 406	97	6.8	37106	1	AY228335	AY228335 Xanthomon	C 479	96	6.7	3037	5	GGU90541	GGU90541 Gallus gall
C 407	97	6.8	37186	1	MSGV244	MSGV244 Burkholde	C 480	96	6.7	3148	4	BTMYOIBA	BTMYOIBA Bos tauru
C 408	97	6.8	63882	7	AY349011	AY349011 Burkholde	C 481	96	6.7	3505	4	BTU03420	BTU03420 Sequence
C 409	97	6.8	110000	1	AE000516_02	AE000516_02 Continuation (3 of	C 482	96	6.7	4515	6	CQ580107	CQ580107 Sequence
C 410	97	6.8	110000	1	AE000516_31	AE000516_31 Continuation (32 o	C 483	96	6.7	4515	6	CQ580107	CQ580107 Sequence
C 411	97	6.8	110000	1	BS571965_37	BS571965_37 Continuation (28 o	C 484	96	6.7	4639	3	AY0521365	AY0521365 Xanthomon
C 412	97	6.8	110000	1	CP000010_27	CP000010_27 Continuation (28 o	C 485	96	6.7	5105	3	AY058497	AY058497 Drosophil
C 413	97	6.8	110000	1	CP000010_28	CP000010_28 Continuation (29 o	C 486	96	6.7	5511	1	AF117980	AF117980 Amycolato
C 414	97	6.8	110000	8	AE016816_5	AE016816_5 Continuation (6 of	C 487	96	6.7	5770	1	RCU84577	RCU84577 Rhodobacter
C 415	97	6.8	117612	10	AL591366	AL591366 Mouse DNA	C 488	96	6.7	11279	6	E34083	E34083 Protein par
C 416	97	6.8	138580	2	CR388100	CR388100 Danio rer	C 489	96	6.7	11908	1	AR005822	AR005822 Caulobact
C 417	97	6.8	148301	2	CR384049	CR384049 Danio rer	C 490	96	6.7	12456	9	AF161886	AF161886 Homo sapi
C 418	97	6.8	185925	5	AL954176	AL954176 Zebrafish	C 491	96	6.7	13656	1	AE002065	AE002065 Deinococc
C 419	97	6.8	193159	9	AC006946	AC006946 Homo sapi	C 492	96	6.7	13656	1	CQ580106	CQ580106 Sequence
C 420	97	6.8	194641	10	AC132462	AC132462 Mus muscu	C 493	96	6.7	23730	6	AF232233	AF232233 Bacteriop
C 421	97	6.8	213184	2	CR749750	CR749750 Danio rer	C 494	96	6.7	40331	9	AC016630	AC016630 Homo sapi
C 422	97	6.8	228327	5	AL844514	AL844514 Zebrafish	C 495	96	6.7	44092	9	AC016629	AC016629 Homo sapi
C 423	97	6.8	299800	1	AP005028	AP005028 Streptomy	C 496	96	6.7	48681	2	AC014181	AC014181 Rhodophil
C 424	97	6.8	301443	1	AE017239	AE017239 Mycobacte	C 497	96	6.7	80609	1	AF116907	AF116907 Rhodococc
C 425	97	6.8	313800	1	SC0939114	SC0939114 Streptomy	C 498	96	6.7	80610	1	AP001204	AP001204 Rhodococc
C 426	97	6.8	318050	1	EX842344	EX842344 Mycobacte	C 499	96	6.7	110000	1	CP000010_18	CP000010_18 Continuation (29 o
C 427	97	6.8	341957	1	EX842572	EX842572 Mycobacte	C 500	96	6.7	110000	2	AP006502_04	AP006502_04 Continuation (19 o
C 428	97	6.8	343050	1	EX248334	EX248334 Mycobacte	C 501	96	6.7	150128	8	AP005409	AP005409 Oryza sat
C 429	97	6.8	348005	1	EX640434	EX640434 Bordetell	C 502	96	6.7	150128	8	AP005409	AP005409 Oryza sat
C 430	97	6.8	346287	1	EX640434	EX640434 Bordetell	C 503	96	6.7	153837	2	AC140157	AC140157 Canis fam
C 431	97	6.8	347894	1	EX640431	EX640431 Bordetell	C 504	96	6.7	157685	2	AC140157	AC140157 Canis fam
C 432	97	6.8	348676	1	EX842581	EX842581 Mycobacte	C 505	96	6.7	163307	8	AP005454	AP005454 Oryza sat
C 433	96.5	6.7	969	6	AX660905	AX660905 Sequence	C 506	96	6.7	163307	8	AP005454	AP005454 Oryza sat
C 434	96.5	6.7	1362	1	AY029248	AY029248 Pseudomon	C 507	96	6.7	167345	5	EX248327	EX248327 Zebrafish
C 435	96.5	6.7	3278	6	AX714327	AX714327 Sequence	C 508	96	6.7	177227	2	AC117009	AC117009 Rattus no
C 436	96.5	6.7	3278	6	AX714327	AX714327 Sequence	C 509	96	6.7	177227	2	AC117009	AC117009 Rattus no
C 437	96.5	6.7	6709	14	MOCERNAP	MOCERNAP Molluscum c	C 510	96	6.7	19046	2	CR846094	CR846094 Danio rer
C 438	96.5	6.7	11873	9	D78345	D78345 Human DNA f	C 511	96	6.7	19046	2	CR846094	CR846094 Danio rer
C 439	96.5	6.7	21013	9	D78345	D78345 Human DNA f	C 512	96	6.7	201313	3	AC010688	AC010688 Drosophil
C 440	96.5	6.7	52797	1	AF068845	AF068845 Mycobacte	C 513	96	6.7	206657	2	CR753834	CR753834 Danio rer
C 441	96.5	6.7	64920	1	AE008925	AE008925 Xanthomon	C 514	96	6.7	207737	2	BX640470	BX640470 Danio rer
C 442	96.5	6.7	101043	9	AC010539	AC010539 Homo sapi	C 515	96	6.7	212505	2	CR759831	CR759831 Danio rer

C 516	96	6.7	22013	2	BX957274	BX957274	Danio rer	C 589	95	6.6	110000	8	AE016818_07	Continuation (8 of
C 517	96	6.7	247903	2	AC127185	AC127185	Rattus no	C 590	95	6.6	114596	9	HS1063B2	AL035683 Human DNA
C 518	96	6.7	273663	2	AC133292	AC133292	Rattus no	C 591	95	6.6	120464	5	AC091751	AC091751 Gallus ga
C 519	96	6.7	281101	3	AE003526	AE003526	Pseudophil	C 592	95	6.6	138203	1	AY310323	AY310323 Streptomy
C 520	96	6.7	301214	1	AE016786	AE016786	Pseudomon	C 593	95	6.6	140812	8	AP001081	AP001081 Oryza sat
C 521	96	6.7	310578	1	AE016873	AE016873	Pseudomon	C 594	95	6.6	149435	8	AC135521	AC135521 Oryza sat
C 522	96	6.7	348771	1	BX640412	BX640412	Bordetelli	C 595	95	6.6	162028	2	AC149108	AC149108 Papio anu
C 523	96	6.7	349028	1	BX640413	BX640413	Bordetelli	C 596	95	6.6	182114	2	AC026296	AC026296 Homo sapi
C 524	96	6.7	349672	1	BX640419	BX640419	Bordetelli	C 597	95	6.6	201244	2	AC146327	AC146327 Gallus ga
C 525	95.5	6.7	3796	9	BC004893	BC004893	Homo sapi	C 598	95	6.6	201156	5	BX530721	BX530721 Zebrafish
C 526	95.5	6.7	3796	9	BC010069	BC010069	Homo sapi	C 599	95	6.6	205035	9	CNS00005	AC049870 Homo chr
C 527	95.5	6.7	3947	6	CQ171209	CQ171209	Sequence	C 600	95	6.6	205161	9	AC010913	AC010913 Homo sapi
C 528	95.5	6.7	3998	9	BC028601	BC028601	Homo sapi	C 601	95	6.6	210867	2	AC104878	AC104878 Pongo pyg
C 529	95.5	6.7	4078	9	HS062531	HS062531	Human AE2 a	C 602	95	6.6	216847	2	AC103459	AC103459 Rattus no
C 530	95.5	6.7	4390	9	BC009386	BC009386	Homo sapi	C 603	95	6.6	227682	2	AC122603	AC122603 Rattus no
C 531	95.5	6.7	4390	9	BC009434	BC009434	Homo sapi	C 604	95	6.6	231413	2	BX640548	BX640548 Danio rer
C 532	95.5	6.7	4503	3	BT004866	BT004866	Drosophila	C 605	95	6.6	234644	2	CR846087	CR846087 Danio rer
C 533	95.5	6.7	10100	9	AP005897	AP005897	Homo sapi	C 606	95	6.6	239841	2	CR749176	CR749176 Danio rer
C 534	95.5	6.7	10659	1	AE012282	AE012282	Xanthomon	C 607	95	6.6	245708	2	AC110145	AC110145 Rattus no
C 535	95.5	6.7	30000	14	BHV130KB	Z48053 Bovine he	Sequence	C 608	95	6.6	262229	2	AC073676	AC073676 Mus muscu
C 536	95.5	6.7	34602	2	FR57P6	Y12334 Takifugu ru	Sequence	C 609	95	6.6	297850	1	AP006577	AP006577 Gloeobact
C 537	95.5	6.7	64492	1	AB086653	AB086653	Streptomy	C 610	95	6.6	297850	1	AP006577	AP006577 Gloeobact
C 538	95.5	6.7	96742	1	AY211023	AY211023	Streptomy	C 611	95	6.6	299850	1	AP005949	AP005949 Bradyrhiz
C 539	95.5	6.7	110000	2	AC096839_2	Continuation (27 o	Continuation	C 612	95	6.6	310266	1	AE015862	AE015862 Pseudomon
C 540	95.5	6.7	110000	2	AC096839_2	Continuation (8 of	Continuation	C 613	94.5	6.6	896	1	AY027570	AY027570 Rhodococ
C 541	95.5	6.7	134127	2	AC150172	AC150172	Gallus ga	C 614	94.5	6.6	1050	6	AR199625	AR199625 Sequence
C 542	95.5	6.7	134127	2	AC150172	AC150172	Gallus ga	C 615	94.5	6.6	1050	6	AR235892	AR235892 Sequence
C 543	95.5	6.7	135301	14	BHV1CGEN	AL513304 Human DNA	Sequence	C 616	94.5	6.6	1050	6	AR366262	AR366262 Sequence
C 544	95.5	6.7	163243	9	AL513304	AL513304	Human DNA	C 617	94.5	6.6	1197	1	PAU50932	PAU50932 Pseudomon
C 545	95.5	6.7	171384	2	AC136212	AC136212	Gallus ga	C 618	94.5	6.6	5946	6	CQ730200	CQ730200 Sequence
C 546	95.5	6.7	177655	10	AC132288	AC132288	Mus muscu	C 619	94.5	6.6	12500	1	AF2323606	AF2323606 Rhodococ
C 547	95.5	6.7	177779	2	AC116870	AC116870	Mus muscu	C 620	94.5	6.6	12500	1	AF2323606	AF2323606 Rhodococ
C 548	95.5	6.7	178746	2	AC150164	AC150164	Gallus ga	C 621	94.5	6.6	12508	6	AR366254	AR366254 Sequence
C 549	95.5	6.7	179952	10	AC124724	AC124724	Mus muscu	C 622	94.5	6.6	12508	6	AR366254	AR366254 Sequence
C 550	95.5	6.7	184010	2	AC018656	AC018656	Homo sapi	C 623	94.5	6.6	12523	6	AR199615	AR199615 Sequence
C 551	95.5	6.7	184851	9	AC146055	AC146055	Pan trogl	C 624	94.5	6.6	12523	6	AR199615	AR199615 Sequence
C 552	95.5	6.7	186929	10	AC090657	AC090657	Mus muscu	C 625	94.5	6.6	12523	6	AR235882	AR235882 Sequence
C 553	95.5	6.7	193047	9	CNS00000Q	AL049874 Human chr	Sequence	C 626	94.5	6.6	12523	6	AR235882	AR235882 Sequence
C 554	95.5	6.7	210308	2	AC132288	AC132288	Mus muscu	C 627	94.5	6.6	14827	10	AY480041	AY480041 Mus muscu
C 555	95.5	6.7	213050	1	AL646079	AL646079	Ralstonia	C 628	94.5	6.6	14853	10	AY480039	AY480039 Mus muscu
C 556	95.5	6.7	254439	2	AC150047	AC150047	Gallus ga	C 629	94.5	6.6	14854	10	AY480034	AY480034 Mus muscu
C 557	95.5	6.7	263785	2	AC128476	AC128476	Rattus no	C 630	94.5	6.6	14906	10	AY480037	AY480037 Mus muscu
C 558	95.5	6.7	288727	2	AC103311	AC103311	Rattus no	C 631	94.5	6.6	14915	10	AY480035	AY480035 Mus muscu
C 559	95.5	6.7	295150	1	SC0939125	AL939125 Streptomy	Sequence	C 632	94.5	6.6	14919	10	AY480033	AY480033 Mus muscu
C 560	95.5	6.7	302300	1	AP005034	AP005034	Streptomy	C 633	94.5	6.6	14944	10	AY480036	AY480036 Mus muscu
C 561	95.5	6.7	303550	1	SC0939118	AL939118 Streptomy	Sequence	C 634	94.5	6.6	14944	10	AY480042	AY480042 Mus muscu
C 562	95.5	6.7	348517	1	BX248354	BX248354	Corynebact	C 635	94.5	6.6	15001	10	AY480040	AY480040 Mus muscu
C 563	95.5	6.7	348580	1	BX572601	BX572601	Rhodococ	C 636	94.5	6.6	15001	10	AY480043	AY480043 Mus muscu
C 564	95	6.6	957	6	AX196016	AX196016	Sequence	C 637	94.5	6.6	15438	10	AY480038	AY480038 Mus muscu
C 565	95	6.6	4599	6	CQ718738	CQ718738	Sequence	C 638	94.5	6.6	24045	1	AB070941	AB070941 Streptomy
C 566	95	6.6	4992	9	BC057255	BC057255	Homo sapi	C 639	94.5	6.6	31310	1	AY131229	AY131229 Streptomy
C 567	95	6.6	5123	14	HEPVTE	X15120 Pseudorabie	Sequence	C 640	94.5	6.6	38786	5	AF170972	AF170972 Agelaius
C 568	95	6.6	6222	1	AE312695	AF312695 Pseudomon	Sequence	C 641	94.5	6.6	42602	2	AC116971	AC116971 Trypanoso
C 569	95	6.6	6246	9	AB007883	AB007883	Homo sapi	C 642	94.5	6.6	42602	2	AC116971	AC116971 Trypanoso
C 570	95	6.6	6394	9	HS0808874	BX648723 Homo sapi	Sequence	C 643	94.5	6.6	110000	2	AC150790_2	Continuation (3 of
C 571	95	6.6	6394	14	SHILL	MS7505 Pseudorabie	Sequence	C 644	94.5	6.6	110000	2	LMFLCHRI16_07	Continuation (8 of
C 572	95	6.6	9121	4	OC7RICH2A	Z19092 O.cuniculus	Sequence	C 645	94.5	6.6	126566	9	AC144385	AC144385 Pan trogl
C 573	95	6.6	11005	1	AE012002	AE012002	Xanthomon	C 646	94.5	6.6	134431	14	AY386265	AY386265 Bovine pa
C 574	95	6.6	11082	1	AE001917	AE001917	Deinococ	C 647	94.5	6.6	137296	2	AC074162	AC074162 Mus muscu
C 575	95	6.6	13766	6	AX553919	AX553919	Sequence	C 648	94.5	6.6	137296	2	AC074162	AC074162 Mus muscu
C 576	95	6.6	30000	6	AX250263	AX250263	Sequence	C 649	94.5	6.6	137296	2	AC074162	AC074162 Mus muscu
C 577	95	6.6	40346	2	AP006490_7	Continuation (8 of	Continuation	C 650	94.5	6.6	150347	2	AC108184	AC108184 Felis cat
C 578	95	6.6	68750	1	AF210843	AF210843	Sorangium	C 651	94.5	6.6	155221	2	AC145688	AC145688 Pan trogl
C 579	95	6.6	68750	6	BD218234	BD218234	Genes for	C 652	94.5	6.6	159125	9	AC139530	AC139530 Homo sapi
C 580	95	6.6	68750	6	AR193029	AR193029	Sequence	C 653	94.5	6.6	160635	2	AC144567	AC144567 Homo sapi
C 581	95	6.6	68750	6	AR199551	AR199551	Sequence	C 654	94.5	6.6	163881	9	AC007436	AC007436 Homo sapi
C 582	95	6.6	68750	6	AR199559	AR199559	Sequence	C 655	94.5	6.6	164977	2	BX957336	BX957336 Danio rer
C 583	95	6.6	68750	6	AR199567	AR199567	Sequence	C 656	94.5	6.6	167857	5	AL844899	AL844899 Zebrafish
C 584	95	6.6	68750	6	AR201097	AR201097	Sequence	C 657	94.5	6.6	167972	2	AC125678	AC125678 Rattus no
C 585	95	6.6	68750	6	AR208671	AR208671	Sequence	C 658	94.5	6.6	180526	2	AC136083	AC136083 Rattus no
C 586	95	6.6	103450	1	AF440781	AF440781	Streptomy	C 659	94.5	6.6	181971	9	AC016182	AC016182 Homo sapi
C 587	95	6.6	109519	6	AX195929	AX195929	Sequence	C 660	94.5	6.6	184541	2	AC073715	AC073715 Mus muscu
C 588	95	6.6	110000	8	AE016815_4	Continuation (5 of	Continuation	C 661	94.5	6.6	189050	1	AL646069	AL646069 Ralstonia

C 662	94.5	6.6	190665	5	EX470086	735	94	6.6	222726	9	AC135069	AC135069 Homo sapi
C 663	94.5	6.6	191356	9	AC005041	C 736	94	6.6	230525	5	EX784028	EX784028 Zebrafish
C 664	94.5	6.6	202844	2	AC110211	C 737	94	6.6	231545	2	EX914198	EX914198 Danio rer
C 665	94.5	6.6	207281	2	CR847891	C 738	94	6.6	240094	2	AC118491	AC118491 Rattus no
C 666	94.5	6.6	234541	2	AC094891	C 739	94	6.6	243836	2	AC116094	AC116094 Rattus no
C 667	94.5	6.6	239623	2	AC121220	C 740	94	6.6	244957	2	EX950211	EX950211 Danio rer
C 668	94.5	6.6	241836	10	AC019302	C 741	94	6.6	260198	2	EX469922	EX469922 Danio rer
C 669	94.5	6.6	252513	2	AC098926	C 742	94	6.6	266132	2	AC099138	AC099138 Rattus no
C 670	94.5	6.6	256759	2	AC126002	C 743	94	6.6	268374	2	AC118769	AC118769 Rattus no
C 671	94.5	6.6	289102	2	AC128976	C 744	94	6.6	299800	1	AP005040	AP005040 Streptomy
C 672	94.5	6.6	299050	1	SC0939119	C 745	94	6.6	300349	1	AE017319	AE017319 Desulfovib
C 673	94.5	6.6	300350	1	AP006574	C 746	94	6.6	300880	1	AE016917	AE016917 Chromobac
C 674	94.5	6.6	300491	2	AC094205	C 747	94	6.6	300880	1	AE016917	AE016917 Chromobac
C 675	94.5	6.6	300600	1	AP005369	C 748	94	6.6	306650	2	AC026340	AC026340 Homo sapi
C 676	94.5	6.6	300900	1	AP005939	C 749	94	6.6	309805	2	AC026340	AC026340 Homo sapi
C 677	94.5	6.6	302178	1	AE016918	C 750	94	6.6	310967	1	AE016869	AE016869 Pseudomon
C 678	94.5	6.6	303550	1	SC0939131	C 751	94	6.6	313846	1	AE017234	AE017234 Mycobacte
C 679	94.5	6.6	325483	1	AP005050	C 752	94	6.6	345012	1	EX572607	EX572607 Rhodopseu
C 680	94.5	6.6	326050	1	EX321864	C 753	94	6.6	345012	1	EX572607	EX572607 Rhodopseu
C 681	94	6.6	612	9	SOE485164	C 754	94	6.5	2313	6	CQ735404	CQ735404 Sequence
C 682	94	6.6	1901	10	RO1131845	C 755	94	6.5	2319	9	HSM805518	HSM805518 Homo sapi
C 683	94	6.6	2130	1	AY299348	C 756	94	6.5	2396	8	AK070971	AK070971 Oryza sat
C 684	94	6.6	2158	9	AK096934	C 757	94	6.5	3542	6	AR338742	AR338742 Sequence
C 685	94	6.6	2444	8	ENU74303	C 758	94	6.5	4632	3	BT009943	BT009943 Homo sapi
C 686	94	6.6	2763	6	AX653205	C 759	94	6.5	5468	6	CQ588087	CQ588087 Drosophil
C 687	94	6.6	4700	10	BC068231	C 760	94	6.5	5630	3	DMU60591	DMU60591 Sequence
C 688	94	6.6	9316	1	AF077869	C 761	94	6.5	5630	3	AR130851	AR130851 Drosophila
C 689	94	6.6	10602	1	AE004874	C 762	94	6.5	5630	6	AR178592	AR178592 Sequence
C 690	94	6.6	11733	1	AE012393	C 763	94	6.5	5630	6	AR211708	AR211708 Sequence
C 691	94	6.6	12842	1	AE005742	C 764	94	6.5	5635	1	AF145039	AF145039 Streptomy
C 692	94	6.6	15497	1	AF134348	C 765	94	6.5	5688	1	AP043350	AP043350 Amycolatops
C 693	94	6.6	18366	1	AF299295	C 766	94	6.5	5688	8	SPBC1115	SPBC1115 S.pombe c
C 694	94	6.6	18767	3	LMFL5649	C 767	94	6.5	10772	1	AE011659	AE011659 Xanthomon
C 695	94	6.6	45998	9	HSU81031	C 768	94	6.5	15724	1	AE005855	AE005855 Caulobact
C 696	94	6.6	58343	1	HO089954	C 769	94	6.5	15724	1	AE004522	AE004522 Pseudomon
C 697	94	6.6	73511	2	HS65A6	C 770	94	6.5	25336	1	MSGX367	MSGX367 Mycobacte
C 698	94	6.6	91395	2	AC150974	C 771	94	6.5	47981	1	AF263245	AF263245 Micromono
C 699	94	6.6	110000	1	AE016822_05	C 772	94	6.5	47981	6	AX112026	AX112026 Sequence
C 700	94	6.6	110000	2	LMFLCHR31_17	C 773	94	6.5	49838	9	HS387E22	HS387E22 Human DNA
C 701	94	6.6	110000	2	LMFLCHR31_18	C 774	94	6.5	66788	6	CQ363727	CQ363727 Sequence
C 702	94	6.6	110000	2	LMFLCHR34_09	C 775	94	6.5	66788	9	AC024884	AC024884 Homo sapi
C 703	94	6.6	119199	2	AP003812	C 776	94	6.5	77314	9	AC024884	AC024884 Homo sapi
C 704	94	6.6	123160	9	AL353719	C 777	94	6.5	103837	1	AE000516_43	AE000516_43 Saccharo
C 705	94	6.6	123828	9	AP000353	C 778	94	6.5	108584	2	AY466441	AY466441 Saccharo
C 706	94	6.6	138780	8	AP004344	C 779	94	6.5	109349	2	Continuation (8 of	Continuation (8 of
C 707	94	6.6	158810	8	AP006286	C 780	94	6.5	110000	1	AP006618_10	AP006618_10 Burkholde
C 708	94	6.6	159174	5	EX005385	C 781	94	6.5	110000	1	EX571965_00	EX571965_00 Continuation (14 of
C 709	94	6.6	160848	2	AC009647	C 782	94	6.5	110000	8	CR380948_3	CR380948_3 Continuation (4 of
C 710	94	6.6	160892	2	CR381637	C 783	94	6.5	110603	9	HSJ421D16	HSJ421D16 Human DNA
C 711	94	6.6	161803	9	AC021028	C 784	94	6.5	118183	8	AC090433	AC090433 Chlamydom
C 712	94	6.6	163194	3	LMFP214	C 785	94	6.5	133765	9	HS67E13	HS67E13 Human DNA
C 713	94	6.6	163698	10	AC115876	C 786	94	6.5	156820	9	AC074323	AC074323 Homo sapi
C 714	94	6.6	170891	2	AC002118	C 787	94	6.5	168794	8	AC087726	AC087726 Chlamydom
C 715	94	6.6	170893	2	AC122297	C 788	94	6.5	174372	2	AC119136	AC119136 Rattus no
C 716	94	6.6	171266	2	EX323586	C 789	94	6.5	174852	2	AC1010195	AC1010195 Homo sapi
C 717	94	6.6	178754	2	AC120264	C 790	94	6.5	184222	9	HS2616N11	HS2616N11 Human DNA
C 718	94	6.6	181157	10	AC121789	C 791	94	6.5	184474	9	AL137026	AL137026 Human DNA
C 719	94	6.6	182760	2	AC120395	C 792	94	6.5	214125	10	AC083948	AC083948 Mus muscu
C 720	94	6.6	185897	2	AC145188	C 793	94	6.5	244800	1	EX842584	EX842584 Mycobacte
C 721	94	6.6	187005	10	AC124470	C 794	94	6.5	265302	2	AC097895	AC097895 Rattus no
C 722	94	6.6	193277	10	AC104324	C 795	94	6.5	278492	1	EX248347	EX248347 Mycobacte
C 723	94	6.6	193394	2	CR388077	C 796	94	6.5	291050	1	SC0939116	SC0939116 Streptomy
C 724	94	6.6	194763	2	AC150852	C 797	94	6.5	298550	1	AP005029	AP005029 Streptomy
C 725	94	6.6	195129	10	AL627069	C 798	94	6.5	299650	1	AP005955	AP005955 Bradyrhiz
C 726	94	6.6	202103	2	CR848044	C 799	94	6.5	300800	1	AE017240	AE017240 Mycobacte
C 727	94	6.6	205642	9	AC016586	C 800	94	6.5	309986	1	AE017240	AE017240 Streptomy
C 728	94	6.6	207454	2	AL129934	C 801	94	6.5	301708	1	AE016792	AE016792 Pseudomon
C 729	94	6.6	210971	5	AC1954188	C 802	94	6.5	302998	1	AE016921	AE016921 Chromobac
C 730	94	6.6	211544	9	AC025165	C 803	94	6.5	303050	1	EX321860	EX321860 Nitrosomo
C 731	94	6.6	213591	2	AC141759	C 804	94	6.5	324050	1	EX248335	EX248335 Mycobacte
C 732	94	6.6	214485	2	AC123416	C 805	94	6.5	347894	1	EX640431	EX640431 Bordetell
C 733	94	6.6	216844	2	AC130788	C 806	94	6.5	348997	1	EX572600	EX572600 Rhodopseu
C 734	94	6.6	217026	2	CR396592	C 807	94	6.5	349640	1	EX572600	EX572600 Rhodopseu

C 808	93	6.5	1024	3	CFCRP10	X13489 Crithidia f	C 881	93	6.5	265382	2	AC114439	AC114439 Rattus no
C 809	93	6.5	1419	9	BC016028	BC016028 Homo sapi	C 882	93	6.5	268510	2	AC095840	AC095840 Rattus no
C 810	93	6.5	1443	4	AF157019	AF157019 Bos tauri	C 883	93	6.5	298900	1	AP005937	AP005937 Bradyrhiz
C 811	93	6.5	1683	1	AX337497	AX337497 Myxococcu	C 884	93	6.5	299991	1	AE016776	AE016776 Pseudomon
C 812	93	6.5	1748	6	AX058217	AX058217 Sequence	C 885	93	6.5	300425	1	AP005038	AP005038 Pseudomon
C 813	93	6.5	2217	6	CQ720538	CQ720538 Sequence	C 886	93	6.5	301457	1	AE016924	AE016924 Chromobac
C 814	93	6.5	3554	6	CQ843120	CQ843120 Sequence	C 887	93	6.5	303855	1	AE017230	AE017230 Mycobacte
C 815	93	6.5	3554	9	AK126087	AK126087 Homo sapi	C 888	93	6.5	310029	1	AE016868	AE016868 Pseudomon
C 816	93	6.5	3573	6	CQ724709	CQ724709 Sequence	C 889	93	6.5	347950	1	AP003013	AP003013 Mesorhizo
C 817	93	6.5	3627	9	HS4576305	HS4576305 Homo sapi	C 890	93	6.5	348171	1	BE640412	BE640412 Bordetell
C 818	93	6.5	4027	1	AE021363	AE021363 Xanthomon	C 891	93	6.5	348525	1	BE640428	BE640428 Bordetell
C 819	93	6.5	4184	9	HS4576307	HS4576307 Homo sapi	C 892	92.5	6.5	978	10	MMU18658	U18658 Mus muscu
C 820	93	6.5	4275	1	XCU28802	U28802 Xanthomonas	C 893	92.5	6.5	1208	4	AF526394	AF526394 Sus scrofa
C 821	93	6.5	8651	1	AY124589	AY124589 Agriomyces	C 894	92.5	6.5	1310	10	AF099020	AF099020 Mus muscu
C 822	93	6.5	9316	1	AF077869	AF077869 Streptomy	C 895	92.5	6.5	2625	8	AK069218	AK069218 Oryza sat
C 823	93	6.5	10381	1	AE012495	AE012495 Xanthomon	C 896	92.5	6.5	2948	10	BC034126	BC034126 Mus muscu
C 824	93	6.5	11320	1	AE012110	AE012110 Xanthomon	C 897	92.5	6.5	3030	6	AR220782	AR220782 Sequence
C 825	93	6.5	11427	1	AE004931	AE004931 Pseudomon	C 898	92.5	6.5	3040	8	AK110154	AK110154 Oryza sat
C 826	93	6.5	1293	1	AE005985	AE005985 Caulobact	C 899	92.5	6.5	3169	8	AK110093	AK110093 Oryza sat
C 827	93	6.5	13068	6	CQ790429	CQ790429 Sequence	C 900	92.5	6.5	3420	9	HS0804095	AL832784 Homo sapi
C 828	93	6.5	13668	1	AE004907	AE004907 Pseudomon	C 901	92.5	6.5	3492	9	BC042651	BC042651 Homo sapi
C 829	93	6.5	14939	1	AE005092	AE005092 Halobacte	C 902	92.5	6.5	3498	9	BC004270	BC004270 Homo sapi
C 830	93	6.5	15081	6	CQ790448	CQ790448 Sequence	C 903	92.5	6.5	3498	9	BC007203	BC007203 Homo sapi
C 831	93	6.5	17753	6	CQ790449	CQ790449 Sequence	C 904	92.5	6.5	3751	9	AK000363	AK000363 Homo sapi
C 832	93	6.5	3276	3	LMFL8942	AL122012 Leishmani	C 905	92.5	6.5	4000	1	XCAVIR	X68781 X.campestri
C 833	93	6.5	35197	9	AC005782	AC005782 Homo sapi	C 906	92.5	6.5	4394	1	HPU80806	U80806 Hydrogenoph
C 834	93	6.5	52754	6	AX695689	AX695689 Sequence	C 907	92.5	6.5	4408	6	CQ850342	CQ850342 Sequence
C 835	93	6.5	88421	6	AX417445	AX417445 Sequence	C 908	92.5	6.5	4408	9	AK127465	AK127465 Homo sapi
C 836	93	6.5	105828	1	AP005965	AP005965 Bradyrhiz	C 909	92.5	6.5	4504	9	AK074115	AK074115 Homo sapi
C 837	93	6.5	108424	10	AL669827	AL669827 Mouse DNA	C 910	92.5	6.5	4663	10	BC053081	BC053081 Mus muscu
C 838	93	6.5	110000	1	AE016822_06	Continuation (7 of	C 911	92.5	6.5	5364	1	SGKSACPG	X77865 S.grieseus g
C 839	93	6.5	110000	1	AE017282_17	Continuation (18 o	C 912	92.5	6.5	5749	8	AF490339	AF490339 Phytophth
C 840	93	6.5	110000	1	AP006618_53	Continuation (54 o	C 913	92.5	6.5	5996	1	BPEBVG	M25401 B.pertussis
C 841	93	6.5	110000	1	AP006618_54	Continuation (55 o	C 914	92.5	6.5	6353	1	AY457916	AY457916 Marine al
C 842	93	6.5	110000	1	BX571966_16	Continuation (17 o	C 915	92.5	6.5	10044	1	AE012020	AE012020 Xanthomon
C 843	93	6.5	110000	2	LMFLCHR36_17	Continuation (18 o	C 916	92.5	6.5	10290	1	AE005865	AE005865 Caulobact
C 844	93	6.5	115866	9	AL627422	AL627422 Human DNA	C 917	92.5	6.5	10511	1	AE012093	AE012093 Xanthomon
C 845	93	6.5	124112	2	AC137573	AC137573 Homo sapi	C 918	92.5	6.5	12837	1	AY057934	AY057934 Xanthomon
C 846	93	6.5	137560	6	CQ830057	CQ830057 Sequence	C 919	92.5	6.5	13104	1	AE004656	AE004656 Pseudomon
C 847	93	6.5	137560	6	AX754989	AX754989 Sequence	C 920	92.5	6.5	13621	1	AE004794	AE004794 Pseudomon
C 848	93	6.5	138701	8	AP0033243	AP0033243 Oryza sat	C 921	92.5	6.5	14857	1	AE009543	AE009543 Brucella
C 849	93	6.5	141469	2	AC148179	AC148179 Zea mays	C 922	92.5	6.5	19601	1	AB070944	AB070944 Streptomy
C 850	93	6.5	141662	5	BX005235	BX005235 Zebrafish	C 923	92.5	6.5	35100	6	I96182	I96182 Sequence 19
C 851	93	6.5	149050	1	ML0672114	AL672114 Mesorhizo	C 924	92.5	6.5	42874	9	HSU63963	U63963 Human CSP-1
C 852	93	6.5	150201	8	CNS080C7	AL928777 Oryza sat	C 925	92.5	6.5	45375	5	AF328738	AF328738 Agelaius
C 853	93	6.5	152040	2	CNS080C7	AC139547 Homo sapi	C 926	92.5	6.5	68254	2	AC117408_3	Continuation (4 of
C 854	93	6.5	153791	2	AC119629	AC119629 Rattus no	C 927	92.5	6.5	84664	10	BX005296	Continuation (4 of
C 855	93	6.5	154076	2	AC023273	AC023273 Homo sapi	C 928	92.5	6.5	85163	1	AY048670	AY048670 Streptomy
C 856	93	6.5	158033	2	AC135991	AC135991 Homo sapi	C 929	92.5	6.5	86431	6	AR406002_7	Continuation (8 of
C 857	93	6.5	162208	8	AP0073321	AP0073321 Homo sapi	C 930	92.5	6.5	110000	1	BX571966_25	Continuation (26 o
C 858	93	6.5	163702	8	AP004849	AP004849 Oryza sat	C 931	92.5	6.5	110000	2	AC087331_3	Continuation (4 of
C 859	93	6.5	163776	2	AC135994	AC135994 Homo sapi	C 932	92.5	6.5	110000	2	LMFLCHR34_16	Continuation (17 o
C 860	93	6.5	164711	2	AC135964	AC135964 Homo sapi	C 933	92.5	6.5	110000	6	AR406002_6	Continuation (7 of
C 861	93	6.5	165711	2	CR759743	CR759743 Danio rer	C 934	92.5	6.5	131918	8	AP003570	AP003570 Oryza sat
C 862	93	6.5	166484	2	AC026830	AC026830 Homo sapi	C 935	92.5	6.5	132825	2	CR457442	CR457442 Danio rer
C 863	93	6.5	176871	2	AC150824	AC150824 Callithiri	C 936	92.5	6.5	137907	2	AC151640	AC151640 Daeyopus n
C 864	93	6.5	180797	2	AC149172	AC149172 Papio anu	C 937	92.5	6.5	143883	9	CNS01DSL	AL121819 Human chr
C 865	93	6.5	183937	2	AC037435	AC037435 Mus muscu	C 938	92.5	6.5	146663	8	AP004558	AP004558 Oryza sat
C 866	93	6.5	184148	2	AC148725	AC148725 Pongo pyg	C 939	92.5	6.5	149500	2	AC138636	AC138636 Leishmani
C 867	93	6.5	184252	2	AC139565	AC139565 Homo sapi	C 940	92.5	6.5	151038	8	AP005441	AP005441 Oryza sat
C 868	93	6.5	184981	9	AC008659	AC008659 Homo sapi	C 941	92.5	6.5	155024	8	AP004665	AP004665 Oryza sat
C 869	93	6.5	188448	9	AC139426	AC139426 Homo sapi	C 942	92.5	6.5	155432	8	AP003247	AP003247 Oryza sat
C 870	93	6.5	188596	9	AC120045	AC120045 Homo sapi	C 943	92.5	6.5	162496	2	AC044846	AC044846 Mus muscu
C 871	93	6.5	190050	1	AL646080	AL646080 Ralstonia	C 944	92.5	6.5	168874	10	AC132135	AC132135 Mus muscu
C 872	93	6.5	200724	9	AL139382	AL139382 Human DNA	C 945	92.5	6.5	170365	9	AL390920	AL390920 Human DNA
C 873	93	6.5	205737	2	AC021445	AC021445 Mus muscu	C 946	92.5	6.5	170459	2	AC150302	AC150302 Papio anu
C 874	93	6.5	208136	2	AC151042	AC151042 Callithiri	C 947	92.5	6.5	172099	2	AC023837	AC023837 Homo sapi
C 875	93	6.5	215050	1	AL646057	AL646057 Ralstonia	C 948	92.5	6.5	172214	2	AC011210	AC011210 Homo sapi
C 876	93	6.5	215131	10	AC119951	AC119951 Mus muscu	C 949	92.5	6.5	172676	9	AC117439	AC117439 Homo sapi
C 877	93	6.5	221805	10	AC116474	AC116474 Mus muscu	C 950	92.5	6.5	174383	2	EX323991	EX323991 Danio rer
C 878	93	6.5	225238	2	AC097825	AC097825 Rattus no	C 951	92.5	6.5	176011	10	AL645862	AL645862 Mouse DNA
C 879	93	6.5	226735	2	AC121120	AC121120 Mus muscu	C 952	92.5	6.5	176258	10	AC147624	AC147624 Mus muscu
C 880	93	6.5	249360	2	AC127920	AC127920 Rattus no	C 953	92.5	6.5	177726	9	AC148671	AC148671 Macaca mu

954	92.5	6.5	178023	10	AC130718	AC130718 Mus muscu	1027	92	6.4	163376	8	OSJN00254	AL731612 Oryza sat
955	92.5	6.5	184346	10	AC122283	Mus muscu	1028	92	6.4	165718	2	AC127508	AC127508 Homo sapi
956	92.5	6.5	186431	6	AX696303	Sequence	1029	92	6.4	166007	9	HSBA425A6	AL121749 Human DNA
c 957	92.5	6.5	191014	9	AC113268	Papio anu	1030	92	6.4	166176	2	EX927372	EX927372 Danio rer
958	92.5	6.5	195485	9	AL591846	Human DNA	c1031	92	6.4	167380	9	AP006242	AP006242 Homo sapi
959	92.5	6.5	197632	2	CR792419	Danio rer	1032	92	6.4	169391	2	AC111190	AC111190 Homo sapi
960	92.5	6.5	210301	9	AF307337	Homo sapi	1033	92	6.4	174164	9	AC116166	AC116166 Homo sapi
961	92.5	6.5	211219	2	CR790363	Danio rer	c1034	92	6.4	181241	9	AC080128	AC080128 Homo sapi
962	92.5	6.5	213050	1	AL646067	Raistonia	c1035	92	6.4	181593	2	CR848006	CR848006 Danio rer
c 963	92.5	6.5	213881	2	AC150564	Bos tauru	1036	92	6.4	187688	9	AP003066	AP003066 Homo sapi
c 964	92.5	6.5	229220	10	AC091519	Mus muscu	1037	92	6.4	192128	2	AC013382	AC013382 Homo sapi
965	92.5	6.5	233144	2	AC110317	AC110317 Rattus no	c1038	92	6.4	195119	5	EX649594	EX649594 Zebrafish
966	92.5	6.5	233755	2	CR812465	Danio rer	1039	92	6.4	195808	2	AL591182	AL591182 Homo sapi
967	92.5	6.5	258174	2	AC079429	Mus muscu	c1040	92	6.4	196451	9	AC112784	AC112784 Homo sapi
968	92.5	6.5	270094	2	AC106083	AC106083 Rattus no	1041	92	6.4	196507	2	AC135177	AC135177 Homo sapi
969	92.5	6.5	287203	2	AC133986	AC133986 Rattus no	c1042	92	6.4	197999	2	AC134688	AC134688 Homo sapi
c 970	92.5	6.5	299425	1	AP005049	AP005049 Streptomy	1043	92	6.4	200966	2	EX927115	EX927115 Danio rer
c 971	92.5	6.5	300717	1	AE017229	Mycobacte	1044	92	6.4	202012	5	EX088583	EX088583 Zebrafish
972	92.5	6.5	345012	1	EX572607	EX572607 Rhodosphe	c1045	92	6.4	202981	2	EX465228	EX465228 Danio rer
973	92.5	6.5	349354	1	EX640416	EX640416 Bordetell	c1046	92	6.4	207822	2	AC109321	AC109321 Homo sapi
c 974	92	6.4	606	9	PT8488168	AJ488168 Pan trogl	c1047	92	6.4	223097	2	AC129874	AC129874 Rattus no
c 975	92	6.4	1236	6	E02708	E02708 DNA sequenc	c1048	92	6.4	223575	10	AC130819	AC130819 Mus muscu
c 976	92	6.4	1881	6	AR541804	AR541804 Sequence	c1049	92	6.4	228783	2	AC094377	AC094377 Rattus no
977	92	6.4	2224	6	AX747800	AX747800 Sequence	c1050	92	6.4	234714	2	EX957235	EX957235 Danio rer
978	92	6.4	2224	9	AK092306	AK092306 Homo sapi	1051	92	6.4	251610	2	AC094526	AC094526 Rattus no
979	92	6.4	2388	1	AY497529	AY497529 Xanthomon	1052	92	6.4	253431	2	AC094604	AC094604 Rattus no
980	92	6.4	2408	8	AY049725	AY049725 Tranetes	c1053	92	6.4	255128	2	AC102905	AC102905 Mus muscu
981	92	6.4	2589	3	BMU16274	U16274 Bombyx mori	1054	92	6.4	267861	2	CH628327	CH628327 Danio rer
c 982	92	6.4	2723	3	BFL580840	AJ580840 Branchios	c1055	92	6.4	277991	2	EX950222	EX950222 Danio rer
c 983	92	6.4	3029	6	AX834352	AX834352 Sequence	c1056	92	6.4	278040	5	AL954847	AL954847 Zebrafish
c 984	92	6.4	3029	9	AK096755	AK096755 Homo sapi	c1057	92	6.4	280810	2	AC046188	AC046188 Homo sapi
985	92	6.4	3054	5	DRE428850	AJ428850 Danio rer	1058	92	6.4	297050	1	AP006569	AP006569 Gloabact
986	92	6.4	3617	10	AB018791	AB018791 Rattus no	c1059	92	6.4	300550	1	AP005021	AP005021 Streptomy
c 987	92	6.4	3764	1	AY148878	AY148878 Methylosi	c1060	92	6.4	301482	1	AE016916	AE016916 Chromobac
c 988	92	6.4	4771	1	AF021263	AF021263 Streptomy	1061	92	6.4	302898	1	AE017238	AE017238 Mycobacte
c 989	92	6.4	9344	14	AB049100	AB049100 Hepatitis	c1062	92	6.4	348068	1	EX572604	EX572604 Rhodosphe
c 990	92	6.4	10222	1	AE004685	AE004685 Pseudomon	c1063	92	6.4	348525	1	EX640428	EX640428 Bordetell
991	92	6.4	10460	1	AE011791	AE011791 Xanthomon	1064	92	6.4	349442	1	EX640447	EX640447 Bordetell
992	92	6.4	10466	1	AE011977	AE011977 Xanthomon	c1065	91.5	6.4	961	10	BC038863	BC038863 Mus muscu
993	92	6.4	11152	1	AE012525	AE012525 Xanthomon	c1066	91.5	6.4	1141	10	MUSTIS11D	M58564 Mouse TIS11
c 994	92	6.4	11213	1	AE004950	AE004950 Xanthomon	c1067	91.5	6.4	1208	6	AX110160	AX110160 Sequence
c 995	92	6.4	11378	1	AE001967	AE001967 Deinococc	c1068	91.5	6.4	1211	6	AX109760	AX109760 Sequence
c 996	92	6.4	13017	1	AE005861	AE005861 Caulobact	c1069	91.5	6.4	1600	9	AF523834	AF523834 Homo sapi
c 997	92	6.4	13349	1	AY599747	AY599747 Pseudomon	c1070	91.5	6.4	1600	9	HS3370184	HS3370184 Novel hum
998	92	6.4	15085	1	AE002038	AE002038 Deinococc	1071	91.5	6.4	1816	9	BC050403	BC050403 Homo sapi
999	92	6.4	22723	9	AF107890	AF107890 Homo sapi	c1072	91.5	6.4	2041	9	AK090885	AK090885 Homo sapi
c1000	92	6.4	28028	2	AC104504	AC104504 Trypanoso	c1073	91.5	6.4	2064	9	AF258570	AF258570 Homo sapi
c1001	92	6.4	35116	9	AC004151	AC004151 Homo sapi	1074	91.5	6.4	2084	1	AY423558	AY423558 Streptomy
c1002	92	6.4	35736	2	AC151604	AC151604 Emiliania	c1075	91.5	6.4	2193	9	ORAIGECA	M15399 Orangutan I
1003	92	6.4	37513	2	AC137639	AC137639 Homo sapi	c1076	91.5	6.4	2507	1	MXAFRZ	J04157 M.xanthus f
1004	92	6.4	37604	9	AP006588	AP006588 Homo sapi	c1077	91.5	6.4	2792	6	AX746933	AX746933 Sequence
1005	92	6.4	37867	1	AF086791	AF086791 Zymomonas	c1078	91.5	6.4	2792	9	AK091359	AK091359 Homo sapi
c1006	92	6.4	40695	9	AC133540	AC133540 Homo sapi	c1079	91.5	6.4	3044	6	AX833814	AX833814 Sequence
1007	92	6.4	64042	2	AC101394	AC101394 Mus muscu	c1080	91.5	6.4	3044	9	AK095851	AK095851 Homo sapi
c1008	92	6.4	84908	8	AC007197	AC007197 Arabidops	c1081	91.5	6.4	3541	1	AF102271	AF102271 Streptomy
c1009	92	6.4	95108	8	AC127818	AC127818 Rattus no	c1082	91.5	6.4	3559	3	BRL223578	AFJ223578 Branchios
c1010	92	6.4	110000	1	AP006618_13	Continuation (14 o	c1083	91.5	6.4	4808	3	BT009988	BT009988 Drosophil
c1011	92	6.4	110000	2	LMFLCHR18_09	Continuation (10 o	c1084	91.5	6.4	8321	6	AX803733	AX803733 Sequence
c1012	92	6.4	122803	5	EX005291	EX005291 Zebrafish	1085	91.5	6.4	8431	4	BTHYR	X02815 Bovine mRNA
1013	92	6.4	124104	9	AC061979	AC061979 Homo sapi	c1086	91.5	6.4	8599	14	BHVUS12	Z38139 Bovine herp
1014	92	6.4	125780	8	OSJN00277	AL731635 Oryza sat	c1087	91.5	6.4	10408	1	AE010409	AE010409 Methanopy
c1015	92	6.4	130596	2	AC018962	AC018962 Homo sapi	1088	91.5	6.4	10635	1	AE008475	AE008475 Streptoco
c1016	92	6.4	131691	9	AC096765	AC096765 Homo sapi	1089	91.5	6.4	10936	1	AE014397	AE014397 Brucella
1017	92	6.4	137300	9	AC090764	AC090764 Homo sapi	c1090	91.5	6.4	11735	1	AE004896	AE004896 Pseudomon
1018	92	6.4	138979	2	AC141667	AC141667 Apis mell	c1091	91.5	6.4	12027	1	AE005728	AE005728 Caulobact
c1019	92	6.4	142525	9	AC105752	AC105752 Homo sapi	c1092	91.5	6.4	12092	1	AE012096	AE012096 Xanthomon
c1020	92	6.4	144000	9	AC123764	AC123764 Homo sapi	1093	91.5	6.4	12652	1	AE005786	AE005786 Caulobact
1021	92	6.4	147184	2	AC135778	AC135778 Homo sapi	1094	91.5	6.4	15080	8	D82879	D82879 Chlorella v
c1022	92	6.4	149637	10	AC133089	AC133089 Mus muscu	1095	91.5	6.4	15516	1	AE012060	AE012060 Xanthomon
c1023	92	6.4	151009	2	AC135784	AC135784 Homo sapi	1096	91.5	6.4	18796	6	CQ363729	CQ363729 Sequence
1024	92	6.4	152559	2	AC135787	AC135787 Homo sapi	1097	91.5	6.4	24798	1	PST297529	PST297529 Pseudomon
1025	92	6.4	157216	2	AC008244	AC008244 Homo sapi	1098	91.5	6.4	49220	7	AX1320035	AX1320035 Bacteriop
1026	92	6.4	158730	2	AC093313	AC093313 Trypanoso	1099	91.5	6.4	49269	8	AX135499	AX135499 Oryza sat

c1100	91.5	6.4	80554	2	AP004143	AP004143 Oryza sat	c1173	91	6.4	2997	6	AX552616	AX552616 Sequence
c1101	91.5	6.4	82662	9	AB104726	AB104726 Homo sapi	1174	91	6.4	3021	6	CQ725525	CQ725525 Sequence
c1102	91.5	6.4	86280	9	HS337018	HS337018 Human DNA	1175	91	6.4	3156	5	AF009012	AF009012 Gallus ga
c1103	91.5	6.4	86829	9	AC011382	AC011382 Homo sapi	c1176	91	6.4	3158	6	AX552614	AX552614 Sequence
c1104	91.5	6.4	92564	9	AY007685	AY007685 Homo sapi	c1177	91	6.4	3241	6	AX833813	AX833813 Sequence
c1105	91.5	6.4	102671	9	BS000241	BS000241 Pan trogl	c1178	91	6.4	3241	9	AK095848	AK095848 Homo sapi
c1106	91.5	6.4	104419	8	AP003995	AP003995 Oryza sat	c1179	91	6.4	3389	3	BT001806	BT001806 Drosophila
c1107	91.5	6.4	107823	2	AC138132	AC138132 Pan trogl	c1180	91	6.4	4138	9	AY193890	AY193890 Homo sapi
c1108	91.5	6.4	110000	1	AE017180_37	Continuation (38 o	c1181	91	6.4	4257	12	CVU07648	U07648 Cloning vec
c1109	91.5	6.4	110000	1	AE017282_12	Continuation (13 o	1182	91	6.4	4358	10	BC060187	BC060187 Mus muscu
c1110	91.5	6.4	110000	1	AP006618_02	Continuation (3 of	1183	91	6.4	4367	10	AK129439	AK129439 Mus muscu
c1111	91.5	6.4	110000	1	AP006618_17	Continuation (18 o	1184	91	6.4	4433	9	AK024506	AK024506 Homo sapi
c1112	91.5	6.4	110000	2	AC127191_2	Continuation (3 of	1185	91	6.4	4734	9	AB007857	AB007857 Homo sapi
c1113	91.5	6.4	124882	9	AC090064	AC090064 Homo sapi	1186	91	6.4	4849	1	MXU08380	MXU08380 Myxococcus
c1114	91.5	6.4	127003	8	CNS0869C	AL732537 Oryza sat	1187	91	6.4	4881	9	BC039204	BC039204 Homo sapi
c1115	91.5	6.4	132544	1	AF521085	AF521085 Streptomy	1188	91	6.4	4882	10	BC046464	BC046464 Mus muscu
c1116	91.5	6.4	132768	9	AC011376	AC011376 Homo sapi	1189	91	6.4	5003	5	BBU18939	BBU18939 Batrachoco
c1117	91.5	6.4	139755	2	AC151511	AC151511 Dasyptus n	1190	91	6.4	5061	1	RLE431175	RLE431175 Rhizobium
c1118	91.5	6.4	142563	10	AL845548	AL845548 Mouse DNA	c1191	91	6.4	5508	1	WXA133131	WXA133131 Myxococcus
c1119	91.5	6.4	145337	8	AP005301	AP005301 Oryza sat	1192	91	6.4	8366	1	AF072709	AF072709 Streptomy
c1120	91.5	6.4	152910	8	AP005537	AP005537 Oryza sat	c1193	91	6.4	8900	8	AB112468	AB112468 Chlamydom
c1121	91.5	6.4	152974	8	AC135497	AC135497 Oryza sat	c1194	91	6.4	9667	3	AY442174	AY442174 Trypanoso
c1122	91.5	6.4	153670	2	AL3555295	AL3555295 Homo sapi	c1195	91	6.4	10249	1	AF088856	AF088856 Vogesella
c1123	91.5	6.4	159810	9	AL356433	AL356433 Human DNA	1196	91	6.4	10542	1	AE004852	AE004852 Pseudomon
c1124	91.5	6.4	161156	9	AL355939	AL355939 Homo sapi	1197	91	6.4	12433	1	AE004828	AE004828 Pseudomon
c1125	91.5	6.4	161531	8	AP004880	AP004880 Homo sapi	c1198	91	6.4	16775	1	AB000735	AB000735 Nocardioid
c1126	91.5	6.4	161795	2	AC126542	AC126542 Homo sapi	1199	91	6.4	21953	6	CQ792619	CQ792619 Sequence
c1127	91.5	6.4	162451	9	AL353597	AL353597 Human DNA	c1200	91	6.4	24081	6	AX598605	AX598605 Sequence
c1128	91.5	6.4	167131	8	CNS0868L	AL731881 Oryza sat	c1201	91	6.4	40962	2	AC006189	AC006189 Homo sapi
c1129	91.5	6.4	167961	2	AP002422	AP002422 Homo sapi	1202	91	6.4	45661	9	AP005888	AP005888 Homo sapi
c1130	91.5	6.4	172654	2	AC067737	AC067737 Homo sapi	c1203	91	6.4	52101	6	AX598593	AX598593 Sequence
c1131	91.5	6.4	173979	2	AC149625	AC149625 Papio anu	1204	91	6.4	82868	1	AJ620477	AJ620477 Angiotoxoc
c1132	91.5	6.4	176148	9	AC010798	AC010798 Homo sapi	1205	91	6.4	82868	6	CQ792587	CQ792587 Sequence
c1133	91.5	6.4	177285	2	AC130354	AC130354 Homo sapi	c1206	91	6.4	82868	6	CQ792604	CQ792604 Sequence
c1134	91.5	6.4	178825	2	AP001203	AP001203 Homo sapi	1207	91	6.4	90502	9	AC108676	AC108676 Homo sapi
c1135	91.5	6.4	182417	2	AC025291	AC025291 Homo sapi	c1208	91	6.4	110000	1	AE018822_19	Continuation (20 o
c1136	91.5	6.4	182735	9	AC129919	AC129919 Homo sapi	c1209	91	6.4	110000	1	AP006618_06	Continuation (7 of
c1137	91.5	6.4	182781	2	AC087814	AC087814 Homo sapi	1210	91	6.4	110000	1	AP006618_36	Continuation (37 o
c1138	91.5	6.4	184469	2	AL365447	AL365447 Homo sapi	c1211	91	6.4	110000	1	BX571965_01	Continuation (2 of
c1139	91.5	6.4	184641	9	AC127455	AC127455 Homo sapi	1212	91	6.4	110000	2	AC095759_2	Continuation (3 of
c1140	91.5	6.4	188956	9	AL591493	AL591493 Human DNA	c1213	91	6.4	110000	2	AP006500_03	Continuation (4 of
c1141	91.5	6.4	188956	9	AL591493	AL591493 Human DNA	c1214	91	6.4	111332	1	AY273869	AY273869 Pseudomon
c1142	91.5	6.4	198177	2	AC141421	AC141421 Pan trogl	1215	91	6.4	115983	8	OSJN00051	OSJN00051 Oryza sat
c1143	91.5	6.4	200089	10	AL683888	AL683888 Mouse DNA	1216	91	6.4	123254	2	AC145054	AC145054 Felis cat
c1144	91.5	6.4	210538	10	AC132455	AC132455 Mus muscu	1217	91	6.4	129505	9	AL590385	AL590385 Human DNA
c1145	91.5	6.4	213612	2	AC148589	AC148589 Pan trogl	c1218	91	6.4	144689	8	AP004307	AP004307 Oryza sat
c1146	91.5	6.4	239893	2	AC107521	AC107521 Rattus no	1219	91	6.4	146313	8	OSJN00261	OSJN00261 Oryza sat
c1147	91.5	6.4	241087	14	AF480884	AF480884 Chimpanze	1220	91	6.4	152418	9	AC100803	AC100803 Homo sapi
c1148	91.5	6.4	274676	1	AE017305	AE017305 Thermsus t	1221	91	6.4	155757	2	AC118548	AC118548 Homo sapi
c1149	91.5	6.4	284300	2	AC111967	AC111967 Rattus no	1222	91	6.4	157419	2	AC025389	AC025389 Homo sapi
c1150	91.5	6.4	299925	1	AP005045	AP005045 Streptomy	1223	91	6.4	159130	2	AC026847	AC026847 Homo sapi
c1151	91.5	6.4	300100	1	SC0939123	AL939123 Streptomy	c1224	91	6.4	159264	2	AC092419	AC092419 Homo sapi
c1152	91.5	6.4	302550	1	AP006581	AP006581 Gloeobact	c1225	91	6.4	159664	2	AL592441	AL592441 Homo sapi
c1153	91.5	6.4	303550	1	SC0939118	AL939118 Streptomy	c1226	91	6.4	160541	2	AC007944	AC007944 Homo sapi
c1154	91.5	6.4	310029	1	AE016861	AE016861 Pseudomon	c1227	91	6.4	160984	9	AC092453	AC092453 Homo sapi
c1155	91.5	6.4	314100	1	SC0939106	AL939106 Streptomy	c1228	91	6.4	162867	9	AC135966	AC135966 Homo sapi
c1156	91.5	6.4	334108	1	AE016857	AE016857 Pseudomon	1229	91	6.4	166005	8	AC120506	AC120506 Oryza sat
c1157	91.5	6.4	346547	1	AP003012	AP003012 Mesorhizo	c1230	91	6.4	166234	9	AC018629	AC018629 Homo sapi
c1158	91.5	6.4	348014	1	EX440430	EX440430 Bordetell	c1231	91	6.4	169347	9	AC007327	AC007327 Homo sapi
c1159	91.5	6.4	349726	1	EX440421	EX440421 Bordetell	1232	91	6.4	171177	9	AC092040	AC092040 Homo sapi
c1160	91	6.4	969	11	BV179107	BV179107 sqm10389	1233	91	6.4	172552	5	BX005365	BX005365 Zebraphish
c1161	91	6.4	1236	6	EO2578	EO2578 DNA encodin	c1234	91	6.4	177466	1	AE001826	AE001826 Deinococc
c1162	91	6.4	1275	9	AE191416	AE191416 Homo sapi	c1235	91	6.4	179354	2	CR354588	CR354588 Danio rer
c1163	91	6.4	1590	6	AR173222	AR173222 Sequence	c1236	91	6.4	180096	2	CR391999	CR391999 Danio rer
c1164	91	6.4	1908	6	AR164599	AR164599 Sequence	c1237	91	6.4	180223	9	AC062017	AC062017 Homo sapi
c1165	91	6.4	2094	9	CR456580	CR456580 Homo sapi	1238	91	6.4	181627	2	AL359264	AL359264 Homo sapi
c1166	91	6.4	2311	6	CQ730056	CQ730056 Sequence	1239	91	6.4	184019	9	AC099544	AC099544 Homo sapi
c1167	91	6.4	2325	9	HS47730	AX747772 Sequence	1240	91	6.4	184543	5	BX571681	BX571681 Zebraphish
c1168	91	6.4	2367	6	AX747772	AX747772 Sequence	c1241	91	6.4	185997	5	BX470139	BX470139 Zebraphish
c1169	91	6.4	2367	9	AK092858	AK092858 Homo sapi	c1242	91	6.4	187201	2	AC113860	AC113860 Rattus no
c1170	91	6.4	2326	5	AY687628	AY687628 Gallus ga	c1243	91	6.4	187578	9	AC096952	AC096952 Homo sapi
c1171	91	6.4	2540	6	EO6801	EO6801 gDNA encodi	1244	91	6.4	188574	2	AC131063	AC131063 Homo sapi
c1172	91	6.4	2698	9	AK091527	AK091527 Homo sapi	1245	91	6.4	196648	2	AC009673	AC009673 Homo sapi

c1246	91	6.4	198261	9	AC016825	AC016825 Homo sapi	1319	90.5	6.3	60385	9	AC009511	Homo sapi
c1247	91	6.4	198502	10	AL450395	Mouse DNA	1320	90.5	6.3	66241	2	AC019757	Drosophila
c1248	91	6.4	202050	1	AL646065	Ralstonia	c1321	90.5	6.3	77457	1	AF210249	Streptomyces
c1249	91	6.4	202301	1	AE017286	AB017286 Desulfovibrio	1322	90.5	6.3	77740	1	AF540993	Pseudomonas
c1250	91	6.4	207383	2	CR381676	CR381676 Danio rerio	c1323	90.5	6.3	78210	1	AB070949	Streptomyces
c1251	91	6.4	210074	9	AC010837	AC010837 Homo sapi	1324	90.5	6.3	97000	9	AP003966	Homo sapi
c1252	91	6.4	210508	2	AC135612	AC135612 Pan troglodytes	c1325	90.5	6.3	103527	2	AC150130	Gallus gallus
c1253	91	6.4	212199	9	AL445199	Human DNA	c1326	90.5	6.3	105027	1	AE016817	Pseudomonas
c1254	91	6.4	217594	1	AP002086	Agrobacterium	c1327	90.5	6.3	110000	1	AE016822	Continuation (7 of)
c1255	91	6.4	220050	1	AL646074	Ralstonia	c1328	90.5	6.3	110000	1	AP006618	Continuation (23 of)
c1256	91	6.4	232760	2	AC141423	AC141423 Pan troglodytes	c1329	90.5	6.3	110000	1	AP006618	Continuation (49 of)
c1257	91	6.4	232893	2	AC096182	AC096182 Rattus norvegicus	1330	90.5	6.3	110000	1	CP000011	Continuation (4 of)
c1258	91	6.4	236522	2	CR376793	CR376793 Danio rerio	c1331	90.5	6.3	110000	2	LMFLCHRI8	Continuation (8 of)
c1259	91	6.4	237725	2	BX293996	BX293996 Danio rerio	1332	90.5	6.3	110000	8	AE016817	Continuation (6 of)
c1260	91	6.4	238108	2	BX248332	BX248332 Danio rerio	c1333	90.5	6.3	120808	10	AL662862	Mouse DNA
c1261	91	6.4	240977	10	AL513352	AL513352 Mouse DNA	1334	90.5	6.3	122437	9	AC022498	AC022498 Homo sapi
c1262	91	6.4	249971	2	AC118143	AC118143 Rattus norvegicus	c1335	90.5	6.3	130528	8	AP003202	AP003202 Oryza sativa
c1263	91	6.4	254464	2	AC117040	AC117040 Rattus norvegicus	c1336	90.5	6.3	133023	10	AL645982	AL645982 Mouse DNA
c1264	91	6.4	270991	2	AC136210	AC136210 Gallus gallus	c1337	90.5	6.3	143300	8	AP003630	AP003630 Oryza sativa
c1265	91	6.4	273413	2	AC079314	AC079314 Homo sapi	1338	90.5	6.3	150272	2	AP005923	AP005923 Oryza sativa
c1266	91	6.4	295150	1	SC0939126	AL939126 Streptomyces	1339	90.5	6.3	154098	9	AC134043	AC134043 Homo sapi
c1267	91	6.4	299600	1	AP005941	AP005941 Bradyrhizobium	1340	90.5	6.3	156561	8	AP006723	AP006723 Oryza sativa
c1268	91	6.4	300327	1	AE017228	AE017228 Mycobacterium	c1341	90.5	6.3	160142	9	AC093684	AC093684 Homo sapi
c1269	91	6.4	300425	1	AP005041	AP005041 Streptomyces	1342	90.5	6.3	164051	6	C0875911	C0875911 Sequence
c1270	91	6.4	300700	1	AP006573	AP006573 Gloeobacterium	c1343	90.5	6.3	167344	3	AC093438	AC093438 Drosophila
c1271	91	6.4	301995	1	AE016779	AE016779 Pseudomonas	1344	90.5	6.3	168008	9	AC008544	AC008544 Homo sapi
c1272	91	6.4	302178	1	AE016918	AE016918 Chromobacterium	c1345	90.5	6.3	170023	3	AC024951	AC024951 Homo sapi
c1273	91	6.4	309267	1	AE017235	AE017235 Mycobacterium	c1346	90.5	6.3	174314	3	AC011066	AC011066 Drosophila
c1274	91	6.4	325352	2	AC120909	AC120909 Rattus norvegicus	1347	90.5	6.3	176027	2	AL732575	AL732575 Mus musculus
c1275	91	6.4	325482	2	EX004858	EX004858 Danio rerio	c1348	90.5	6.3	176051	9	AC023490	AC023490 Homo sapi
c1276	91	6.4	343243	1	EX640414	EX640414 Bordetella pertussis	1349	90.5	6.3	176146	2	AC023124	AC023124 Homo sapi
c1277	91	6.4	348014	1	EX640430	EX640430 Bordetella pertussis	1350	90.5	6.3	180136	10	AL732557	AL732557 Mouse DNA
c1278	90.5	6.3	861	9	HS3339387	AJ339387 Homo sapi	c1351	90.5	6.3	181103	3	AC011065	AC011065 Drosophila
c1279	90.5	6.3	1017	13	AY487480	AY487480 Uncultured	c1352	90.5	6.3	181253	2	AC099065	AC099065 Homo sapi
c1280	90.5	6.3	1370	8	AK069887	AK069887 Oryza sativa	c1353	90.5	6.3	183155	9	AC099065	AC099065 Homo sapi
c1281	90.5	6.3	1722	9	BC047320	BC047320 Homo sapi	1354	90.5	6.3	185080	9	AL954258	AL954258 Pan troglodytes
c1282	90.5	6.3	1904	9	HS0801326	AL133055 Homo sapi	c1355	90.5	6.3	186063	9	AC104417	AC104417 Homo sapi
c1283	90.5	6.3	1962	6	C0733707	C0733707 Sequence	1356	90.5	6.3	186553	2	AC150177	AC150177 Gallus gallus
c1284	90.5	6.3	2105	6	BD132812	BD132812 Plant and animal	c1357	90.5	6.3	190211	2	AC150083	AC150083 Gallus gallus
c1285	90.5	6.3	2105	6	AX031231	AX031231 Sequence	1358	90.5	6.3	192863	2	AC147313	AC147313 Pan troglodytes
c1286	90.5	6.3	2170	9	BC041015	BC041015 Homo sapi	1359	90.5	6.3	193689	2	AC066603	AC066603 Homo sapi
c1287	90.5	6.3	2183	14	AF214005	AF214005 Banana staminal	c1360	90.5	6.3	205794	9	AC010864	AC010864 Homo sapi
c1288	90.5	6.3	2364	9	AK000271	AK000271 Homo sapi	1361	90.5	6.3	211414	2	AC150057	AC150057 Gallus gallus
c1289	90.5	6.3	2835	6	AX136351	AX136351 Sequence	c1362	90.5	6.3	214387	2	AC137537	AC137537 Canis familiaris
c1290	90.5	6.3	2835	6	BD123628	BD123628 Secretary	c1363	90.5	6.3	218067	2	AC150058	AC150058 Gallus gallus
c1291	90.5	6.3	2835	9	AK075543	AK075543 Homo sapi	c1364	90.5	6.3	219205	10	AL611985	AL611985 Mouse DNA
c1292	90.5	6.3	3210	9	BC050477	BC050477 Homo sapi	1365	90.5	6.3	222605	1	AP002555	AP002555 Escherichia coli
c1293	90.5	6.3	3340	10	BC079869	BC079869 Mus musculus	1366	90.5	6.3	239347	2	AC099240	AC099240 Rattus norvegicus
c1294	90.5	6.3	3823	1	AB021364	AB021364 Xanthomonas	1367	90.5	6.3	248717	2	EX470107	EX470107 Danio rerio
c1295	90.5	6.3	4324	1	SO1300305	AJ300305 Streptomyces	c1368	90.5	6.3	265341	3	AE003634	AE003634 Drosophila
c1296	90.5	6.3	6036	6	C0586932	C0586932 Sequence	c1369	90.5	6.3	265524	3	AE003541	AE003541 Drosophila
c1297	90.5	6.3	6126	14	PV1318065	AJ318065 Pseudorabies	1370	90.5	6.3	287510	2	CR753823	CR753823 Danio rerio
c1298	90.5	6.3	7441	6	C0597803	CQ597803 Sequence	c1371	90.5	6.3	296500	1	SC0939128	SC0939128 Streptomyces
c1299	90.5	6.3	8223	6	C0586931	CQ586931 Sequence	1372	90.5	6.3	298550	1	AP005047	AP005047 Streptomyces
c1300	90.5	6.3	9277	6	CQ729952	CQ729952 Sequence	c1373	90.5	6.3	299450	1	AP006580	AP006580 Gloeobacterium
c1301	90.5	6.3	9287	9	HW00017A1	L02870 Human alpha	1374	90.5	6.3	299925	1	AP005039	AP005039 Streptomyces
c1302	90.5	6.3	10029	1	AE012787	AE012787 Chlorobacterium	1375	90.5	6.3	300052	1	AE017232	AE017232 Mycobacterium
c1303	90.5	6.3	11565	1	AE011677	AE011677 Xanthomonas	1376	90.5	6.3	300425	1	AP005022	AP005022 Streptomyces
c1304	90.5	6.3	11589	1	AE002079	AE002079 Deinococcus	1377	90.5	6.3	301675	1	AP005027	AP005027 Streptomyces
c1305	90.5	6.3	1296	1	AE001950	AE001950 Deinococcus	c1378	90.5	6.3	311000	1	SC0939122	SC0939122 Streptomyces
c1306	90.5	6.3	13431	1	AE005044	AE005044 Halobacterium	c1379	90.5	6.3	311963	1	AE016872	AE016872 Pseudomonas
c1307	90.5	6.3	20256	6	C0875919	CQ875919 Sequence	c1380	90.5	6.3	339650	1	SC0939108	SC0939108 Streptomyces
c1308	90.5	6.3	29132	1	STH575648	AJ575648 Streptomyces	c1381	90.5	6.3	346274	1	EX640443	EX640443 Bordetella pertussis
c1309	90.5	6.3	32896	1	AY52397285	AY523976 Azospirillum	c1382	90	6.3	612	9	CJA488165	CJA488165 Callithrix jacchus
c1310	90.5	6.3	32881	2	AC020288	AC020288 Drosophila	1383	90	6.3	624	9	CCA488163	CCA488163 Cebus cap
c1311	90.5	6.3	34875	6	C0861683	CQ861683 Sequence	c1384	90	6.3	1173	1	AY259141	AY259141 Streptomyces
c1312	90.5	6.3	34875	9	AC005329	AC005329 Homo sapi	1385	90	6.3	1195	6	AR321627	AR321627 Sequence
c1313	90.5	6.3	35881	9	AC005331	AC005331 Homo sapi	c1386	90	6.3	1402	6	AX463508	AX463508 Sequence
c1314	90.5	6.3	35868	3	AC011617	AC011617 Leishmania	1387	90	6.3	2003	6	CQ718085	CQ718085 Streptomyces
c1315	90.5	6.3	38516	1	AF540992	AF540992 Pseudomonas	1388	90	6.3	2456	8	AK072099	AK072099 Oryza sativa
c1316	90.5	6.3	48423	6	BD184770	BD184770 Nucleic acid	c1389	90	6.3	2550	6	CQ730790	CQ730790 Sequence
c1317	90.5	6.3	49208	6	AR204241	AR204241 Sequence	c1390	90	6.3	2878	9	BC0228710	BC0228710 Homo sapi
c1318	90.5	6.3	49208	2	AP004374	AP004374 Oryza sativa	c1391	90	6.3	3306	9	BC022938	BC022938 Homo sapi

1332	90	6.3	3333	1	AY492259	AY492259 Corynebacterium	1332	90	6.3	193050	1	AL646062	AL646062 Ralstonia
1333	90	6.3	3426	1	AY495678	AY495678 Xanthomonas	1333	90	6.3	193059	2	AL149253	AL149253 Papilio anu
1334	90	6.3	4434	6	CQ735134	CQ735134 Sequence	1334	90	6.3	194244	2	BX322553	BX322553 Homo sapi
1335	90	6.3	5005	9	AB011099	AB011099 Homo sapi	1335	90	6.3	195652	9	AC093572	AC093572 Pan trogl
1336	90	6.3	7234	1	AY101609	AY101609 Myxococcus	1336	90	6.3	200249	2	AC145063	AC145063 Pan trogl
1337	90	6.3	7282	9	HSNMDAR1A	Z32772 H. sapiens g	1337	90	6.3	200836	2	AC011965	AC011965 Homo sapi
1338	90	6.3	8312	1	AB178023	AB178023 Ralstonia	1338	90	6.3	201088	9	AL589733	AL589733 Human DNA
1339	90	6.3	9752	1	AJ746243	AJ746243 Stenotroph	1339	90	6.3	205050	1	AL646082	AL646082 Ralstonia
1340	90	6.3	10135	1	AE006017	AE006017 Caulobact	1340	90	6.3	205930	10	AC113533	AC113533 Mus muscu
1341	90	6.3	11064	1	AE004853	AE004853 Pseudomon	1341	90	6.3	207050	1	AL646063	AL646063 Ralstonia
1342	90	6.3	11512	1	AE011729	AE011729 Xanthomon	1342	90	6.3	209859	5	BX005398	BX005398 Zebrafish
1343	90	6.3	11691	1	AE004947	AE004947 Pseudomon	1343	90	6.3	217335	1	AE016946	AE016946 Bacteroid
1344	90	6.3	11702	1	AE004529	AE004529 Pseudomon	1344	90	6.3	225614	2	BX936454	BX936454 Danio rer
1345	90	6.3	12299	1	AE006000	AE006000 Caulobact	1345	90	6.3	228633	5	BX649600	BX649600 Zebrafish
1346	90	6.3	12444	1	AE004777	AE004777 Pseudomon	1346	90	6.3	230945	10	AC122898	AC122898 Mus muscu
1347	90	6.3	12608	1	AE000073	AE000073 Rhizobium	1347	90	6.3	250313	2	CR788310	CR788310 Danio rer
1348	90	6.3	14149	1	AE005986	AE005986 Caulobact	1348	90	6.3	254977	2	AC117353	AC117353 Rattus no
1349	90	6.3	14750	1	AE005796	AE005796 Caulobact	1349	90	6.3	258871	2	AC095418	AC095418 Rattus no
1350	90	6.3	17112	1	AE004997	AE004997 Halobacte	1350	90	6.3	258581	2	CR394526	CR394526 Danio rer
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VERSION AY358467.1 GI:37182057
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3580)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,

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Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Wleand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
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Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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CSRA"

ORIGIN

Alignment Scores:

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US-10-015-388A-54 (1-280) x AY358467 (1-3580)

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Qy 21 ThrValProGluAspLeuPhePheLeuGluGluGlyProSerTyrAlaPheGluValAsp 40
Db 267 ACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGGTCTCCCTCATATGCTTTGAGGTGGAC 326
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Db 447 AGTGACGGAGTGGGGGCTTCATGAGGAAAATCACCCACACCTACCCAGCCTGGGA 506
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Wed Mar 30 09:32:46 2005

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LOCUS			
DEFINITION Homo sapiens congenital dyserythropoietic anemia, type I, mRNA			

ACCESSION BC052568
VERSION BC052568.1
KEYWORDS GI:30851636
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4354)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 4354)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigr.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

(cDNA clone IMAGE:6645406), partial cds.
BC052568
BC052568.1 GI:30851636
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4354)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 4354)
Strausberg,R.
Direct Submission
Submitted (16-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigr.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IMAGE Plate: 47 Row: 0 Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 9
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ACCESSION AF525398
VERSION AF525398.1 GI:27451597
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4725)
AUTHORS Dgany,O., Avidan,N., Delaunay,J., Krasnov,T., Shalmon,L.,
Shalev,H., Eidelitz-Markus,T., Kapelushnik,J., Catlan,D.,
Pariente,A., Tulliez,M., Cretien,A., Schischmanoff,P.O.,
Iolascon,A., Fibach,E., Koren,A., Roessler,J., Le Merrier,M.,
Yaniv,I., Zaizov,R., Ben-Asher,E., Olender,T., Lancet,D.,
Beckmann,J.S. and Tamary,H.
Congenital dyserythropoietic anemia type I is caused by mutations
in codanin-1
Am. J. Hum. Genet. 71 (6), 1467-1474 (2002)
JOURNAL 22340442
MEDLINE 12434312
PUBMED 2 (bases 1 to 4725)
REFERENCE Ben-Asher,E.
AUTHORS Direct Submission
TITLE Submitted (27-JUN-2002) Molecular Genetics, The Weizmann Institute
JOURNAL of Science and the Schneider Medical Center, Hertzfel Street,
Rehovot 76100, Israel
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Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 23 Row: d Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

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Location/Qualifiers
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BC008334

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC008334 3212 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, clone IMAGE:3506174, mRNA, partial cds.

BC008334

BC008334.1 GI:14249908

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3212)

Strausberg, R.

Direct Submission

Submitted (25-MAY-2001) National Institutes of Health, Mammalian

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USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Stacey

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 23 Row: d Column: 13.

Location/Qualifiers

FEATURES

Alignment Scores:

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Score:

Percent Similarity:

Best Local Similarity:

Query Match:

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99.64% Conservative: 0

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US-10-015-388a-54 (1-280) x BC008333 (1-3212)

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ORIGIN
Alignment Scores:
Pred. No.: 9,928-97 Length: 3212
Score: 1424.00 Matches: 279
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 1
Query Match: 99.44% Indels: 0
DB: 9 Gaps: 0

US-10-015-388A-54 (1-280) x BC008334 (1-3212)
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DB 1381 TGTCAAGGAAGAGCCCTGGGGCTGTGTGGGGCTGTCTCCAGAGGAGAGCCCGGCGCC 1440
QY 221 ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrp 240
DB 1441 GTTCTGACAGCTGCAGAGAACATTGCTGTGGGGCTTGCACACAGAGAAAGCCCTGTCTGG 1500
QY 241 LeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLysAlaAlaValSerArgThr 260
DB 1501 CTGTGAGCAACATCAGACGACTGATCAGGAGGAGGTGAAAGCAGCAGTGTGTCGACCA 1560
QY 261 LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgArgGlyCysSerArgAla 280
DB 1561 CTTGAGCCAGGGTCTGTAACCTGCTGCCCGGGGAGCGAGGGGCTGCTCCCGCGCC 1620

RESULT 9
AC016400 Homo sapiens, WORKING DRAFT SEQUENCE, 19 unordered pieces.
LOCUS AC016400
DEFINITION AC016400.1 GI:6468793
ACCESSION AC016400
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 129517)
AUTHORS Ben-Asher,E., Avidan,N., Olender,T., Lancet,D., Salmon,L. and Tamary,H.
TITLE Sequencing of human chromosome 15 D15S488 region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 129517)
AUTHORS Ben-Asher,E., Avidan,N., Olender,T., Lancet,D., Salmon,L. and Tamary,H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Dept. of Molecular Genetics, Weizmann Institute of Science, P.O.Box 26, Rehovot 76100, Israel
COMMENT center: The Weizmann Institute, Crown Genome Center Web site: http://bioinfo.weizmann.ac.il/genome_center/sequencing.html
Contact: igbenashew@weizmann.ac.il
Statistics Sequencing vector: PUC18 Chemistry: Big Dye terminators.
* NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 6440: contig of 6440 bp in length
* * gap of unknown length
* 6441 8285: contig of 1845 bp in length
* * gap of unknown length
* 8286 9535: contig of 1250 bp in length
* * gap of unknown length
* 9536 10785: contig of 1250 bp in length
* * gap of unknown length
* 10786 18051: contig of 7266 bp in length
* * gap of unknown length
* 18052 31986: contig of 13935 bp in length
* * gap of unknown length
* 31987 41836: contig of 9850 bp in length
* * gap of unknown length
* 41837 45535: contig of 3699 bp in length

```


Db 91080 TCTGAGTCGGAATGAGGCAAGGGCTGGAAGACGAGAGGTTTCAGAAAGCCCTGGGGATTCC 91021
QY 17 ----- 17
Db 91020 CATCATCTCAGAGGTGGCTGCTTTTGAAGCTGGCGCTACACCTGGGACCGTGCAGGAGG 90961
QY 18 -----Glnile 19
Db 90960 TGGGGTGGGTGGGTGGGGGTCTCTGAAGTTGACCTGAATTGTGACTGTCTTGGCAGATT 90901
QY 20 ProThrValProGluAspLeuPheLeuGluGluGlyProSerTyrAlaPheGluVal 39
Db 90900 CCCACAGTCCCTCAGGACTGTCTTCTTCTGGAAGAGGGTCCCTCATATGCTTTGAGGTG 90841
QY 40 AspThrValAlaProGluHisGlyLeu----- 48
Db 90840 GACACAGTAGCCCCAGAGCATGGCTT-GGTGAGTGTCTGGGTTCGCGAGAGCCATGGGA 90782
QY 48 ----- 48
Db 90781 AACTCAGGAATAAGGAAGTGGGTGCTCTGGGAGGCCAGCCAGGGGCAGATGTAAACC 90722
QY 48 ----- 48
Db 90721 TTGTAAAGCCCTGCCAACTGCTCTTCTGGGTGCGCTGGGGAGGGGAGTCTGCTG 90662
QY 49 -----AspAlaAlaProValValAspGlnGlnLeuLeuTyrThr 61
Db 90661 ACACCAACCTTTTCTCCCGAGCAATGCGCTGTGTGGTGGACAGCAGCTGCTCTACACC 90602
QY 62 CysCysProTyrIle----- 66
Db 90601 TGCTGCCCCATCATCGGTGAGCACCGGTCTTCCCTGGAGCGTCTTGGTGTCTGCTCCTCCA 90542
QY 66 ----- 66
Db 90541 TGAGTACCCAAAGGACCCCTTGGCCAGCTCCCTTGGATATTGCTCCGTTTCATATGC 90482
QY 66 ----- 66
Db 90481 ATTCTGGGTATCTGAGCCTTTGACTCCACAAGTAAAGTCCATGATACTTAGGAGGGG 90422
QY 67 -----GlyGluLeuArgLysLeuLe 73
Db 90421 AGAGGGTCTCGAACTGAGAACTTGGACTTCACTGATACAGAGAGCTCCGAAACTGCT 90362
QY 73 uAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLysIleThrPr 93
Db 90361 CGCTTCGTGGGTGTCAAGGCACTGTGACGAGTGGGGCTTTCATGAGGAAATCACGCC 90302
QY 93 oThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu----- 110
Db 90301 CACCACTACACAGCCTGGAGCCAGCTTCCAGACCAGCCAGGGGCTCAGGTAAG 90242
QY 110 ----- 110
Db 90241 GGCAGGCGGAGACACCCGTGGGGAATAATGAGGGGGGTGGGGCGGGGACAGGAGGC 90182
QY 111 -----GlnAlaGlnLeuAlaGlnAlaPhePh 119
Db 90181 TGGAGGAAGCCTTGTGCTCTCCCTCCCTCCCGCCAGGACAGCTCGCCCGAGCCCTTTT 90122
QY 119 eHisAnGlnProProSerLeuArgThrValGluPheValAlaGluArgIleGlySe 139
Db 90121 CCACAAACCGCCGCTCTCTGCGCGGACCGGTAGAGTTCTGTGGCAAGAAATTTGGATC 90062
QY 139 rAnCysValLysHisIleLysAla----- 147
Db 90061 AAACGTGTGTAACAATATCAAGTA-ACAGTGGGTTAAGGATCCTGTCTCATCGCCCTAC 90003
QY 147 ----- 147

Db 90002 CATTTTTCCTCTTTTCTCAGTTGCTAAACTGAGAAGGTACGCCAGAGGGTGGGTGTG 89943
QY 147 ----- 147
Db 89942 GGGCTGAATGGGTGACACATTTTGAAGCAAAATTTCTGACCAAAATTTCCCATAAATTTTCA 89883
QY 148 -----Th 148
Db 89882 GCCTCTTTCGATTAAACCTCCCAACCATCCCAACCTTGTCTCCCTGTCTGAGGGGTAC 89823
QY 148 -----Th 148
Db 148 rLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGluGlnGluGlnLeuValThrG 168
Db 89822 ACTGTGGCAGATCTGTGTGGCCAGGAGAGTCACTTCTCAAGAGCAGCTGGTGACACA 89763
QY 168 nGlyGluGluGlyGlyAspProAlaGlnLeuLeuGluLeuLeuLeuLeuLeuLeuLeuPr 188
Db 89762 GGGAGAGAGGGGAGAGAGCCAGCCAGCTGTGTGGAGATCTTGTGTTCAGCTGTGCCC 89703
QY 188 oHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu----- 199
Db 89702 TCACGGGGCCCGAGCAATTGGCCCTGGGGCGGAGTAAGCAGCGCTGTCTCCATTTGATCCA 89643
QY 199 ----- 199
Db 89642 CTCTCTCTTGGCTTCTCTGTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 89583
QY 199 ----- 199
Db 89582 TCCTCTCTCATGCTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 89523
QY 199 ----- 199
Db 89522 GGCTGTAGCCTTCTGTGGCACAAAGCCAAACCTAGTGTGGGAGCGTGTGTGTGTGTGT 89463
QY 199 ----- 199
Db 89462 TGGGGCTGGCAGTTGGGCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 89403
QY 199 ----- 199
Db 89402 GGTGCTCTCTTCCAAAGGTACAGCTCCAGGTCTGAGGGCTTGTGTGTGTGTGTGTGTGT 89343
QY 200 -----ph 200
Db 89342 CTCTGACGCGAGCTGAAATACCCAGAGATCACTGACCCCATCTGTCTCTCTCTCTCTCT 89283
QY 200 eCysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAl 220
Db 89282 CTGTCAAAGGAAGAGCCCTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGTGGGGCTGT 89223
QY 220 a----- 220
Db 89222 -CGTACGTGTGAGGGAGCCCTGCAGCTAGCAGGCCAGGCAAGTGTGTGGGAGGTGTGACGGA 89164
QY 220 ----- 220
Db 89163 GTAGTCTGAGGTGCGGAGGGTGTGTGGGGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGT 89104
QY 221 -----ValLeuSe 223
Db 89103 TTGTGACCCAGGCCCTCCCTAGCCCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 89044
QY 223 rSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaIleTrpLeuSerAl 243
Db 89043 CAGTGCAGAGAACATTTGTGTGGGGCTTGGCAACAGAGAAAGCTGTGTGTGTGTGTGTGTGT 88984
QY 243 aAsnIle----- 245
Db 88983 CAACAT-CACAGGTAAGTCTCTGATGGGGAGGTGGTGTGTGTGTGTGTGTGTGTGTGTGT 88925
QY 245 ----- 245
Db 88924 ACTGCGAGAGCTCAGAGCATCTTGTGGGGGATGGGACTGTGAGCCAGTAGGAAACAGC 88865

QY 245 ----- 245

Db 88864 AAAAGGCATGGTGTAGCATGTGTAACCTGTGTGAGGCGCCCTCCGCGATTCTCTTCCCAT 88805

QY 246 -----ThralaLeulleaArgGluVallyAlaAlaValSerArgThrle 261

Db 88804 CTCCTCTGCCCCCAGCAGCAGTGTGAGGAGGAGTGAAGCAGCAGTGAGTCGCACACT 88745

QY 261 uArgAlaGlnGlyProGluPuAlaAlaArgGlyGluArgGlyCysSerArgAla 280

Db 88744 TCGAGCCAGGCTCTGTAACCTGTGTGCGGGGAGCGAGGCGTCTCTCCGCGCC 88687

RESULT 11

AC099267

LOCUS Rattus norvegicus clone CH230-2231.3, *** SEQUENCING IN PROGRESS

DEFINITION *** 11 unordered pieces.

ACCESSION AC099267.5 GI:30578709

VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus

REFERENCE 1 (bases 1 to 260033)

AUTHORS Muzny D, Marie, Metzker M, Lee, Abramson S., Adams C., Alder J., Allen C., Allen H., Albrooks S., Amin A., Anguiano D., Anyalebechi V., Aoyagi A., Ayodeji M., Baca S., Baden H., Baldwin D., Bandaranaike D., Barber M., Barnstead M., Benahmed F., Biswal K., Blair J., Blankenburg K., Blyth P., Brown M., Bryant N., Buhay C., Burch P., Burrell K., Calderon E., Cardenas V., Carter K., Cavazos I., Ceasar H., Center A., Chacko J., Chavez D., Chen G., Chen R., Chen Y., Chen Z., Chu J., Cleveland C., Cockrell R., Cox C., Coyle M., Cree A., D'Souza L., Davila M., Davis C., Davy-Carroll L., De Anda C., Dederich D., Delgado O., Denson S., Deramo C., Ding Y., Dinh H., Divya K., Draper H., Dugan-Rocha S., Dunn A., Durbin K., Duval B., Eaves K., Egan A., Escotto M., Eugene C., Evans C.A., Falls T., Fan G., Fernandez S., Finley M., Flagg N., Forbes L., Foster M., Foster P., Fraser C.M., Gabisi A., Ganta R., Garcia A., Garner T., Garza M., Gebregregis E., Geer K., Gill R., Grady M., Guerra R., Guevara W., Gunaratne P., Haaland M., Hamill C., Hamilton C., Hamilton K., Harvey Y., Havlak P., Hawes A., Henderson N., Hernandez J., Hollins R., Hines S., Hladun S.L., Hodgson A., Hognes M., Hollins B., Howells S., Hulyk S., Hume J., Idlebird D., Jackson A., Jackson L., Jacob L., Jiang H., Johnson B., Johnson R., Jolivet A., Karpathy S., Kelly S., Kelly S., Khan Z., King L., Kovar C., Kowis C., Kraft C.L., Lebow H., Levan J., Lewis L., Li Z., Liu J., Liu J., Liu W., Liu Y., London P., Longacre S., Lopez J., Lorensuhewa L., Loulsegged H., Lozano R.J., Lu X., Ma J., Maheshwari M., Mahindaratne M., Mahmoud M., Malloy K., Mangum A., Mangum B., Mapua P., Martin K., Martin R., Martinez E., Mawhinney S., McLeod M.P., McNeill T.Z., Meenen E., Milosavljevic A., Miner G., Minja E., Montemayor J., Morgan M., Morris K., Morris S., Munidasa M., Murphy M., Nair L., Nankervis C., Neal D., Newton N., Nguyen N., Norris S., Parks K., Nwakoelameh O., Okwunou G., Olarnpunsagoon A., Pal S., Parks K., Paternak S., Paul H., Perez A., Perez L., Pfanckoch C., Plopper F., Poindexter A., Popovic D., Primus E., Pu L.-L., Puazo M., Quiroz J., Rachlin E., Reeves K., Regier M.A., Reigh R., Reilly B., Reilly M., Ren Y., Reuter M., Richards S., Riggs F., Rives C., Rodkey T., Rojas A., Rose M., Rose R., Ruiz S.J., Sanders W., Savery G., Scherer S., Scott G., Shatsman S., Shen H., Shetty J., Shvartsbeyn A., Sisson I., Sitter C.D., Smajda D., Sneed A., Sodergren E., Song X.-Z., Sorelle R., Sosa J., Steimle M., Strong R., Sutton A., Svatek A., Tabor P., Taylor C., Taylor T., Thomas N., Thomas S., Tingey A., Trejos Z., Usmani K., Valas R., Vera V., Villasana D., Waldron L., Walker B., Wang J., Wang Q., Wang S., Warren J., Warren R., Wei X., White F., Williams G., Willson R., Wleczyk R., Woodson H., Worley K., Wright D., Wright R., Wu J., Yakub S., Yen J., Yoon L., Yoon V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished

2 (bases 1 to 260033)

Worley, K. C.

Direct Submission

Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 260033)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:2321447.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GJNH

Center clone name: CH230-2231.3

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 234700 bases at least Q40

Consensus quality: 239776 bases at least Q30

Consensus quality: 242937 bases at least Q20

Estimated insert size: 248755; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 226385: contig of 226385 bp in length

* 226386 226485: gap of unknown length

* 226486 232811: contig of 6326 bp in length

* 232812 232911: gap of unknown length

* 232912 244866: contig of 11955 bp in length

* 244867 244966: gap of unknown length

* 244967 248097: contig of 3131 bp in length

* 248098 248197: gap of unknown length

* 248198 249262: contig of 1065 bp in length

* 249263 250548: gap of unknown length

* 250549 250648: gap of unknown length

* 250649 252327: contig of 1678 bp in length

* 252328 253828: gap of unknown length

* 253829 253928: gap of unknown length

* 253929 255915: contig of 1987 bp in length

Db 11420 TGGGTTGTCATGACTAGCCCTTGCAGGAGACATTCGAGTCAATCTGTTTCC 11361

Qy 247 -----AlaLeuIleArgArgGluValIleAlaValSerArgThrLeuArgA 263
|||||

Db 11360 TCTGCTGGCAGCGCTGATTAGAGGGAAGTGAAGAGCGCGTGAAGTGCATGCTACGAG 11301
|||||

Qy 263 laGInGlyProGluProAlaAlaArgGlyGluArgArgGlyCysSerArgAla 280
|||||

Db 11300 CCCAGGTCCTGAGCAACTGCCCGGTGGAGCGGAGGGCTGCTCCCGAGCC 11248
|||||

RESULT 13

AC106723_0

WPCOMMENT

Sequence split into 4 fragments LOCUS AC106723 Accession AC106723

Fragment Name Begin End

AC106723_0 1 110000

AC106723_1 100001 210000

AC106723_2 200001 310000

AC106723_3 300001 398804

LOCUS AC106723 398804 bp DNA linear HTG 09-MAY-2002

DEFINITION Homo sapiens chromosome 12 clone RP11-166C15, WORKING DRAFT

ACCESSION AC106723

VERSION AC106723.4 GI:20335948

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 398804)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C., Albrooks,S.D., Amaraturung,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brivea,M., Brown,M., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.K.J., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Honsi,P., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lorado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtonson,J., Newtonson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S., Ogih,M., Okuwonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peary,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scheraz,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vaequez,L., Verd,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 398804)

AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Worley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 398804)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:18449801.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HDRB
Center clone name: RP11-166C15
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 406565 bases at least Q40
Consensus quality: 434376 bases at least Q30
Consensus quality: 451165 bases at least Q20
Estimated insert size: 160028; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1
2262: contig of 2262 bp in length
2263: gap of unknown length
2363: contig of 2105 bp in length
4468: gap of unknown length
4568: contig of 2764 bp in length
7332: gap of unknown length
7432: contig of 2140 bp in length
9571: gap of unknown length
9671: contig of 2125 bp in length
11797: gap of unknown length
11897: contig of 2486 bp in length
14383: gap of unknown length
14383: contig of 3407 bp in length
17889: gap of unknown length
17990: contig of 2245 bp in length
20234: gap of unknown length
20335: contig of 2500 bp in length
22835: gap of unknown length
22935: contig of 2186 bp in length
25121: gap of unknown length
25221: contig of 2371 bp in length
27592: gap of unknown length
27692: contig of 2205 bp in length
29897: gap of unknown length
29997: contig of 2180 bp in length
32177: gap of unknown length
32277: contig of 2801 bp in length
35078: gap of unknown length
35178: contig of 2567 bp in length
37745: gap of unknown length
37845: contig of 3459 bp in length
41303: gap of unknown length
41404: contig of 2472 bp in length

* 43876 43975: gap of unknown length
* 43976 46887: contig of 2912 bp in length
* 46888 46987: gap of unknown length
* 46989 50531: contig of 3544 bp in length
* 50532 54502: contig of 3871 bp in length
* 54503 54602: gap of unknown length
* 54603 57296: contig of 2694 bp in length
* 57297 57396: gap of unknown length
* 57397 61113: contig of 3717 bp in length
* 61114 61213: gap of unknown length
* 61214 64199: contig of 2986 bp in length
* 64200 64299: gap of unknown length
* 64300 67530: contig of 3231 bp in length
* 67531 67630: gap of unknown length
* 67631 70324: contig of 2694 bp in length
* 70325 70424: gap of unknown length
* 70425 72781: contig of 2357 bp in length
* 72782 72881: gap of unknown length
* 72882 76879: contig of 3998 bp in length
* 76880 76879: gap of unknown length
* 76880 82091: contig of 5112 bp in length
* 82092 82191: gap of unknown length
* 82192 86320: contig of 4129 bp in length
* 86321 86420: gap of unknown length
* 86421 89443: contig of 3023 bp in length
* 89444 93543: gap of unknown length
* 93544 93359: contig of 3716 bp in length
* 93360 97402: contig of 4043 bp in length
* 97403 97502: gap of unknown length
* 97503 101314: contig of 3812 bp in length
* 101315 101414: gap of unknown length
* 101415 105395: contig of 3981 bp in length
* 105396 105495: gap of unknown length
* 105496 110258: contig of 4763 bp in length
* 110259 110358: gap of unknown length
* 110359 113890: contig of 3532 bp in length
* 113891 113990: gap of unknown length
* 113991 116843: contig of 2853 bp in length
* 116844 116943: gap of unknown length
* 116944 121662: contig of 4719 bp in length
* 121663 121762: gap of unknown length
* 121763 125530: contig of 3768 bp in length
* 125531 125630: gap of unknown length
* 125631 129673: contig of 4043 bp in length
* 129674 129773: gap of unknown length
* 129774 135858: contig of 6085 bp in length
* 135859 140422: gap of unknown length
* 140423 140522: gap of unknown length
* 140523 145465: contig of 4943 bp in length
* 145466 145565: gap of unknown length
* 145566 150799: contig of 5134 bp in length
* 150799 150799: gap of unknown length
* 150800 156717: contig of 5918 bp in length
* 156718 156817: gap of unknown length
* 156818 161426: contig of 4609 bp in length
* 161427 161526: gap of unknown length
* 161527 166773: contig of 5247 bp in length
* 166774 166873: gap of unknown length
* 166874 171242: contig of 4369 bp in length
* 171243 171342: gap of unknown length
* 171343 177494: contig of 6151 bp in length
* 177494 183721: gap of unknown length
* 183721 183721: contig of 6128 bp in length

Alignment Scores:
Pred. No.: 5,7e-31 Length: 110000
Score: 566.50 Matches: 170
Percent Similarity: 34.07% Conservative: 0
Best Local Similarity: 34.07% Mismatches: 6
Query Match: 39.56% Indels: 326

DB: 2 Gaps: 5
US-10-015-388a-54 (1-280) x AC106723_0 (1-110000)
Qy 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
Db 58150 GCCTCTCCCTCCTCCCC-----CAGGCACAGCTCGCCAGGCTTTTTCAC 58197
Qy 121 AsnGlnProSerLeuArgArgThrValGluPheValAlaGluArgGlyGlySerAsn 140
Db 58198 AACAGCGCGCCCTCCTTGCAGCCAGCTAGATTCTGCGCAGAAAGATTTGATCAAC 58257
Qy 141 CysVallyHisIleLysAla----- 147
Db 58258 TGTGTCAACATATCAAGTA-AGAGTGGTTAAGGATCTGGTCTCATCGCCCTACCATT 58316
Qy 147 ----- 147
Db 58317 TTTTCCCTTTTCTCAGTTGCTTAAACTGAGAGGTGAGCCAGGGTGGTGGGCG 58376
Qy 147 ----- 147
Db 58377 TGAATGGCTGACACATTTTGAAGCAATTTCTGACCAATTTCCATAAATTTTCAGCCT 58436
Qy 148 -----Thrlu 149
Db 58437 CTTTCCGATTAACTCCCAACCATCCCTTGTCTGCTGCTGCGAGGGCTACACTG 58496
Qy 150 ValAlaSerLeuValArgGlnAlaGlnSerLeuLeuGlnGlnLeuValThrGlnGly 169
Db 58497 GTGGCAGATCTGTGCGCCAGGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGA 58556
Qy 170 GluGlnGlyGlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuCysProHis 189
Db 58557 GAGGAGGGGAGACCCAGCCAGCTGTTGAGATCTTGTGTTCCAGCTGTGCCCTAC 58616
Qy 190 GlyAlaGlnAlaLeuAlaLeuGlyArgGlu----- 199
Db 58617 GGGGCCAGGCAATTGGCCCTGGGGCGGAGTAAGCAGCGCTGGTCCATTTGATCCACTCT 58676
Qy 199 ----- 199
Db 58677 CCTCTGGCTTTCTCTGTCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 58736
Qy 199 ----- 199
Db 58737 CTCTTCAGCTCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 58796
Qy 199 ----- 199
Db 58797 GTAGGCTTCTGTGGCACAAGGCAAAAGCAACCTAGGTTTGGGAGCGTGTGTGATGCTGG 58856
Qy 199 ----- 199
Db 58857 GCTGCACTTGGGCTTGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 58916
Qy 199 ----- 199
Db 58917 GCCTCTTCCAGGTACAGCTCCAGGCTCAGGGCTTGGTGCACTCGGGGCAATTTACTT 58976
Qy 200 -----PheCy 201
Db 58977 CTGAGCCAGGCTGAATATACCCAGAGATCACTGACCCCATCTGTCTTCTTCTTCTTCT 59036
Qy 201 sGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAla-- 220
Db 59037 TCAAGGAGAGGCTTGGGGCTGTGCGGGCTGTGCGGGCTGTGCGGGCTGTGCGGGCTGTGCG 59095
Qy 220 ----- 220
Db 59096 TACGTGTGAGGGAGGCTTGCAGCTAGCAGGCCAGGCTTGTGGGGAGGTGTCAGGAGTA 59155
Qy 220 ----- 220

Db 59156 GTCTGAGGCTGCGGAGGGTGTGTGGGGCGGGTCACTGCTGAGTCTGGCATCCTTTG 59215
Qy 221 -----ValLeuSerSe 224
Db 59216 TTGCACCCAGCCCTCCCTAGCCCTGACTCTGTAGTTCTGCTGAGGTTCTGAGCAG 59275
Qy 224 rAlaGluAnIleAlaValGlyVleuAlaThrGluLysAlaCysAlaTrpLeuSerAlaAs 244
Db 59276 TCACAGAAACATTTGCTGTGGGCTTTCACAGAAAGCCTGTGCTGTGCTGTCAGCCAA 59335
Qy 244 nile----- 245
Db 59336 CAT-CACAGGTAAGTCTGGATGGGAGTGGCTGTAATCAAGTGTTTAAAAAGTGGACT 59394
Qy 245 ----- 245
Db 59395 GGCAGAGAGTCAGAGCATCTTTTGGGCGATGGGACTGAGAGCCAGTAGGAACAGCAA 59454
Qy 245 ----- 245
Db 59455 AGGCATGGTTAGCATGTGTGAACCTGTGCAGGGCCCTCCCGTGATTCCTTTCCCATTTCTC 59514
Qy 246 -----ThrAlaLeuLeuArgArgGluValLysAlaAlaValSerArgThrLeuAr 262
Db 59515 CCTTCGCCACAGCAGCAGTATCAGGAGGAGGTGAAGCAGCAGTGAGTGGCAGCAGCTTCG 59574
Qy 262 gAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyCysSerArgAla 280
Db 59575 AGCCAGGCTCTGAACCTGTGTCGCCGGGAGCGGAGGGCTGCTCCCGGCC 59629

RESULT 14
BX537330/c
LOCUS 166294 bp DNA linear HTG 06-OCT-2004
DEFINITION Danio rerio clone DKEYP-104A11, WORKING DRAFT SEQUENCE.
ACCESSION BX537330
VERSION BX537330.8 GI:53850156
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 166294)
Leongamornlert, D.
Direct Submission
Submitted (05-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Oct 6, 2004 this sequence version replaced gi:52213873.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
----- Project Information
Center project name: zkp104A11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Consensus quality: 166177 bases at least Q40
Consensus quality: 166251 bases at least Q30
Consensus quality: 166280 bases at least Q20
Insert size: 166294; sum-of-contigs
Insert size: 156143; 4.0% error; agarose-fp
Quality coverage: 7.07x in Q20 bases; sum-of-contigs Quality
coverage: 7.57x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have

* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 166294: contig of 166294 bp in length.

FEATURES

source
1..166294
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-104A11"
/clone_lib="DanioKeyPilot"
1..166294
/note="assembly_fragment:00001
clone_end:SP6
vector_side:left"

misc_feature

ORIGIN

Alignment Scores:
Pred. No.: 3.27e-16 Length: 166294
Score: 371.50 Matches: 122
Percent Similarity: 32.48% Conservative: 31
Best Local Similarity: 25.90% Mismatches: 43
Query Match: 25.94% Indels: 277
DB: 2 Gaps: 7
US-10-015-388A-54 (1-280) x BX537330 (1-166294)
Qy 49 AspAsnAlaProValValAspGlnLeuLeuThrCysCysProTyrIle----- 66
Db 10286 GACACATCCCATTAGTGGACCAACAGCTTCTACACTTGTCTCCATATTT-GGGTAA 10228
Qy 66 ----- 66
Db 10227 GAGCAAGCTCCTCTGGRAAAATGTCTTCAGAAATTATCATTTGCACAAAGAAATACAGTA 10168
Qy 67 -----GlyLeuLeuArg 70
Db 10167 CATTTCTAATGATGGTGATGATTATCTTTTACATCATTTCTTTTGAAGGGAGTTCT 10108
Qy 71 LysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLys 90
Db 10107 AAACCTTCTGCTCTTTGTGGTGGTAGCACATCCAAGAGTGGAGGCTTGATTCGCAG 10048
Qy 91 IleThrProThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu 110
Db 10047 ATCACCCCCAGCTCTGCAGAACCAAGGGTCTCTTCGACTACACGTTACAGCAGCAAACTT 9988
Qy 111 GlnAlaGln----- 113
Db 9987 CAGGT-AAACTGCCAGCAAAATGTCTTCATCTGTAGTATAATCGATAGTATGTTTTTAAT 9929
Qy 114 -----LeuAlaGlnAlaPhePhe 119
Db 9928 GAGAGTTCAATTAATGTTTTTGGATGTTTAAACAAGGTTGACCTGGACAGGAGGCTTTT 9869
Qy 120 HisAsnGlnProProSerLeuArgArgThrValGluPheValAlaGluArgIleGlySer 139
Db 9868 CACAACCAACCCCTTCTCTGAGGCGTACTGTAGAGTTTGTGTGAGAGGTCGCGCTCC 9809
Qy 140 AsnCysValLysHisIleLys----- 146
Db 9808 AACTGCGTCAAAACACATTAAAGTCAGTCTCCAAGATTTTTTGACCCCTTTTCTTTCTAGTC 9749
Qy 146 ----- 146
Db 9748 CATGCAATTAATTTTACATTTGTTTTTATCATTTTCCCTAATTTCTGTGTGGCAGA 9689
Qy 147 AlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeuVal 166
Db 9688 GCAACACTTGTGTTGGAGCTTGTGAGGGGTGGTGAAGAACTCTCAGGGATAGTTG--- 9632
Qy 167 ThrGlnGlyGluGluGlyGlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeu 186

Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml. DKEY-72L18 is from a Zebrafish BAC library VECTOR: pIndigoBAC-5.
Location/Qualifiers
1..170138
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-72L18"
/clone_lib="DanioKey"

FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 3.36e-16 Length: 170138
Score: 371.50 Matches: 122
Percent Similarity: 32.48% Conservative: 31
Best Local Similarity: 25.30% Mismatches: 43
Query Match: 25.94% Indels: 277
DB: 5 Gaps: 7
US-10-015-388A-54 (1-280) x BX569781 (1-170138)
QY 49 AspAsnAlaProValValAspGlnGlnLeuLeuThrCysCysProTyrlle----- 66
Db 112256 GACACATCCCATAGTAGTGACCAACAGCTTCTTACACTTGTCTGCCATATTTT-GGGTAA 112198
QY 66----- 66
Db 112197 GAGCAAGCTCTCTGGAAAAATGTGCTTCAGAAATTATGCTTGCACAAAGAAATACAGTA 112138
QY 67-----GlyGluLeuArg 70
Db 112137 CATTTCTAATTGATGTGATGATTATCTTTTACATCATCTTTTGAAGGGGAGTTTCGT 112078
QY 71 LysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLys 90
Db 112077 AAACATCTCTGCTGCTTTTGTGCTGTAGCACATCCAGAGTGGAGGCTTGATTCGCAAG 112018
QY 91 IleThrProThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu 110
Db 112017 ATCACCCCAACGCTCTGTCAGAACCAAGGGGTCTCTCGACTACACGTTTCACAGCAAGAACTT 111958

9631 -----GATATGAGGGCGTAAACACTGCCAAGCTAAACGACTATATCTGTCTCAGCTG 9578
QY 187 CysProHisGlyAlaGlnAlaLeu-----AlaLeu-GlyArg----- 198
Db 9577 TGTGATCGGGCATGCAAGCTCTGGAGAGAGCAACCAAGTCAATGGCTTGTCTTTTCTT 9518
QY 198----- 198
Db 9517 TTAAGTATTGGCAACACTTTATTATTTGAGCGTCCGTTTGAGTATTAGTAGACTGTCTGCT 9458
QY 198----- 198
Db 9457 TAATATCTGTTGATATCTGTTAATATCTGCTCTTCAACAGACTTTCAACTGACTATAAG 9398
QY 198----- 198
Db 9397 AAACCTTTGCAAGTACATGTCATTTTACCAACCCCTAACCTCAACCCCTAACCTA 9338
QY 198----- 198
Db 9337 ACAGCTAATTATTAATCTAATGAGAATTAGTTGGCATGATGATGATGATGATGATGAT 9278
QY 198----- 198
Db 9277 TAGCAACGGACCATCAAAATAAAGTCTGACCAAGTTTTTTGTTAAAGTAAACATGTT 9218
QY 199-----GluPheCysG1 202
Db 9217 TTCTAAACATCTTTTATCTAGTATGCTTTTGTCTCATCATGTCATGATGATGATGATGAT 9158
QY 202 nArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrProAlaAla----- 220
Db 9157 TGAGATGCTCCAGGAGCTGTCGAGTCTTCTTCTCTGGAGACCTCTCTCTCTGTCGAG 9098
QY 220----- 220
Db 9097 TAAACAGCTGTTAGTTCGTTAGTTCAGTCCATTAATACTCGCTTATTTATTTGTTAATT 9038
QY 220----- 220
Db 9037 TAAAAAACAAAGCTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8978
QY 221 -----ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaC 238
Db 8977 TGGTTAGTCTTGACCAAGCTAGAGCATCACCCTGTTGGCTACAGAAAGGCTT 8918
QY 238 YeAlaTrpLeuSerAlaAsnIleThrAla 247
Db 8917 GCAGCTGGCTGTCTCTCCAAACATCACAAAGT 8889

RESULT 15
BX569781/c
LOCUS
DEFINITION
Zebrafish DNA sequence from clone DKEY-72L18 in linkage group 17,
complete sequence.
ACCESSION
BX569781
VERSION
BX569781.7
KEYWORDS
GI:50057770
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 170138)
Direct Submission
Submitted (07-JUL-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 8, 2004 this sequence version replaced gi:46802300.
----- Genome Center
Center: Wellcome Trust Sanger Institute

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Run on: March 29, 2005, 08:32:35 ; Search time 487 Seconds
(without alignments)
3403.547 Million cell updates/sec

Title: US-10-015-388A-54

Perfect score: 1432

Sequence: 1 MCFINKULLLVGLWLFQIP.....LRAQGPFAARGRRGCSRA 280

Scoring table: BLOSUM62

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AAC58112	standard; cDNA; 3580 BP.			
DE	Human PRO1295 nucleotide sequence	SEQ ID NO:28.			
PN	WO200053750-A1.				
PD	14-SEP-2000.				
PA	(GETH) GENENTECH INC.				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
Mismatches:	0				
Indels:	0				
RESULT 2					
ID	AAF37037	standard; cDNA; 3580 BP.			
DE	Human PRO1295 (UNQ664) cDNA sequence	SEQ ID NO:53.			
PN	WO200012708-A2.				
PD	09-MAR-2000.				
PA	(GETH) GENENTECH INC.				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
Mismatches:	0				
Indels:	0				
RESULT 3					
ID	AAF54239	standard; DNA; 3580 BP.			
DE	DNA encoding protein of the invention	#16.			
PN	WO200078961-A1.				
PD	28-DEC-2000.				
PA	(GETH) GENENTECH INC.				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
Mismatches:	0				
Indels:	0				
RESULT 4					
ID	AC068276	standard; cDNA; 3580 BP.			
DE	Novel human secreted and transmembrane protein	PRO1295 cDNA.			
PN	US2003073130-A1.				
PD	17-APR-2003.				
PA	(GETH) GENENTECH INC.				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
Mismatches:	0				
Indels:	0				
RESULT 5					
ID	ACH04378	standard; cDNA; 3580 BP.			
DE	Human cDNA encoding secreted/transmembrane protein	PRO1295.			
PN	US2003044841-A1.				
PD	06-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
Mismatches:	0				
Indels:	0				

RESULT 6

ID ACD67922 standard; cDNA; 3580 BP.

DE Novel human secreted and transmembrane protein PRO1295 cDNA.

PN US2003073129-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 7

ID ADC17922 standard; cDNA; 3580 BP.

DE Human PRO polynucleotide #16.

PN US2003064925-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 8

ID ADD70568 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003099625-A1.

PD 29-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 9

ID ADD39645 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003083462-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 10

ID ADD70091 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003054406-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 11

ID ADD38212 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003096955-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 12

ID ADD39168 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003096954-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 13

ID ADD38691 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 14

ID ADD40122 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

RESULT 15

ID ADD40122 standard; cDNA; 3580 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Query Match: 100.00%

Mismatches: 0

Indels: 0

Wed Mar 30 09:32:46 2005

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ID ADE50343 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ADE19955 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ADE49866 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ADE21424 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ADF29849 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ADF55742 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ADH9246 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADE96426 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADF25737 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ADF24636 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADF29372 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ADE96903 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ADH02941 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ADH03895 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ADH03418 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ADH04372 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ADH61373 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ADL94572 standard; cDNA; 3580 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1295.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ADO05609 standard; cDNA; 4725 BP.
DE Human erythrocyte differentiation factor, Codanin-1 encoding DNA.
```

PN WO2004035535-A2.
 PD 29-APR-2004.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 Best Local Similarity: 100.00% Mismatches: 0
 Indels: 0
 Query Match: 100.00%
 RESULT 34
 ID AB211689 standard; cDNA; 1833 BP.
 DE Human polynucleotide SEQ ID NO 571.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 100.00% Mismatches: 0
 Indels: 0
 Query Match: 88.34%
 RESULT 35
 ID ADM44207 standard; cDNA; 2240 BP.
 DE Novel human arginine-rich protein cDNA #571.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Best Local Similarity: 100.00% Mismatches: 0
 Indels: 0
 Query Match: 88.34%
 RESULT 36
 ID AAH99000 standard; cDNA; 403 BP.
 DE Human EST-derived coding sequence SEQ ID NO: 857.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 98.45% Mismatches: 2
 Indels: 0
 Query Match: 46.58%
 RESULT 37
 ID ABL19883 standard; DNA; 3904 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11122.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 22.94% Mismatches: 87
 Indels: 58
 Query Match: 8.94%
 RESULT 38
 ID ABL19882 standard; DNA; 7602 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11119.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 22.94% Mismatches: 87
 Indels: 58
 Query Match: 8.94%
 RESULT 39
 ID ABL03786 standard; cDNA; 18737 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5840.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 22.94% Mismatches: 87
 Indels: 58
 Query Match: 8.94%
 RESULT 40
 ID AD087067 standard; cDNA; 2340 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3943.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 24.04% Mismatches: 119
 Indels: 81
 Query Match: 7.86%
 RESULT 41
 ID ABK42709 standard; DNA; 17761 BP.
 DE Genomic sequence #608 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 27.66% Mismatches: 97

Query Match: 7.82% Indels: 88
 RESULT 42
 ID AAK79415 standard; DNA; 17761 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 27.66% Mismatches: 97
 Indels: 88
 Query Match: 7.82%
 RESULT 43
 ID ADS60865 standard; DNA; 17761 BP.
 DE Connective tissue related genomic DNA #608.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 27.66% Mismatches: 97
 Indels: 88
 Query Match: 7.82%
 RESULT 44
 ID ACA38667 standard; DNA; 1104 BP.
 DE Prokaryotic essential gene #20324.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 25.42% Mismatches: 89
 Indels: 60
 Query Match: 7.79%
 RESULT 45
 ID AB271082 standard; DNA; 1104 BP.
 DE Mycobacterium tuberculosis protein encoding DNA SEQ ID NO:42.
 PN WO2003000721-A2.
 PD 03-JAN-2003.
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 Best Local Similarity: 25.42% Mismatches: 89
 Indels: 60
 Query Match: 7.79%
 RESULT 46
 ID ACA40617 standard; DNA; 1107 BP.
 DE Prokaryotic essential gene #22274.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 25.42% Mismatches: 89
 Indels: 60
 Query Match: 7.79%
 RESULT 47
 Best Local Similarity: 25.42% Mismatches: 89
 Indels: 60
 Query Match: 7.79%
 RESULT 48
 Best Local Similarity: 25.42% Mismatches: 89
 Indels: 60
 Query Match: 7.79%
 RESULT 49
 Best Local Similarity: 27.36% Mismatches: 98
 Indels: 34
 Query Match: 7.72%
 RESULT 50
 Best Local Similarity: 27.36% Mismatches: 98
 Indels: 34
 Query Match: 7.72%
 RESULT 51
 ID AAT61835 standard; DNA; 1712 BP.
 DE Pseudomonas aeruginosa exoenzyme S gene.
 PN US5599665-A.
 PD 04-FEB-1997.
 PA (MCWR-) MCW RES FOUND INC.
 Best Local Similarity: 23.36% Mismatches: 128
 Indels: 123
 Query Match: 7.61%
 RESULT 52
 ID ABL63712 standard; DNA; 1457 BP.
 DE Breast cancer related gene sequence SEQ ID NO:2049.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Best Local Similarity: 26.43% Mismatches: 104
 Indels: 77
 Query Match: 7.58%
 RESULT 53
 ID ADF65592 standard; DNA; 1457 BP.
 DE Human mRNA for B-HLH binding protein DNA.
 PN WO2003072827-A1.

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PD 04-SEP-2003.	PA (FIVE-) FIVE PRIME THERAPEUTICS INC.	
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	Best Local Similarity: 22.01%	Mismatches: 124
Best Local Similarity: 26.43%	Indels: 123	
Query Match: 7.58%		
RESULT 54		
ID AAS94864 standard; DNA; 1678 BP.		
DE Human DNA sequence #119 expressed during foam cell differentiation.		
PD WO200177389-A2.		
PD 18-OCT-2001.		
PA (INCY-) INCYTE GENOMICS INC.		
Best Local Similarity: 28.42%	Mismatches: 90	
Query Match: 7.51%	Indels: 86	
RESULT 55		
ID ADP65052 standard; DNA; 1396 BP.		
DE Human twist homologue (acrocephalosyndactyly 3) DNA sequence.		
PD WO2003072827-A1.		
PD 04-SEP-2003.		
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.		
Best Local Similarity: 28.32%	Mismatches: 95	
Query Match: 7.37%	Indels: 78	
RESULT 56		
ID ADQ22344 standard; DNA; 1664 BP.		
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5164.		
PD WO2004048938-A2.		
PD 10-JUN-2004.		
PA (PROT-) PROTEIN DESIGN LABS INC.		
Best Local Similarity: 28.32%	Mismatches: 95	
Query Match: 7.37%	Indels: 78	
RESULT 57		
ID AAS67977 standard; cDNA; 1980 BP.		
DE DNA encoding novel human diagnostic protein #3781.		
PD WO200175067-A2.		
PD 11-OCT-2001.		
PA (HYSE-) HYSEQ INC.		
Best Local Similarity: 26.99%	Mismatches: 108	
Query Match: 7.37%	Indels: 96	
RESULT 58		
ID ABD02086 standard; DNA; 1350 BP.		
DE Pseudomonas aeruginosa polynucleotide #690.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 59		
ID ABD02116 standard; DNA; 3054 BP.		
DE Pseudomonas aeruginosa polynucleotide #720.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 60		
ID ABD02056 standard; DNA; 6885 BP.		
DE Pseudomonas aeruginosa polynucleotide #660.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 25.23%	Mismatches: 98	
Query Match: 7.30%	Indels: 127	
RESULT 61		
ID ABD03071 standard; DNA; 1131 BP.		
DE Pseudomonas aeruginosa polynucleotide #1675.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 22.45%	Mismatches: 110	
Query Match: 7.23%	Indels: 121	
RESULT 62		
ID ADN98622 standard; cDNA; 3180 BP.		
DE Novel human cDNA sequence #222.		
PD WO2004038003-A2.		
PD 06-MAY-2004.		
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 63		
ID ADO00191 standard; cDNA; 3180 BP.		
DE Novel human cDNA sequence #1006.		
PD WO2004038003-A2.		
PD 06-MAY-2004.		
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 64		
ID ADC30771 standard; cDNA; 3438 BP.		
DE Human novel cDNA sequence, SEQ ID NO:853.		
PD WO2003029271-A2.		
PD 10-APR-2003.		
PA (HYSE-) HYSEQ INC.		
Best Local Similarity: 22.01%	Mismatches: 124	
Query Match: 7.23%	Indels: 123	
RESULT 65		
ID ABD09457 standard; DNA; 1236 BP.		
DE Pseudomonas aeruginosa polynucleotide #8061.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.19%	Indels: 101	
RESULT 66		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 67		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 68		
ID ABD09598 standard; DNA; 2556 BP.		
DE Pseudomonas aeruginosa polynucleotide #8202.		
PD US6551795-B1.		
PD 22-APR-2003.		
PA (GENO-) GENOME THERAPEUTICS CORP.		
Best Local Similarity: 23.12%	Mismatches: 114	
Query Match: 7.16%	Indels: 98	
RESULT 69		
ID ADS63367 standard; cDNA; 1101 BP.		
DE Bacterial polynucleotide #15354.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 26.70%	Mismatches: 82	
Query Match: 7.12%	Indels: 45	
RESULT 70		
ID ADS63734 standard; cDNA; 1104 BP.		
DE Bacterial polynucleotide #15721.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Best Local Similarity: 26.70%	Mismatches: 82	
Query Match: 7.12%	Indels: 45	
RESULT 71		
ID ADS64120 standard; cDNA; 1374 BP.		
DE Bacterial polynucleotide #16107.		
PD US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		

PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 26.70% Mismatches: 82
 Query Match: 7.12% Indels: 45
 RESULT 72
 ID ADL46198 standard; DNA; 903 BP.
 DE Ashbya gossypii GTP cyclohydrolase II-encoding DNA, SEQ ID NO:1.
 PN WO2004022776-A2.
 PD 18-MAR-2004.
 PA (BADI) BASF AG.
 Best Local Similarity: 24.36% Mismatches: 100
 Query Match: 7.09% Indels: 51
 RESULT 73
 ID ADK6552 standard; DNA; 1052 BP.
 DE A gossypii riboflavin synthesis rib1 coding sequence.
 PN DE10159396-A1.
 PD 12-JUN-2003.
 PA (BADI) BASF AG.
 Best Local Similarity: 24.36% Mismatches: 100
 Query Match: 7.09% Indels: 51
 RESULT 74
 ID AAT03514 standard; cDNA to mRNA; 1329 BP.
 DE Ashbya gossypii Rib 1 gene (GTP-cyclohydrolase II).
 PN DE4420785-A1.
 PD 05-OCT-1995.
 PA (BADI) BASF AG.
 Best Local Similarity: 24.36% Mismatches: 100
 Query Match: 7.09% Indels: 51
 RESULT 75
 ID ADL46200 standard; DNA; 2528 BP.
 DE Ashbya gossypii GTP cyclohydrolase II gene (rib1), SEQ ID NO:3.
 PN WO2004022776-A2.
 PD 18-MAR-2004.
 PA (BADI) BASF AG.
 Best Local Similarity: 24.36% Mismatches: 100
 Query Match: 7.09% Indels: 51
 RESULT 76
 ID ADI27110 standard; DNA; 3400 BP.
 DE Human LRP binding family protein DNA #4.
 PN WO2003106657-A2.
 PD 24-DEC-2003.
 PA (STOW-) STOWERS INST MEDICAL RES.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 77
 ID AAA94049 standard; DNA; 5680 BP.
 DE Human DAN/Cerberus-related protein 6 (hDCR6) gene.
 PN WO200055193-A2.
 PD 21-SEP-2000.
 PA (REG-) REGENERON PHARM INC.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 78
 ID AAD27577 standard; DNA; 7099 BP.
 DE Human osteolevin gene.
 PN WO200198491-A2.
 PD 27-DEC-2001.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (UVIN-) UNIV INSTELLING ANTWERPEN UIA.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 79
 ID AAA29064 standard; DNA; 9301 BP.
 DE Human TGF-beta binding protein (BEER) genomic DNA.
 PN WO200032773-A1.
 PD 08-JUN-2000.
 PA (DARW-) DARWIN DISCOVERY LTD.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 80
 ID ACF79823 standard; DNA; 21501 BP.
 DE Human SOST gene encoding sclerostin.
 PN WO2003073991-A2.

PD 12-SEP-2003.
 PA (CELL-) CELLTech R & D INC.
 PA (SUTH/) KUNG SUTHERLAND M S.
 PA (GEOG/) GEOGHEGAN J C.
 PA (YUCC/) YU C.
 PA (LATH/) LATHAM J.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 81
 ID ADF11646 standard; DNA; 94752 BP.
 DE Human chromosome 17 clone HPRC905N1 nucleic acid.
 PN WO2003087763-A2.
 PD 23-OCT-2003.
 PA (CELL-) CELLTech R & D INC.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 82
 ID ADF11613 standard; DNA; 130320 BP.
 DE Human sclerostin gene region.
 PN WO2003087763-A2.
 PD 23-OCT-2003.
 PA (CELL-) CELLTech R & D INC.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 Best Local Similarity: 25.65% Mismatches: 85
 Query Match: 7.09% Indels: 62
 RESULT 83
 ID ADL45243 standard; DNA; 1810 BP.
 DE Human ovarian cancer DNA marker #19133.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Best Local Similarity: 27.48% Mismatches: 80
 Query Match: 7.05% Indels: 64
 RESULT 84
 ID ADQ38777 standard; DNA; 2064 BP.
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 440.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 7.05% Indels: 65
 RESULT 85
 ID ADQ38776 standard; DNA; 2106 BP.
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 439.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 7.05% Indels: 65
 RESULT 86
 ID ADP65591 standard; DNA; 797 BP.
 DE Human basic helix-loop-helix binding protein (TWIST) gene, DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Best Local Similarity: 31.02% Mismatches: 79
 Query Match: 7.02% Indels: 29
 RESULT 87
 ID ABT06509 standard; DNA; 1800 BP.
 DE Twist gene promoter sequence.
 PN WO200259347-A2.
 PD 01-AUG-2002.
 PA (UVJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Best Local Similarity: 31.63% Mismatches: 79
 Query Match: 7.02% Indels: 33
 RESULT 88
 ID ADC07759 standard; DNA; 2143 BP.
 DE Rice DNA sequence Seq ID25 related to grain filling.
 PN WO2003000905-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 22.77% Mismatches: 85

Query Match:	7.02%	Indels:	135
RESULT 89			
ID ACN38185 standard; cDNA; 2213 BP.			
DE Tumour-associated antigenic target (TAT) cDNA DNA324544, SEQ ID NO:1540.			
PN WO2004030615-A2.			
PD 15-APR-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 23.55%		Mismatches:	99
Query Match:	7.02%	Indels:	98
RESULT 90			
ID ADE54144 standard; cDNA; 5408 BP.			
DE Human prostate cancer cDNA #491.			
PN US2003190640-A1.			
PD 09-OCT-2003.			
PA (FARI/) FARIS M.			
PA (PEAR/) PEARSON C I.			
Best Local Similarity: 24.56%		Mismatches:	103
Query Match:	7.02%	Indels:	115
RESULT 91			
ID ADO26000 standard; DNA; 2285 BP.			
DE Corn chalcone synthase (CHS) polynucleotide seqid 38.			
PN WO2004046336-A2.			
PD 03-JUN-2004.			
PA (MONS) MONSANTO TECHNOLOGY LLC.			
Best Local Similarity: 25.19%		Mismatches:	81
Query Match:	6.98%	Indels:	84
RESULT 92			
ID AAA08834 standard; DNA; 5040 BP.			
DE Murine APC-2 gene.			
PN WO200018913-A1.			
PD 06-APR-2000.			
PA (UYUT-) RIJKSUNIV UTRECHT.			
Best Local Similarity: 24.51%		Mismatches:	120
Query Match:	6.98%	Indels:	115
RESULT 93			
ID AAH18204 standard; cDNA; 6193 BP.			
DE Human cDNA sequence SEQ ID NO:18123.			
PN EP1074617-A2.			
PD 07-FEB-2001.			
PA (HELI-) HELIX RES INST.			
Best Local Similarity: 25.41%		Mismatches:	84
Query Match:	6.98%	Indels:	66
RESULT 94			
ID ADO07830 standard; cDNA; 6825 BP.			
DE Mouse polynucleotide #43.			
PN US2004071700-A1.			
PD 15-APR-2004.			
PA (LIFE-) LIFE SCI DEV CORP.			
Best Local Similarity: 24.51%		Mismatches:	120
Query Match:	6.98%	Indels:	115
RESULT 95			
ID ADM83716 standard; DNA; 1800 BP.			
DE Human twist promoter.			
PN US2003138783-A1.			
PD 24-JUL-2003.			
PA (SUKU/) SUKUMAR S.			
PA (EVRO/) EVRON E.			
PA (DOOL/) DOOLEY W C.			
PA (SACC/) SACCHI N.			
PA (DAVI/) DAVIDSON N.			
PA (FACK/) FACKLER M J.			
Best Local Similarity: 31.63%		Mismatches:	79
Query Match:	6.95%	Indels:	33
RESULT 96			
ID ADG91050 standard; DNA; 2120 BP.			
DE Hepatic specific nucleic acid encoding sequence #239.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 97			
ID ADG91053 standard; DNA; 2280 BP.			
DE Hepatic specific nucleic acid encoding sequence #242.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 98			
ID ADG91049 standard; DNA; 2457 BP.			
DE Hepatic specific nucleic acid encoding sequence #238.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 99			
ID ADG91048 standard; DNA; 2489 BP.			
DE Hepatic specific nucleic acid encoding sequence #237.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 100			
ID ADG91047 standard; DNA; 2520 BP.			
DE Hepatic specific nucleic acid encoding sequence #236.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 101			
ID ADG91054 standard; DNA; 2641 BP.			
DE Hepatic specific nucleic acid encoding sequence #243.			
PN WO2003066877-A2.			
PD 14-AUG-2003.			
PA (DIAD-) DIADEXUS INC.			
Best Local Similarity: 24.17%		Mismatches:	111
Query Match:	6.95%	Indels:	53
RESULT 102			
ID ADQ17684 standard; DNA; 2870 BP.			
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 501.			
PN WO2004048938-A2.			
PD 10-JUN-2004.			
PA (PROT-) PROTEIN DESIGN LABS INC.			
Best Local Similarity: 31.63%		Mismatches:	79
Query Match:	6.95%	Indels:	33
RESULT 103			
ID ABZ11230 standard; cDNA; 7057 BP.			
DE Human polynucleotide SEQ ID NO 112.			
PN WO200270539-A2.			
PD 12-SEP-2002.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 23.93%		Mismatches:	107
Query Match:	6.95%	Indels:	95
RESULT 104			
ID ADM43748 standard; cDNA; 7057 BP.			
DE Novel human arginine-rich protein cDNA #112.			
PN US2004053250-A1.			
PD 18-MAR-2004.			
PA (TANG/) TANG Y T.			
PA (XUEA/) XUE A.			
PA (DRMA/) DRMANAC R T.			
Best Local Similarity: 23.93%		Mismatches:	107
Query Match:	6.95%	Indels:	95
RESULT 105			
ID ACN45066 standard; DNA; 27189 BP.			
DE Human genomic sequence HCG30694.			
PN WO2003073826-A2.			
PD 12-SEP-2003.			
PA (SAGR-) SAGRES DISCOVERY.			
Best Local Similarity: 24.16%		Mismatches:	117
Query Match:	6.95%	Indels:	89
RESULT 106			

ID AAQ04485 standard; DNA; 1236 BP.
 DE Plasmid pSEUKS1id encoding UK-S1.
 PN EP370205-A.
 PD 30-MAY-1990.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 27.10% Mismatches: 90
 Query Match: 6.91% Indels: 44
 RESULT 107

ID ABD07632 standard; DNA; 1419 BP.
 DE Pseudomonas aeruginosa polynucleotide #6236.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.10% Mismatches: 129
 Query Match: 6.91% Indels: 123
 RESULT 108

ID ABD07463 standard; DNA; 1476 BP.
 DE Pseudomonas aeruginosa polynucleotide #6067.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.10% Mismatches: 129
 Query Match: 6.91% Indels: 123
 RESULT 109

ID AAC39340 standard; DNA; 1601 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24273.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 24.51% Mismatches: 74
 Query Match: 6.91% Indels: 88
 RESULT 110

ID ABD10451 standard; DNA; 1893 BP.
 DE Pseudomonas aeruginosa polynucleotide #9055.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.36% Mismatches: 121
 Query Match: 6.88% Indels: 136
 RESULT 111

ID ABL54590 standard; cDNA; 2242 BP.
 DE Human CREB conjugated protein 30.8 encoding cDNA SEQ ID NO 1.
 PN CN1326942-A.
 PD 19-DEC-2001.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Best Local Similarity: 21.63% Mismatches: 99
 Query Match: 6.88% Indels: 115
 RESULT 112

ID ADQ83748 standard; cDNA; 2555 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #562.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 21.63% Mismatches: 99
 Query Match: 6.88% Indels: 115
 RESULT 113

ID ABL12402 standard; cDNA; 90104 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31688.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 22.49% Mismatches: 68
 Query Match: 6.88% Indels: 69
 RESULT 114

ID ABQ81844 standard; DNA; 349980 BP.
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1100.
 PN EP1227152-A1.
 PD 31-JUL-2002.
 PA (NEST) SOC PROD NESTLE SA.
 Best Local Similarity: 27.83% Mismatches: 71
 Query Match: 6.88% Indels: 58
 RESULT 115

ID ABK34884 standard; cDNA; 1204 BP.
 DE Human cDNA encoding secreted protein #22.
 PN WO200177288-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Best Local Similarity: 28.91% Mismatches: 101
 Query Match: 6.84% Indels: 52
 RESULT 116

ID AAC87527 standard; DNA; 1493 BP.
 DE Human RAP (receptor associated protein) cDNA.
 PN WO200071714-A2.
 PD 30-NOV-2000.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 117

ID AAL48893 standard; cDNA; 1493 BP.
 DE Human receptor-associated protein coding sequence.
 PN WO200260951-A2.
 PD 08-AUG-2002.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 118

ID ABR84062 standard; cDNA; 1493 BP.
 DE Human cDNA differentially expressed in granulocytic cells #633.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 119

ID ADJ74840 standard; DNA; 1493 BP.
 DE Marker gene SEQ ID NO:92.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 120

ID ADR24896 standard; DNA; 1493 BP.
 DE Breast cancer prognosis marker #757.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 121

ID ADP23134 standard; cDNA; 1493 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 122

ID ADA71052 standard; DNA; 2934 BP.
 DE Rice gene, SEQ ID 4375.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 26.35% Mismatches: 110
 Query Match: 6.84% Indels: 66
 RESULT 123

ID ADP23134 standard; cDNA; 1493 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 124

ID ADP23134 standard; cDNA; 1493 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:228.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 28.27% Mismatches: 83
 Query Match: 6.84% Indels: 65
 RESULT 125

ID ACH89545 standard; DNA; 609 BP.
 DE Human genome derived single exon probe #22740.
 DE Human genome derived single exon probe #22740.

PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Best Local Similarity: 32.70%
 Query Match: 6.81%
 Mismatches: 67
 Indels: 23
 RESULT 126
 ID AAZ87298 standard; DNA; 11220 BP.
 DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.
 PN WO20000620-A2.
 PD 06-JAN-2000.
 PA (MINU) UNIV MINNESOTA.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 127
 ID ADJ91917 standard; DNA; 11220 BP.
 DE Streptomyces macrolide biosynthetic protein (PikAII) coding sequence.
 PN US2003194784-A1.
 PD 16-OCT-2003.
 PA (SHER/) SHERMAN D H.
 PA (LIUH/) LIU H.
 PA (XUEY/) XUE Y.
 PA (ZHAO/) ZHAO L.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 128
 ID AAZ87318 standard; DNA; 36778 BP.
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster.
 PN WO20000620-A2.
 PD 06-JAN-2000.
 PA (MINU) UNIV MINNESOTA.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 129
 ID ADJ91933 standard; DNA; 36778 BP.
 DE Streptomyces venezuelae pik gene cluster coding sequence.
 PN US2003194784-A1.
 PD 16-OCT-2003.
 PA (SHER/) SHERMAN D H.
 PA (LIUH/) LIU H.
 PA (XUEY/) XUE Y.
 PA (ZHAO/) ZHAO L.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 130
 ID AAZ87285 standard; DNA; 37948 BP.
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.
 PN WO20000620-A2.
 PD 06-JAN-2000.
 PA (MINU) UNIV MINNESOTA.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 131
 ID AAZ75633 standard; DNA; 38506 BP.
 DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.
 PN US6117659-A.
 PD 12-SEP-2000.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 132
 ID AAZ56001 standard; DNA; 38506 BP.
 DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.
 PN WO9861599-A2.
 PD 02-DEC-1999.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 133
 ID ADA09418 standard; DNA; 38506 BP.
 DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.
 PN US6509455-B1.

PD 21-JAN-2003.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 134
 ID ADH53462 standard; DNA; 38506 BP.
 DE S. venezuelae pKOS023-27 cosmid DNA.
 PN US2003162262-A1.
 PD 28-AUG-2003.
 PA (ASHL/) ASHLEY G.
 PA (BETL/) BETLACH M C.
 PA (BETL/) BETLACH M.
 PA (MCDA/) MCDANIEL R.
 PA (TANG/) TANG L.
 Best Local Similarity: 25.17%
 Query Match: 6.81%
 Mismatches: 91
 Indels: 101
 RESULT 135
 ID ABS56090 standard; DNA; 38506 BP.
 DE S. venezuelae DNA inserted into cosmid pKOS023-27.
 PN WO200297062-A2.
 PD 05-DEC-2002.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 23.71%
 Query Match: 6.81%
 Mismatches: 101
 Indels: 87
 RESULT 136
 ID ABD05377 standard; DNA; 858 BP.
 DE Pseudomonas aeruginosa polynucleotide #3981.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.85%
 Query Match: 6.77%
 Mismatches: 91
 Indels: 50
 RESULT 137
 ID ACA26285 standard; DNA; 1347 BP.
 DE Prokaryotic essential gene #7942.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 25.38%
 Query Match: 6.77%
 Mismatches: 106
 Indels: 55
 RESULT 138
 ID ABD05446 standard; DNA; 1482 BP.
 DE Pseudomonas aeruginosa polynucleotide #4050.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.85%
 Query Match: 6.77%
 Mismatches: 91
 Indels: 50
 RESULT 139
 ID AAZ33614 standard; cDNA; 1499 BP.
 DE Human breast tumour-associated EST 4.
 PN DE19813839-A1.
 PD 23-SEP-1999.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Best Local Similarity: 28.21%
 Query Match: 6.77%
 Mismatches: 87
 Indels: 59
 RESULT 140
 ID ABD05293 standard; DNA; 1605 BP.
 DE Pseudomonas aeruginosa polynucleotide #3897.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.85%
 Query Match: 6.77%
 Mismatches: 91
 Indels: 50
 RESULT 141
 ID ADD25545 standard; DNA; 3120 BP.
 DE Binding domain-immunoglobulin fusion protein-associated DNA #57.
 PN US2003118592-A1.
 PD 26-JUN-2003.
 PA (GENE-) GENE-CRAFT INC.
 Best Local Similarity: 27.19%
 Query Match: 6.77%
 Mismatches: 89
 Indels: 49
 RESULT 142

ID ADK61414 standard; DNA; 3120 BP.
 DE Ovarian cancer-related DNA #569 with altered ovarian cancer expression.
 PN WO2003068054-A2.
 PD 21-AUG-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 143
 ID ADP09696 standard; cDNA; 3120 BP.
 DE Human IL17R cDNA.
 PN JP2004135545-A.
 PD 13-MAY-2004.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 144
 ID ADP13348 standard; DNA; 3120 BP.
 DE Renal cell carcinoma differentially expressed gene #84.
 PN WO2004048933-A2.
 PD 10-JUN-2004.
 PA (AMHP) WYETH.
 PA (TWIN) TWINE N C.
 PA (BUREC) BURCZYNSKI M E.
 PA (TREP) TREPICCHIO W L.
 PA (DORN) DORNER A.
 PA (STOV) STOVER J A.
 PA (SLON) SLONI D K.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 145
 ID AAT33801 standard; cDNA to mRNA; 3223 BP.
 DE Human interleukin-17 receptor cDNA.
 PN WO9629408-A1.
 PD 26-SEP-1996.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 146
 ID AAV27592 standard; cDNA to mRNA; 3223 BP.
 DE Human interleukin-17 receptor cDNA.
 PN WO9823284-A1.
 PD 04-JUN-1998.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 147
 ID AAX01922 standard; cDNA to mRNA; 3223 BP.
 DE Human IL-17R cDNA.
 PN US5869286-A.
 PD 09-FEB-1999.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 148
 ID AAA51988 standard; cDNA to mRNA; 3223 BP.
 DE Human interleukin-17 receptor coding sequence.
 PN US6100235-A.
 PD 08-AUG-2000.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 149
 ID AA52146 standard; cDNA to mRNA; 3223 BP.
 DE Human interleukin-17 receptor coding sequence.
 PN US6096305-A.
 PD 01-AUG-2000.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 150
 ID AAA59871 standard; cDNA; 3223 BP.
 DE Human interleukin-17 (IL-17) receptor nucleotide sequence.

PN US6072033-A.
 PD 06-JUN-2000.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 151
 ID AAA61240 standard; cDNA; 3223 BP.
 DE Human IL-17R cDNA.
 PN US6072037-A.
 PD 06-JUN-2000.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 152
 ID AAF57188 standard; cDNA; 3223 BP.
 DE Human IL-17R (hCTLA-8 receptor) polypeptide encoding cDNA.
 PN US6197525-B1.
 PD 06-MAR-2001.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 153
 ID AD02815 standard; DNA; 3223 BP.
 DE Human Interleukin-17 receptor (IL-17R) or CTLA-8 receptor DNA.
 PN US6191104-B1.
 PD 20-FEB-2001.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 154
 ID ADJ88264 standard; cDNA to mRNA; 3223 BP.
 DE Human IL-17 receptor nucleic acid sequence.
 PN US6680057-B1.
 PD 20-JAN-2004.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 155
 ID ADL24268 standard; DNA; 3223 BP.
 DE Human IL-17 receptor coding sequence.
 PN WO2004019866-A2.
 PD 11-MAR-2004.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 156
 ID ADQ91251 standard; cDNA; 3223 BP.
 DE Human cDNA encoding the interleukin-17 receptor, IL-17R.
 PN US2004120898-A1.
 PD 24-JUN-2004.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 157
 ID ADR01307 standard; cDNA to mRNA; 3223 BP.
 DE Human interleukin-17 receptor, IL-17R, cDNA to mRNA.
 PN US2004120899-A1.
 PD 24-JUN-2004.
 PA (IMMV) IMMUNEX CORP.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 158
 ID ADG32974 standard; DNA; 3429 BP.
 DE Human DNA differentially expressed in patients with SLE SeqID298.
 PN WO2003090694-A2.
 PD 06-NOV-2003.
 PA (EXPR) EXPRESSION DIAGNOSTICS INC.
 Best Local Similarity: 27.19% Mismatches: 89
 Query Match: 6.77% Indels: 49
 RESULT 159
 ID ABT08140 standard; DNA; 7438 BP.
 DE Recombinase domain-containing fusion protein-related vector 1.
 PN WO200238613-A2.

Query Match:	6.77%	Indels:	104
RESULT 171			
ID ADA49192 standard; DNA; 969 BP.			
DE Maize gene conferring disease resistance in plants.			
PN WO2003000906-A2.			
PD 03-JAN-2003.			
PA (SYGN) SYNGENTA PARTICIPATIONS AG.			
Best Local Similarity: 26.58%		Mismatches:	70
Query Match: 6.74%		Indels:	74
RESULT 172			
ID ADJ44454 standard; cDNA; 969 BP.			
DE Plant cDNA #5454.			
PN US2004016025-A1.			
PD 22-JAN-2004.			
PA (BUDW/) BUDWORTH P.			
PA (MOUG/) MOUGHAMER T.			
PA (BRIG/) BRIGGS S P.			
PA (COOP/) COOPER B.			
PA (GLAZ/) GLAZEBROOK J.			
PA (GOFF/) GOFF S A.			
PA (KATA/) KATAGIRI F.			
PA (KREP/) KREPS J.			
PA (PROV/) PROVANT N.			
PA (RICK/) RICKE D.			
PA (ZHUT/) ZHU T.			
Best Local Similarity: 26.58%		Mismatches:	70
Query Match: 6.74%		Indels:	74
RESULT 173			
ID ABD07251 standard; DNA; 1311 BP.			
DE Pseudomonas aeruginosa polynucleotide #5855.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 21.71%		Mismatches:	83
Query Match: 6.74%		Indels:	91
RESULT 174			
ID ADA53443 standard; cDNA; 3278 BP.			
DE Human coding sequence, SEQ ID 1011.			
PN EP1293569-A2.			
PD 19-MAR-2003.			
PA (HELI-) HELIX RES INST.			
PA (KEAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 21.20%		Mismatches:	111
Query Match: 6.74%		Indels:	101
RESULT 175			
ID ADG30703 standard; DNA; 3291 BP.			
DE Xanthomonas axonopodis pv citri plant pathology-related XACb0015 DNA.			
PN WO2003089647-A1.			
PD 30-OCT-2003.			
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.			
Best Local Similarity: 23.61%		Mismatches:	121
Query Match: 6.74%		Indels:	61
RESULT 176			
ID AAA83998 standard; DNA; 999 BP.			
DE ORF2-16 encoding Pseudomonas bto gene cluster regulator, SEQ ID NO:18.			
PN JP2000093180-A.			
PD 04-APR-2000.			
PA (TOFU) TONEN CORP.			
Best Local Similarity: 26.64%		Mismatches:	68
Query Match: 6.70%		Indels:	68
RESULT 177			
ID ACH87698 standard; DNA; 1433 BP.			
DE Human genome derived single exon probe #20893.			
PN US2003194704-A1.			
PD 16-OCT-2003.			
PA (PENN/) PENN S G.			
PA (RANK/) RANK D R.			
PA (HANZ/) HANZEL D K.			
Best Local Similarity: 28.91%		Mismatches:	101
Query Match: 6.70%		Indels:	52
RESULT 178			
ID ACH87093 standard; DNA; 1458 BP.			
DE Human genome derived single exon probe #20888.			

PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN//) PENN S G.
 PA (RANK//) RANK D R.
 PA (HANZ//) HANZEL D K.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 179
 ID AAL61513 standard; DNA; 1813 BP.
 DE Human inhibitor-kappa B-R DNA #3.
 PN WO2003042360-A2.
 PD 22-MAY-2003.
 PA (ISIS-) ISIS PHARM INC.
 Best Local Similarity: 25.31%
 Query Match: 6.70%
 Mismatches: 89
 Indels: 67
 RESULT 180
 ID ADI32145 standard; cDNA; 1813 BP.
 DE Human cDNA #1471.
 PN US6607879-B1.
 PD 19-AUG-2003.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 25.31%
 Query Match: 6.70%
 Mismatches: 89
 Indels: 67
 RESULT 181
 ID ACA31501 standard; DNA; 1831 BP.
 DE Prokaryotic essential gene #13158.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 29.22%
 Query Match: 6.70%
 Mismatches: 82
 Indels: 49
 RESULT 182
 ID ADN99012 standard; cDNA; 2205 BP.
 DE Novel human cDNA sequence #612.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 183
 ID ADO00581 standard; cDNA; 2205 BP.
 DE Novel human cDNA sequence #1396.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 184
 ID ADE54125 standard; cDNA; 2661 BP.
 DE Human prostate cancer cDNA #472.
 PN US2003190640-A1.
 PD 09-OCT-2003.
 PA (FARI//) FARIS M.
 PA (PEAR//) PEARSON C I.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 185
 ID ABL67218 standard; DNA; 2678 BP.
 DE Thyroid cancer related gene sequence SEQ ID NO:5555.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 186
 ID ACA56631 standard; cDNA; 2678 BP.
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1229.
 PN US6500938-B1.
 PD 31-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 187

ID ADI56427 standard; DNA; 2678 BP.
 DE Human polynucleotide probe #1229.
 PN US2004010136-A1.
 PD 15-JAN-2004.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 188
 ID ADQ85883 standard; cDNA; 2683 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2755.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD//) WU T D.
 PA (ZHOU//) ZHOU Y.
 Best Local Similarity: 28.91%
 Query Match: 6.70%
 Mismatches: 101
 Indels: 52
 RESULT 189
 ID ABL07083 standard; cDNA; 4515 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15731.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 24.48%
 Query Match: 6.70%
 Mismatches: 120
 Indels: 67
 RESULT 190
 ID ADQ89769 standard; DNA; 4515 BP.
 DE Antagonist of cell cycle progression nucleotide sequence #100.
 PN WO2004063362-A2.
 PD 29-JUL-2004.
 PA (CYCL-) CYCLACEL LTD.
 Best Local Similarity: 24.48%
 Query Match: 6.70%
 Mismatches: 120
 Indels: 67
 RESULT 191
 ID AAA38389 standard; DNA; 11279 BP.
 DE Pseudomonas sp. WF505 bto gene cluster, SEQ ID NO:1.
 PN JP2000093180-A.
 PD 04-APR-2000.
 PA (TOFU) TONEN CORP.
 Best Local Similarity: 26.64%
 Query Match: 6.70%
 Mismatches: 68
 Indels: 68
 RESULT 192
 ID ABL07082 standard; cDNA; 26370 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15728.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 24.48%
 Query Match: 6.70%
 Mismatches: 120
 Indels: 67
 RESULT 193
 ID ADP64454 standard; DNA; 76994 BP.
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
 PN WO2004053065-A2.
 PD 24-JUN-2004.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 29.69%
 Query Match: 6.70%
 Mismatches: 99
 Indels: 36
 RESULT 194
 ID ADC24078 standard; DNA; 1011 BP.
 DE DNA sequence (SeqID 345) encoding a nitrilase enzyme.
 PN WO2003000840-A2.
 PD 03-JAN-2003.
 PA (DIVE-) DIVERSA CORP.
 PA (MADD//) MADDEN D.
 Best Local Similarity: 23.66%
 Query Match: 6.67%
 Mismatches: 114
 Indels: 66
 RESULT 195
 ID ADH36179 standard; DNA; 1011 BP.
 DE Chemical process monitoring-related nitrilase gene sequence SeqID345.
 PN WO2003098187-A2.
 PD 27-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 23.66%
 Mismatches: 114
 Indels: 66

Query Match: 6.67% Indels: 66
RESULT 196
ID ADG93879 standard; DNA; 1011 BP.
DE Nitrilase enzyme gene sequence SeqID345.
PN WO2003097810-A2.
PD 27-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 23.66% Mismatches: 114
Query Match: 6.67% Indels: 66
RESULT 197
ID ADI62477 standard; DNA; 1011 BP.
DE DNA encoding nitrilase polypeptide #173.
PN WO2003106415-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 23.66% Mismatches: 114
Query Match: 6.67% Indels: 66
RESULT 198
ID ADI64598 standard; DNA; 1011 BP.
DE DNA encoding nitrilase seq id 173.
PN US2004014195-A1.
PD 22-JAN-2004.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 23.66% Mismatches: 114
Query Match: 6.67% Indels: 66
RESULT 199
ID ABI10626 standard; DNA; 1965 BP.
DE Pseudomonas aeruginosa polynucleotide #9230.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 28.88% Mismatches: 86
Query Match: 6.67% Indels: 61
RESULT 200
ID AAS71429 standard; cDNA; 2253 BP.
DE DNA encoding novel human diagnostic protein #7233.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.05% Mismatches: 113
Query Match: 6.67% Indels: 70
RESULT 201
ID ADC32348 standard; cDNA; 2253 BP.
DE Human novel cDNA contig sequence, SEQ ID NO:2430.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.05% Mismatches: 113
Query Match: 6.67% Indels: 70
RESULT 202
ID ADC32347 standard; cDNA; 2253 BP.
DE Human novel cDNA contig sequence, SEQ ID NO:2429.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.05% Mismatches: 113
Query Match: 6.67% Indels: 70
RESULT 203
ID ACA37877 standard; DNA; 2493 BP.
DE Prokaryotic essential gene #19534.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 26.96% Mismatches: 91
Query Match: 6.67% Indels: 52
RESULT 204
ID ABD10460 standard; DNA; 2805 BP.
DE Pseudomonas aeruginosa polynucleotide #9064.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 28.88% Mismatches: 86
Query Match: 6.67% Indels: 61

RESULT 205
ID ABD09496 standard; DNA; 3453 BP.
DE Pseudomonas aeruginosa polynucleotide #8100.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.31% Mismatches: 94
Query Match: 6.67% Indels: 55
RESULT 206
ID ADF72496 standard; DNA; 3758 BP.
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 3.
PN JP2003334094-A.
PD 25-NOV-2003.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 23.96% Mismatches: 106
Query Match: 6.67% Indels: 115
RESULT 207
ID ADF72500 standard; DNA; 3897 BP.
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 7.
PN JP2003334094-A.
PD 25-NOV-2003.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 23.96% Mismatches: 106
Query Match: 6.67% Indels: 115
RESULT 208
ID ACN38747 standard; cDNA; 3961 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325047, SEQ ID NO:2455.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.26% Mismatches: 104
Query Match: 6.67% Indels: 115
RESULT 209
ID ADF72498 standard; DNA; 3996 BP.
DE Osteoclast bicarbonate/chloride exchanger coding sequence, SEQ ID 5.
PN JP2003334094-A.
PD 25-NOV-2003.
PA (SANY) SANKYO CO LTD.
Best Local Similarity: 23.96% Mismatches: 106
Query Match: 6.67% Indels: 115
RESULT 210
ID ADK16023 standard; DNA; 64492 BP.
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.
PN US2004053274-A1.
PD 18-MAR-2004.
PA (TOKD) TOKYO INST TECHNOLOGY.
Best Local Similarity: 28.47% Mismatches: 99
Query Match: 6.67% Indels: 73
RESULT 211
ID ACH87373 standard; DNA; 875 BP.
DE Human genome derived single exon probe #20568.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 212
ID AAK53011 standard; cDNA; 1330 BP.
DE Human polynucleotide SEQ ID NO 2540.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 22.52% Mismatches: 106
Query Match: 6.63% Indels: 122
RESULT 213
ID AAN71338 standard; DNA; 2304 BP.
DE Modified prourokinase.
PN EP36040-A.
PD 09-SEP-1987.
PA (COLB) COLLABORATIVE RES INC.
Best Local Similarity: 24.63% Mismatches: 96

Query Match: 6.63% Indels: 79
RESULT 214
ID ACN43531 standard; cDNA; 3448 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2406.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 21.92% Mismatches: 99
Query Match: 6.63% Indels: 98
RESULT 215
ID AAS74203 standard; cDNA; 5254 BP.
DE DNA encoding novel human diagnostic protein #10007.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 216
ID ADR24155 standard; DNA; 5960 BP.
DE Breast cancer prognosis marker #16.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NSCA-) NETHERLANDS CANCER INST.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 217
ID AAK52019 standard; cDNA; 6044 BP.
DE Human polynucleotide SEQ ID NO 564.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 218
ID AAK53003 standard; cDNA; 6051 BP.
DE Human polynucleotide SEQ ID NO 2532.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 219
ID ACD13189 standard; cDNA; 6075 BP.
DE cDNA encoding novel human protein NOV4a.
PN WO200298900-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 27.23% Mismatches: 96
Query Match: 6.63% Indels: 52
RESULT 220
ID AAQ73500 standard; DNA; 8438 BP.
DE DNA encoding Pseudorabies virus large latency transcript.
PN US5352596-A.
PD 04-OCT-1994.
PA (USDA) US SEC OF AGRIC.
Best Local Similarity: 27.41% Mismatches: 96
Query Match: 6.63% Indels: 82
RESULT 221
ID AAD46790 standard; DNA; 13766 BP.
DE pGRN145 plasmid DNA.
PN WO200274935-A2.
PD 26-SEP-2002.
PA (GERO-) GERON CORP.
Best Local Similarity: 23.89% Mismatches: 94
Query Match: 6.63% Indels: 72
RESULT 222
ID AA255887 standard; DNA; 68750 BP.
DE Sorangium cellulosum 68.75 kb contig.
PN WO9966028-A2.
PD 23-DEC-1999.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Best Local Similarity: 30.49% Mismatches: 91
Query Match: 6.63% Indels: 46
RESULT 223
ID ADJ72363 standard; DNA; 90597 BP.
DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Best Local Similarity: 26.00% Mismatches: 96
Query Match: 6.63% Indels: 67
RESULT 224
ID ADJ72363 standard; DNA; 90597 BP.
DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Best Local Similarity: 24.70% Mismatches: 119
Query Match: 6.63% Indels: 97
RESULT 225
ID ABQ78872 standard; DNA; 90600 BP.
DE S. roseosporus daptomycin biosynthetic gene cluster 90kb region.
PN WO200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALT/) BALTZ R H.
PA (SILV/) SILVA C J.
Best Local Similarity: 26.00% Mismatches: 96
Query Match: 6.63% Indels: 67
RESULT 226
ID ABQ78872 standard; DNA; 90600 BP.
DE S. roseosporus daptomycin biosynthetic gene cluster 90kb region.
PN WO200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALT/) BALTZ R H.
PA (SILV/) SILVA C J.
Best Local Similarity: 24.70% Mismatches: 119
Query Match: 6.63% Indels: 97
RESULT 227
ID ABX04971 standard; DNA; 103599 BP.
DE S. cinnamonensis monensin type I polyketide synthase gene cluster.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
Best Local Similarity: 21.99% Mismatches: 129
Query Match: 6.63% Indels: 99
RESULT 228
ID AAS08693 standard; DNA; 109519 BP.
DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
PN WO200049177-A2.
PD 24-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 230
ID AAL43629 standard; DNA; 1050 BP.
DE Rhodococcus picric acid degradation F420-dependent dehydrogenase #2 ORF.
PN US2002042117-A1.
PD 11-APR-2002.
PA (ROUV/) ROUVIERE P E.
PA (WALT/) WALTERS D M.
PA (RUSS/) RUSS R.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 231
ID ABK51847 standard; DNA; 1050 BP.

DE R. erythropolis HL PM-1 picric acid degradation gene cluster ORF9.
PN US635470-B1.
PD 12-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 232
ID AAD27248 standard; DNA; 1050 BP.
DE Rhodococcus erythropolis HL-PM1 picric acid degradation gene ORF8.
PN US6329151-B1.
PD 11-DEC-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 233
ID ACA26216 standard; DNA; 1629 BP.
DE Prokaryotic essential gene #7873.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-), ELITRA PHARM INC.
Best Local Similarity: 21.76% Mismatches: 84
Query Match: 6.60% Indels: 78
RESULT 234
ID ADH71207 standard; DNA; 2268 BP.
DE Human gene of the invention NOV61 SEQ ID NO:103.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-), CURAGEN CORP.
Best Local Similarity: 23.05% Mismatches: 117
Query Match: 6.60% Indels: 92
RESULT 235
ID ACA45234 standard; DNA; 2286 BP.
DE Prokaryotic essential gene #28891.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-), ELITRA PHARM INC.
Best Local Similarity: 23.51% Mismatches: 91
Query Match: 6.60% Indels: 119
RESULT 236
ID AAS78878 standard; cDNA; 2653 BP.
DE DNA encoding novel human diagnostic protein #14682.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-), HYSEQ INC.
Best Local Similarity: 24.89% Mismatches: 61
Query Match: 6.60% Indels: 83
RESULT 237
ID ADO07393 standard; DNA; 7033 BP.
DE Modified human hepsin plasmid pIRESpuro2W/hepEK.
PN WO200403630-A2.
PD 22-APR-2004.
PA (SCHD), SCHERING AG.
Best Local Similarity: 22.99% Mismatches: 102
Query Match: 6.60% Indels: 72
RESULT 238
ID AAS3941 standard; DNA; 12508 BP.
DE 12.5 kb picric acid degradation cluster.
PN WO200049177-A2.
PD 24-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 24.00% Mismatches: 109
Query Match: 6.60% Indels: 83
RESULT 239
ID AAS3941 standard; DNA; 12508 BP.
DE 12.5 kb picric acid degradation cluster.
PN WO200049177-A2.
PD 24-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 240
ID AAD27240 standard; DNA; 12508 BP.
DE Rhodococcus erythropolis strain HL-PM1 picric acid degradation gene.

PN US6329151-B1.
PD 11-DEC-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 24.00% Mismatches: 109
Query Match: 6.60% Indels: 83
RESULT 241
ID AAD27240 standard; DNA; 12508 BP.
DE Rhodococcus erythropolis strain HL-PM1 picric acid degradation gene.
PN US6329151-B1.
PD 11-DEC-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 242
ID AAL43619 standard; DNA; 12523 BP.
DE Rhodococcus erythropolis 12kb picric acid degradation gene cluster.
PN US2002042117-A1.
PD 11-APR-2002.
PA (ROUV/), ROUVIERE P E.
PA (WALT/), WALTERS D M.
PA (RUSS/), RUSS R.
Best Local Similarity: 24.00% Mismatches: 109
Query Match: 6.60% Indels: 83
RESULT 243
ID AAL43619 standard; DNA; 12523 BP.
DE Rhodococcus erythropolis 12kb picric acid degradation gene cluster.
PN US2002042117-A1.
PD 11-APR-2002.
PA (ROUV/), ROUVIERE P E.
PA (WALT/), WALTERS D M.
PA (RUSS/), RUSS R.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 244
ID ABK51837 standard; DNA; 12523 BP.
DE Rhodococcus erythropolis HL PM-1 picric acid degradation gene cluster.
PN US6355470-B1.
PD 12-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 24.00% Mismatches: 109
Query Match: 6.60% Indels: 83
RESULT 245
ID ABK51837 standard; DNA; 12523 BP.
DE Rhodococcus erythropolis HL PM-1 picric acid degradation gene cluster.
PN US6355470-B1.
PD 12-MAR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Best Local Similarity: 27.90% Mismatches: 81
Query Match: 6.60% Indels: 69
RESULT 246
ID AAL62889 standard; DNA; 88624 BP.
DE Human alpha-2 macroglobulin genomic DNA.
Best Local Similarity: 28.95% Mismatches: 30
Query Match: 6.60% Indels: 29
RESULT 247
ID ABD11923 standard; DNA; 891 BP.
DE Pseudomonas aeruginosa polynucleotide #10527.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-), GENOME THERAPEUTICS CORP.
Best Local Similarity: 31.48% Mismatches: 45
Query Match: 6.56% Indels: 16
RESULT 248
ID ABD11931 standard; DNA; 1320 BP.
DE Pseudomonas aeruginosa polynucleotide #10535.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-), GENOME THERAPEUTICS CORP.
Best Local Similarity: 31.48% Mismatches: 45
Query Match: 6.56% Indels: 16
RESULT 249
ID ABD12035 standard; DNA; 1473 BP.
DE Pseudomonas aeruginosa polynucleotide #10639.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 31.48% Mismatches: 45
Query Match: 6.56% Indels: 16
RESULT 250
ID ABD15515 standard; DNA; 1767 BP.
DE Pseudomonas aeruginosa polynucleotide #14119.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 26.72% Mismatches: 108
Query Match: 6.56% Indels: 49
RESULT 251
ID ADH71189 standard; DNA; 2106 BP.
DE Human gene of the invention NOV6c SEQ ID NO:85.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 26.16% Mismatches: 125
Query Match: 6.56% Indels: 49
RESULT 252
ID ACA45338 standard; DNA; 2215 BP.
DE Prokaryotic essential gene #26995.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 22.99% Mismatches: 95
Query Match: 6.56% Indels: 91
RESULT 253
ID ADA69752 standard; DNA; 2763 BP.
DE Rice gene, SEQ ID 3075.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 26.24% Mismatches: 95
Query Match: 6.56% Indels: 82
RESULT 254
ID ACN43529 standard; cDNA; 3508 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2404.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.55% Mismatches: 76
Query Match: 6.56% Indels: 78
RESULT 255
ID ACN43534 standard; cDNA; 3637 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2409.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.55% Mismatches: 76
Query Match: 6.56% Indels: 78
RESULT 256
ID ACA42635 standard; DNA; 4248 BP.
DE Prokaryotic essential gene #24292.
PN WO200271183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 28.14% Mismatches: 109
Query Match: 6.56% Indels: 31
RESULT 257
ID ABD15556 standard; DNA; 4287 BP.
DE Pseudomonas aeruginosa polynucleotide #14160.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 26.72% Mismatches: 108
Query Match: 6.56% Indels: 49
RESULT 258
ID ADK41004 standard; DNA; 5159 BP.
DE Novel human kinase gene #24.
PN WO2003057841-A2.

PD 17-JUL-2003.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Best Local Similarity: 25.43% Mismatches: 77
Query Match: 6.56% Indels: 75
RESULT 259
ID ADRI5718 standard; DNA; 5159 BP.
DE Kinase 40980 hCT14735 1 coding sequence, SEQ ID 111.
PN WO2004069154-A2.
PD 19-AUG-2004.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Best Local Similarity: 25.43% Mismatches: 77
Query Match: 6.56% Indels: 75
RESULT 260
ID ABD14206 standard; DNA; 1230 BP.
DE Pseudomonas aeruginosa polynucleotide #12810.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 29.38% Mismatches: 68
Query Match: 6.53% Indels: 51
RESULT 261
ID AA158354 standard; cDNA; 3542 BP.
DE Human polynucleotide SEQ ID NO 557.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 94
Query Match: 6.53% Indels: 82
RESULT 262
ID ADQ98563 standard; cDNA; 3542 BP.
DE DNA encoding human GPCR-like protein seqid 233.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 94
Query Match: 6.53% Indels: 82
RESULT 263
ID ADB48323 standard; cDNA; 3542 BP.
DE Novel human cDNA SEQ ID NO 233.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Best Local Similarity: 24.23% Mismatches: 94
Query Match: 6.53% Indels: 82
RESULT 264
ID ABL12403 standard; cDNA; 5468 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31691.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 24.74% Mismatches: 123
Query Match: 6.53% Indels: 59
RESULT 265
ID AAV22647 standard; cDNA; 5630 BP.
DE Drosophila melanogaster kuzbanian (kuz) gene.
PN WO9808933-A1.
PD 05-MAR-1998.
PA (REGC) UNIV CALIFORNIA.
PA (UYTA) UNIV YALE.
Best Local Similarity: 24.74% Mismatches: 123
Query Match: 6.53% Indels: 59
RESULT 266
ID AAK51968 standard; cDNA; 6248 BP.
DE Human polynucleotide SEQ ID NO 513.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Best Local Similarity: 26.21% Mismatches: 97
 Query Match: 6.53% Indels: 86
 RESULT 267
 ID AD114148 standard; DNA; 17596 BP.
 DE M. megalomicea cosmid KOS205-57-2.3B SEQ ID NO:2.
 PD WO2004003169-A2.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 24.63% Mismatches: 102
 Query Match: 6.53% Indels: 71
 RESULT 268
 ID AAF30757 standard; DNA; 47981 BP.
 DE Micromonospora megalomicea megalomicin biosynthetic gene cluster.
 PD WO2004003169-A2.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 24.63% Mismatches: 102
 Query Match: 6.53% Indels: 71
 RESULT 269
 ID AAS59515 standard; DNA; 66788 BP.
 DE Propionibacterium acnes immunogenic protein encoding DNA #10.
 PD WO200181581-A2.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 24.10% Mismatches: 100
 Query Match: 6.53% Indels: 80
 RESULT 270
 ID ACF64444 standard; DNA; 66788 BP.
 DE Propionibacterium acnes DNA contig sequence #10.
 PD WO2003033515-A1.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 24.10% Mismatches: 100
 Query Match: 6.53% Indels: 80
 RESULT 271
 ID ACF64444 standard; DNA; 66788 BP.
 DE Propionibacterium acnes DNA contig sequence #10.
 PD WO2003033515-A1.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 24.10% Mismatches: 100
 Query Match: 6.53% Indels: 80
 RESULT 272
 ID ACF64444 standard; DNA; 66788 BP.
 DE Propionibacterium acnes DNA contig sequence #10.
 PD WO2003033515-A1.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 24.10% Mismatches: 100
 Query Match: 6.53% Indels: 80
 RESULT 273
 ID ABD02895 standard; DNA; 990 BP.
 DE Pseudomonas aeruginosa polynucleotide #1499.
 PD US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.19% Mismatches: 103
 Query Match: 6.49% Indels: 112
 RESULT 274
 ID ABD08329 standard; DNA; 1101 BP.
 DE Pseudomonas aeruginosa polynucleotide #6933.
 PD US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.19% Mismatches: 103
 Query Match: 6.49% Indels: 112
 RESULT 275
 ID ABD08256 standard; DNA; 1320 BP.
 DE Pseudomonas aeruginosa polynucleotide #6860.
 PD US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.19% Mismatches: 103
 Query Match: 6.49% Indels: 112
 RESULT 276
 ID ABD08161 standard; DNA; 1359 BP.
 DE Pseudomonas aeruginosa polynucleotide #6765.
 PD US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.19% Mismatches: 103
 Query Match: 6.49% Indels: 112
 RESULT 277
 ID AAF32672 standard; cDNA; 1748 BP.
 DE Human cDNA encoding intracellular signalling molecule INTRA35.
 PD WO200077040-A2.

PD 21-DEC-2000.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 28.75% Mismatches: 79
 Query Match: 6.49% Indels: 63
 RESULT 278
 ID ADM87079 standard; cDNA; 1909 BP.
 DE Human protein encoding cDNA SEQ ID NO:172.
 PD WO2004009834-A2.
 PA (NUVE-) NUVELO INC.
 Best Local Similarity: 25.00% Mismatches: 63
 Query Match: 6.49% Indels: 88
 RESULT 279
 ID AAK74278 standard; DNA; 2388 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29090.
 PD WO200157182-A2.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 27.47% Mismatches: 86
 Query Match: 6.49% Indels: 59
 RESULT 280
 ID AD064606 standard; cDNA; 3554 BP.
 DE Novel human cDNA sequence #1767.
 PD EPI440981-A2.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 23.82% Mismatches: 129
 Query Match: 6.49% Indels: 126
 RESULT 281
 ID AAL44297 standard; DNA; 8651 BP.
 DE Agromyces mediolanus Y1 operon (C50 carotenoid producing operon).
 PD WO200241833-A2.
 PA (CRGI) CARGILL INC.
 Best Local Similarity: 25.61% Mismatches: 112
 Query Match: 6.49% Indels: 72
 RESULT 282
 ID ADL71890 standard; cDNA; 13068 BP.
 DE Temperature inducible alphavirus vector pCytTs2.1.
 PD WO2004018506-A2.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 Best Local Similarity: 23.25% Mismatches: 105
 Query Match: 6.49% Indels: 75
 RESULT 283
 ID ADL71909 standard; cDNA; 15081 BP.
 DE Expression vector pCytTs-Orp.
 PD WO2004018506-A2.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 Best Local Similarity: 23.25% Mismatches: 105
 Query Match: 6.49% Indels: 75
 RESULT 284
 ID ADL71910 standard; cDNA; 17753 BP.
 DE Expression vector pCytTs-OPE.
 PD WO2004018506-A2.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 Best Local Similarity: 23.25% Mismatches: 105
 Query Match: 6.49% Indels: 75
 RESULT 285
 ID AB033451 standard; DNA; 46338 BP.
 DE Murine cancer-associated (CA) gene MD07-086.
 PD WO2004058146-A2.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Best Local Similarity: 23.45% Mismatches: 62
 Query Match: 6.49% Indels: 95
 RESULT 286
 ID ADA02798 standard; DNA; 52754 BP.
 DE Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.
 PD WO2003057146-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%		Mismatches: 113
Query Match: 6.49%		Indels: 95
RESULT 287		
ID ADB72536 standard; DNA; 52754 BP.		
DE Human TNFSF11 gene.		
PN W02003008583-A2.		
PD 30-JAN-2003.		
PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%		Mismatches: 113
Query Match: 6.49%		Indels: 95
RESULT 288		
ID ADC85278 standard; DNA; 52754 BP.		
DE Human TNFSF11 genomic sequence.		
PN W02003045230-A2.		
PD 05-JUN-2003.		
PA (SAGR-) SAGRES DISCOVERY.		
Best Local Similarity: 22.59%		Mismatches: 113
Query Match: 6.49%		Indels: 95
RESULT 289		
ID ADM74393 standard; DNA; 52754 BP.		
DE Human carcinoma associated (CA) nucleic acid #31.		
PN US2004072154-A1.		
PD 15-APR-2004.		
PA (MORR-) MORRIS D W.		
PA (ENGE/) ENGELHARD E K.		
Best Local Similarity: 22.59%		Mismatches: 113
Query Match: 6.49%		Indels: 95
RESULT 290		
ID ALA40781 standard; DNA; 88421 BP.		
DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.		
PN W0200231155-A2.		
PD 18-APR-2002.		
PA (ECOP-) ECOPIA BIOSCIENCES INC.		
Best Local Similarity: 26.92%		Mismatches: 84
Query Match: 6.49%		Indels: 66
RESULT 291		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 292		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 293		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 294		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 295		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 296		
Best Local Similarity: 26.77%		Mismatches: 56
Query Match: 6.49%		Indels: 22
RESULT 297		
ID ADP74816 standard; DNA; 137560 BP.		
DE Parapoxvirus ovis genome DNA sequence SeqID1.		
PN W09306215-A1.		
PD 01-APR-1993.		
PA (SALK) SALK INST BIOLOGICAL STUDIES.		
Best Local Similarity: 24.58%		Mismatches: 70
Query Match: 6.46%		Indels: 91
RESULT 299		
ID ADH71215 standard; DNA; 2268 BP.		
DE Human gene of the invention NOV6p SEQ ID NO:111.		
PN W02003102155-A2.		
PD 11-DEC-2003.		
PA (CURA-) CURAGEN CORP.		

Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 300	
ID ADH71213 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6o	SEQ ID NO:109.
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 301	
ID ADH71185 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6a	SEQ ID NO:81.
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 302	
ID ADH71211 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6n	SEQ ID NO:107.
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 303	
ID ADH71209 standard; DNA; 2268 BP.	
DE Human gene of the invention NOV6m	SEQ ID NO:105.
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.05%	Mismatches: 117
Query Match: 6.46%	Indels: 92
RESULT 304	
ID ADH71187 standard; DNA; 2280 BP.	
DE Human gene of the invention NOV6b	SEQ ID NO:83.
FN W02003102155-A2.	
PD 11-DEC-2003.	
PA (CURA-) CURAGEN CORP.	
Best Local Similarity: 23.44%	Mismatches: 126
Query Match: 6.46%	Indels: 86
RESULT 305	
ID ADS62026 standard; cDNA; 2766 BP.	
DE Bacterial polynucleotide #14013.	
FN US2003233675-A1.	
PD 18-DEC-2003.	
PA (CAOY/) CAO Y.	
PA (HINK/) HINKLE G J.	
PA (SLAT/) SLATER S C.	
PA (CHEN/) CHEN X.	
PA (GOLD/) GOLDMAN B S.	
Best Local Similarity: 21.75%	Mismatches: 91
Query Match: 6.46%	Indels: 117
RESULT 306	
ID ACN44719 standard; cDNA; 2858 BP.	
DE Human mRNA sequence hCT1785697.	
FN W02003073826-A2.	
PD 12-SEP-2003.	
PA (SAGR-) SAGRES DISCOVERY.	
Best Local Similarity: 21.38%	Mismatches: 109
Query Match: 6.46%	Indels: 105
RESULT 307	
ID ABS70366 standard; cDNA; 3030 BP.	
DE Human bone remodelling gene #23.	
FN US6426186-B1.	
PD 30-JUL-2002.	
PA (INCY-) INCYTE GENOMICS INC.	
Best Local Similarity: 21.38%	Mismatches: 109
Query Match: 6.46%	Indels: 105
RESULT 308	
ID AAD59099 standard; DNA; 3389 BP.	
DE Human antiCD3/CD28-RATL 5-h6 contig DNA.	

PN US200314196-A1.
 PD 31-JUL-2003.
 PA (BOWE/) BOWEN M. A.
 PA (FINGER/) FINGER J.
 Best Local Similarity: 21.38% Mismatches: 109
 Query Match: 6.46% Indels: 105
 RESULT 309
 ID ADM86984 standard; cDNA; 3493 BP.
 DE Human protein encoding cDNA SEQ ID NO:77.
 PN WO2004009834-A2.
 PD 29-JAN-2004.
 PA (NUVE-) NUVELO INC.
 Best Local Similarity: 21.38% Mismatches: 109
 Query Match: 6.46% Indels: 105
 RESULT 310
 ID ADF12845 standard; DNA; 3498 BP.
 DE Reference mRNA sequence #59.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Best Local Similarity: 21.38% Mismatches: 109
 Query Match: 6.46% Indels: 105
 RESULT 311
 ID ADS14592 standard; DNA; 3750 BP.
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2305, SEQ ID 147.
 PN WO2004083385-A2.
 PD 30-SEP-2004.
 PA (IOWA) UNIV IOWA RES FOUND.
 Best Local Similarity: 28.45% Mismatches: 86
 Query Match: 6.46% Indels: 61
 RESULT 312
 ID ADRO7305 standard; cDNA; 4408 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 811.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 25.97% Mismatches: 68
 Query Match: 6.46% Indels: 24
 RESULT 313
 ID ACM44718 standard; DNA; 20478 BP.
 DE Human genomic sequence HCG1747365.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity: 21.38% Mismatches: 109
 Query Match: 6.46% Indels: 105
 RESULT 314
 ID AAM63350 standard; DNA; 21185 BP.
 DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.
 PN WO20040596-A1.
 PD 13-JUL-2000.
 PA (REGC) UNIV CALIFORNIA.
 Best Local Similarity: 25.65% Mismatches: 76
 Query Match: 6.46% Indels: 67
 RESULT 315
 ID AAV20441 standard; DNA; 35100 BP.
 DE Human c-fos oncogene.
 PN US5734039-A.
 PD 31-MAR-1998.
 PA (UYJB-) UNIV JEFFERSON THOMAS.
 Best Local Similarity: 24.52% Mismatches: 89
 Query Match: 6.46% Indels: 125
 RESULT 316
 ID AAS98633 standard; DNA; 38258 BP.
 DE DNA encoding Colony stimulating factor 1 receptor (CSF1R).
 PN WO20040596-A1.
 PD 13-JUL-2000.
 PA (REGC) UNIV CALIFORNIA.
 Best Local Similarity: 24.52% Mismatches: 89
 Query Match: 6.46% Indels: 125
 RESULT 317
 ID AAG63348 standard; DNA; 63164 BP.
 DE Streptomyces globisporus C-1027 gene cluster.
 PN WO20040596-A1.
 PD 13-JUL-2000.
 PA (REGC) UNIV CALIFORNIA.

Best Local Similarity: 25.65% Mismatches: 76
 Query Match: 6.46% Indels: 67
 RESULT 318
 Best Local Similarity: 25.00% Mismatches: 75
 Query Match: 6.48% Indels: 95
 RESULT 319
 ID ADI39160 standard; DNA; 86941 BP.
 DE Streptomyces hygrosopicus herbimycin gene cluster, SEQ ID NO:2.
 PN WO2003106653-A2.
 PD 24-DEC-2003.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 26.49% Mismatches: 106
 Query Match: 6.46% Indels: 80
 RESULT 320
 Best Local Similarity: 25.00% Mismatches: 75
 Query Match: 6.46% Indels: 95
 RESULT 321
 ID ADH17387 standard; cDNA; 1321 BP.
 DE Human NOV9a cDNA - SEQ ID 77.
 PN WO2003093432-A2.
 PD 13-NOV-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 23.61% Mismatches: 98
 Query Match: 6.42% Indels: 110
 RESULT 322
 ID ABD09161 standard; DNA; 1461 BP.
 DE Pseudomonas aeruginosa polynucleotide #7765.
 PN US551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.02% Mismatches: 133
 Query Match: 6.42% Indels: 96
 RESULT 323
 ID ACA42339 standard; DNA; 1608 BP.
 DE Prokaryotic essential gene #23996.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 23.00% Mismatches: 99
 Query Match: 6.42% Indels: 93
 RESULT 324
 ID ADS14623 standard; DNA; 1608 BP.
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2573, SEQ ID 178.
 PN WO2004083385-A2.
 PD 30-SEP-2004.
 PA (IOWA) UNIV IOWA RES FOUND.
 Best Local Similarity: 23.00% Mismatches: 99
 Query Match: 6.42% Indels: 93
 RESULT 325
 ID ABX70825 standard; cDNA; 1879 BP.
 DE Novel human cDNA sequence #50.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.03% Mismatches: 60
 Query Match: 6.42% Indels: 108
 RESULT 326
 ID ADF44669 standard; cDNA; 2094 BP.
 DE Bacterial polynucleotide #19420.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 27.91% Mismatches: 108
 Query Match: 6.42% Indels: 30
 RESULT 327
 ID ADB63171 standard; cDNA; 2224 BP.
 DE Human cDNA encoding clone SPLN20073500.

PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 26.74% Mismatches: 108
Query Match: 6.42% Indels: 115
RESULT 328
ID ADM02791 standard; cDNA; 3029 BP.
DE Human cDNA of the invention SEQ ID NO:1476.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 24.28% Mismatches: 88
Query Match: 6.42% Indels: 90
RESULT 329
ID AAS27829 standard; DNA; 22452 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1489.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 26.62% Mismatches: 88
Query Match: 6.42% Indels: 88
RESULT 330
ID AAS27827 standard; DNA; 22452 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1487.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 26.62% Mismatches: 88
Query Match: 6.42% Indels: 88
RESULT 331
ID ADB94632 standard; DNA; 22452 BP.
DE Novel human protein DNA #241.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 26.62% Mismatches: 88
Query Match: 6.42% Indels: 88
RESULT 332
ID ADB94630 standard; DNA; 22452 BP.
DE Novel human protein DNA #239.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 26.62% Mismatches: 88
Query Match: 6.42% Indels: 88
RESULT 333
ID ADI00878 standard; DNA; 22773 BP.
DE Human mucin MUC5B genomic DNA 5' fragment.
PN US2003096219-A1.
PD 22-MAY-2003.
PA (WURR/) WU R.
PA (CHEN/) CHEN Y.
Best Local Similarity: 24.09% Mismatches: 106
Query Match: 6.42% Indels: 126
RESULT 334
ID ACN44185 standard; cDNA; 956 BP.
DE Mouse mRNA sequence mct18732.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.74% Mismatches: 96
Query Match: 6.39% Indels: 54
RESULT 335
ID AAH00902 standard; DNA; 1208 BP.
DE Sporothrix schenckii nucleotide sequence SEQ ID NO:893.
PN WO200123604-A2.
PD 05-APR-2001.
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Best Local Similarity: 22.12% Mismatches: 100
Query Match: 6.39% Indels: 92
RESULT 336
ID AAH00502 standard; DNA; 1211 BP.
DE Sporothrix schenckii nucleotide sequence SEQ ID NO:493.
PN WO200123604-A2.
PD 05-APR-2001.
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
Best Local Similarity: 22.12% Mismatches: 100
Query Match: 6.39% Indels: 92
RESULT 337
ID ACM49920 standard; DNA; 1425 BP.
DE Prokaryotic essential gene #31577.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 23.15% Mismatches: 77
Query Match: 6.39% Indels: 55
RESULT 338
ID ACN40783 standard; cDNA; 1600 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326842, SEQ ID NO:5787.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 23.97% Mismatches: 102
Query Match: 6.39% Indels: 104
RESULT 339
ID AAL45648 standard; cDNA; 2064 BP.
DE Human cancer cell growth inhibitor related cDNA SEQ ID NO: 4.
PN CN1324819-A.
PD 05-DEC-2001.
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
Best Local Similarity: 23.97% Mismatches: 102
Query Match: 6.39% Indels: 104
RESULT 340
ID AAL45649 standard; DNA; 2064 BP.
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 6.
PN CN1324819-A.
PD 05-DEC-2001.
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.
Best Local Similarity: 23.97% Mismatches: 102
Query Match: 6.39% Indels: 104
RESULT 341
ID ADB62304 standard; cDNA; 2792 BP.
DE Human cDNA encoding clone FCBBF20059660.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.97% Mismatches: 102
Query Match: 6.39% Indels: 104
RESULT 342
ID ADM02253 standard; cDNA; 3044 BP.
DE Human cDNA of the invention SEQ ID NO:938.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.97% Mismatches: 102
Query Match: 6.39% Indels: 104
RESULT 343
ID AAD51683 standard; cDNA; 3073 BP.
DE Human nucleic acid associated protein (NAAP)-9 encoding cDNA.
PN WO200299115-A2.
PD 12-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
PA (YUEH/) YUE H.
Best Local Similarity: 22.50% Mismatches: 125
Query Match: 6.39% Indels: 124
RESULT 344
ID AAD59100 standard; DNA; 3393 BP.
DE Human RAT1 5h6 DNA.
PN US2003144196-A1.
PD 31-JUL-2003.

PA (BOWE/) BOWEN M A.
 PA (FING/) FINGER J. Mismatches: 110
 Best Local Similarity: 21.38% Indels: 105
 Query Match: 6.39%
 RESULT 345
 ID AAS92479 standard; cDNA; 4014 BP.
 DE DNA encoding novel human diagnostic protein #28283.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 21.45% Mismatches: 75
 Query Match: 6.39% Indels: 138
 RESULT 346
 ID ABX34460 standard; cDNA; 4709 BP.
 DE Human mdt cDNA SEQ ID 21.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 347
 ID AAX58463 standard; DNA; 4857 BP.
 DE Thermophilus thermophilus DNA polymerase dnaE gene.
 PN WO9913060-A1.
 PD 18-MAR-1999.
 PA (ENZY-) ENZYCO INC.
 Best Local Similarity: 23.51% Mismatches: 99
 Query Match: 6.39% Indels: 62
 RESULT 348
 ID ADI23903 standard; DNA; 8321 BP.
 DE Streptomyces fradiae A541 locus contig 3.
 PN US2003198981-A1.
 PD 23-OCT-2003.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 22.14% Mismatches: 116
 Query Match: 6.39% Indels: 63
 RESULT 349
 ID AAG59517 standard; DNA; 18796 BP.
 DE Propionibacterium acnes immunogenic protein encoding DNA #12.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.87% Mismatches: 134
 Query Match: 6.39% Indels: 74
 RESULT 350
 ID ACP64446 standard; DNA; 18796 BP.
 DE Propionibacterium acnes DNA contig sequence #12.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.87% Mismatches: 134
 Query Match: 6.39% Indels: 74
 RESULT 351
 ID ACN44184 standard; DNA; 20956 BP.
 DE Mouse genomic sequence mCG15594.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity: 25.74% Mismatches: 96
 Query Match: 6.39% Indels: 54
 RESULT 352
 ID AAX87248 standard; DNA; 23580 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 353
 ID AAS28556 standard; DNA; 23580 BP.
 DE Genomic sequence #336 encoding for novel human respiratory antigen.
 PN WO200155448-A1.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 354
 ID ADG41752 standard; DNA; 23580 BP.
 DE Human respiratory system associated genomic DNA seq id 990.
 PN US2003215893-A1.
 PD 20-NOV-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 355
 ID ADI97526 standard; DNA; 23580 BP.
 DE Human respiratory system associated polypeptide-related DNA SeqID990.
 PN US2003077704-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 356
 ID ABQ88164 standard; cDNA; 86080 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 357
 ID ABK83561 standard; cDNA; 86080 BP.
 DE Human cDNA differentially expressed in granulocytic cells #132.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 358
 ID ADD71054 standard; DNA; 86080 BP.
 DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.
 PN WO2003061564-A2.
 PD 31-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (LGBI-) LG BIOMEDICAL INST.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 359
 ID ADQ18878 standard; DNA; 86080 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1697.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 360
 ID ADQ97263 standard; DNA; 100864 BP.
 DE Mouse cancer associated sequence MD2-08-023, SEQ ID 239.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Best Local Similarity: 25.74% Mismatches: 96
 Query Match: 6.39% Indels: 54
 RESULT 361
 ID AAG7248 standard; DNA; 23580 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.97% Mismatches: 102
 Query Match: 6.39% Indels: 104
 RESULT 362
 ID ABD10328 standard; DNA; 678 BP.
 DE Pseudomonas aeruginosa polynucleotide #8932.
 PN US651795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 28.71% Mismatches: 77
 Query Match: 6.35% Indels: 54
 RESULT 363

ID	ACA37660 standard; DNA; 1113 BP.	PA	(WUTD/) WU T D.	
DE	Prokaryotic essential gene #19317.	PA	(ZHOU/) ZHOU Y.	
PD	WO200277183-A2.		Best Local Similarity: 23.58%	Mismatches: 115
PA	(ELIT-) ELITRA PHARM INC.		Query Match: 6.35%	Indels: 44
Best Local Similarity: 22.92%				
Query Match: 6.35%				
RESULT 364				
ID	ADJ63193 standard; DNA; 1275 BP.	ID	AD863143 standard; cDNA; 2367 BP.	
DE	Human zygote arrest 1 (Zar1) DNA sequence #2.	DE	Human cDNA encoding clone SPLEN20024770.	
PD	WO2003091400-A2.	PD	EPI308459-A2.	
PD	06-NOV-2003.	PD	07-MAY-2003.	
PA	(BAYU) BAYLOR COLLEGE MEDICINE.	PA	(HELI-) HELIX RES INST.	
PA	(AMHP) WYETH.	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
Best Local Similarity: 28.57%		Best Local Similarity: 26.38%		Mismatches: 118
Query Match: 6.35%		Query Match: 6.35%		Indels: 80
RESULT 365		RESULT 373		
ID	AAS18432 standard; DNA; 1590 BP.	ID	AAK74279 standard; DNA; 2386 BP.	
DE	Contig 143a DNA encoding S. narbonensis polyketide synthase.	DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29091.	
PD	US6303767-B1.	PD	WO200157182-A2.	
PD	16-OCT-2001.	PD	09-AUG-2001.	
PA	(KOSA-) KOSAN BIOSCIENCES INC.	PA	(HOMA-) HUMAN GENOME SCI INC.	
Best Local Similarity: 23.38%		Best Local Similarity: 27.47%		Mismatches: 87
Query Match: 6.35%		Query Match: 6.35%		Indels: 59
RESULT 366		RESULT 374		
ID	ADJ91888 standard; DNA; 1590 BP.	ID	AA051488 standard; DNA; 2540 BP.	
DE	Streptomyces narbonolide polyketide synthase coding sequence #1.	DE	Orrithine carbamoyl transferase (OCTase) gene.	
PD	US2003194784-A1.	PD	EP570096-A2.	
PD	16-OCT-2003.	PD	18-NOV-1993.	
PA	(SHER/) SHERMAN D H.	PA	(OJIP) OJI PAPER CO.	
PA	(LIUH/) LIU H.	PA	(OJIP) NEW OJI PAPER CO LTD.	
PA	(XUEY/) XUE Y.	Best Local Similarity: 24.28%		Mismatches: 98
PA	(ZHAO/) ZHAO L.	Query Match: 6.35%		Indels: 62
Best Local Similarity: 23.38%		RESULT 375		
Query Match: 6.35%		ID	AAL50615 standard; cDNA; 3158 BP.	
RESULT 367		DE	Human glutamate receptor 14691 coding sequence.	
ID	ADC30856 standard; cDNA; 1635 BP.	PD	EP1245574-A1.	
DE	Human novel cDNA sequence, SEQ ID NO:938.	PD	02-OCT-2002.	
PD	WO2003029271-A2.	PA	(MILL-) MILLENNIUM PHARM INC.	
PD	10-APR-2003.	Best Local Similarity: 24.16%		Mismatches: 88
PA	(HYSE-) HYSEQ INC.	Query Match: 6.35%		Indels: 90
Best Local Similarity: 25.50%		RESULT 376		
Query Match: 6.35%		ID	ADM02252 standard; cDNA; 3241 BP.	
RESULT 368		DE	Human cDNA of the invention SEQ ID NO:937.	
ID	AA016105 standard; cDNA; 1908 BP.	PD	EPI347046-A1.	
DE	Human intracellular regulatory molecule, KWC02 cDNA.	PD	24-SEP-2003.	
PD	US6274312-B1.	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
PD	14-AUG-2001.	Best Local Similarity: 23.91%		Mismatches: 88
PA	(SCHE) SCHERING CORP.	Query Match: 6.35%		Indels: 90
Best Local Similarity: 23.87%		RESULT 377		
Query Match: 6.35%		ID	ADL61747 standard; DNA; 3255 BP.	
RESULT 369		DE	P. aeruginosa pathogenic virulence factor encoding DNA SEQ ID NO:17.	
ID	ACA23718 standard; DNA; 2064 BP.	PD	WO2004024937-A2.	
DE	Prokaryotic essential gene #5375.	PD	25-MAR-2004.	
PD	WO200277183-A2.	PA	(GEHO) GEN HOSPITAL CORP.	
PD	03-OCT-2002.	Best Local Similarity: 24.45%		Mismatches: 86
PA	(ELIT-) ELITRA PHARM INC.	Query Match: 6.35%		Indels: 89
Best Local Similarity: 24.22%		RESULT 378		
Query Match: 6.35%		ID	AAZ22251 standard; DNA; 4257 BP.	
RESULT 370		DE	Nucleotide sequence of pPur vector.	
ID	AA071369 standard; DNA; 2304 BP.	PD	WO9947921-A1.	
DE	Modified prourokinase (ALA).	PD	23-SEP-1999.	
PD	EP236040-A.	PA	(PHAR-) PHARMACOPEDIA INC.	
PD	09-SEP-1987.	Best Local Similarity: 24.05%		Mismatches: 109
PA	(COJB) COLLABORATIVE RES INC.	Query Match: 6.35%		Indels: 57
Best Local Similarity: 27.65%		RESULT 379		
Query Match: 6.35%		ID	ABT16611 standard; DNA; 4257 BP.	
RESULT 371		DE	Artificial plant chromosome related plasmid DNA SEQ ID NO 22.	
ID	AD086010 standard; cDNA; 2313 BP.	PD	WO200296923-A1.	
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #2882.	PD	05-DEC-2002.	
PD	WO2004060270-A2.	PA	(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.	
PD	22-JUL-2004.	PA	(AGRI-) AGRISOMA INC.	
PA	(GETH) GENENTECH INC.	Best Local Similarity: 24.05%		Mismatches: 109
		Query Match: 6.35%		Indels: 57
		RESULT 380		
		ID	ACC44641 standard; DNA; 4257 BP.	

DE Plasmid pUR nucleotide sequence SEQ ID NO:30.
 PN WO200297059-A2.
 PD 05-DEC-2002.
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 Best Local Similarity: 24.05% Mismatches: 109
 Query Match: 6.35% Indels: 57
 RESULT 381
 ID ABR16615 standard; DNA; 4346 BP.
 DE Artificial plant chromosome related plasmid DNA SEQ ID NO:26.
 PN WO200296923-A1.
 PD 05-DEC-2002.
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 PA (AGRI-) AGRISOMA INC.
 Best Local Similarity: 24.05% Mismatches: 109
 Query Match: 6.35% Indels: 57
 RESULT 382
 ID ACC44716 standard; DNA; 4346 BP.
 DE Plasmid pSV40193attPeasePUR nucleotide sequence SEQ ID NO:113.
 PN WO200297059-A2.
 PD 05-DEC-2002.
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 Best Local Similarity: 24.05% Mismatches: 109
 Query Match: 6.35% Indels: 57
 RESULT 383
 ID ADR24153 standard; DNA; 4608 BP.
 DE Breast cancer prognosis marker #14.
 PN WO20004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Best Local Similarity: 25.88% Mismatches: 99
 Query Match: 6.35% Indels: 45
 RESULT 384
 ID ACNA0091 standard; cDNA; 4608 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA326249, SEQ ID NO:4656.
 PN WO20004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 25.88% Mismatches: 99
 Query Match: 6.35% Indels: 45
 RESULT 385
 ID ADJ63204 standard; DNA; 6002 BP.
 DE Human zygote arrest 1 (Zar1) DNA sequence #3.
 PN WO2003091400-A2.
 PD 06-NOV-2003.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (AMHP) WYETH.
 Best Local Similarity: 28.57% Mismatches: 89
 Query Match: 6.35% Indels: 51
 RESULT 386
 ID ADJ63176 standard; DNA; 7405 BP.
 DE Human zygote arrest 1 (Zar1) DNA sequence #1.
 PN WO2003091400-A2.
 PD 06-NOV-2003.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (AMHP) WYETH.
 Best Local Similarity: 28.57% Mismatches: 89
 Query Match: 6.35% Indels: 51
 RESULT 387
 ID AAD54223 standard; DNA; 24081 BP.
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.
 PN WO200288176-A2.
 PD 07-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 26.38% Mismatches: 94
 Query Match: 6.35% Indels: 50
 RESULT 388
 ID ADF31997 standard; DNA; 39949 BP.
 DE Full length cosmid 2A7.
 PN WO200309993-A2.
 PD 04-DEC-2003.
 PA (AVET) AVENTIS PHARM INC.
 Best Local Similarity: 21.07% Mismatches: 134

Query Match: 6.35% Indels: 39
 RESULT 389
 ID ADF31998 standard; DNA; 48200 BP.
 DE Cosmid 2A7.
 PN WO200309993-A2.
 PD 04-DEC-2003.
 PA (AVET) AVENTIS PHARM INC.
 Best Local Similarity: 21.07% Mismatches: 134
 Query Match: 6.35% Indels: 39
 RESULT 390
 ID AAD54217 standard; DNA; 52101 BP.
 DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.
 PN WO200288176-A2.
 PD 07-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 26.38% Mismatches: 94
 Query Match: 6.35% Indels: 50
 RESULT 391
 ID AD059147 standard; DNA; 70782 BP.
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.
 PN DE10241152-A1.
 PD 18-MAR-2004.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Best Local Similarity: 27.60% Mismatches: 73
 Query Match: 6.35% Indels: 86
 RESULT 392
 ID ADL81732 standard; DNA; 84830 BP.
 DE P. aeruginosa PA14 large pathogenicity island PAPI-1 DNA SEQ ID NO:2.
 PN WO20004024937-A2.
 PD 25-MAR-2004.
 PA (GEHO) GEN HOSPITAL CORP.
 Best Local Similarity: 24.45% Mismatches: 86
 Query Match: 6.35% Indels: 89
 RESULT 393
 ID AAS69335 standard; cDNA; 690 BP.
 DE DNA encoding novel human diagnostic protein #5139.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 31.25% Mismatches: 40
 Query Match: 6.32% Indels: 37
 RESULT 394
 ID ABD15563 standard; DNA; 933 BP.
 DE Pseudomonas aeruginosa polynucleotide #14167.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.11% Mismatches: 93
 Query Match: 6.32% Indels: 84
 RESULT 395
 ID ADC24016 standard; DNA; 1017 BP.
 DE DNA sequence (SeqID 283) encoding a nitrilase enzyme.
 PN WO2003000840-A2.
 PD 03-JAN-2003.
 PA (DIVE-) DIVERSA CORP.
 PA (MADD) MADDEN D.
 Best Local Similarity: 23.16% Mismatches: 109
 Query Match: 6.32% Indels: 78
 RESULT 396
 ID ADH36117 standard; DNA; 1017 BP.
 DE Chemical process monitoring-related nitrilase gene sequence SeqID283.
 PN WO2003098187-A2.
 PD 27-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 23.16% Mismatches: 109
 Query Match: 6.32% Indels: 78
 RESULT 397
 ID ADG93818 standard; DNA; 1017 BP.
 DE Nitrilase enzyme gene sequence SeqID283.
 PN WO2003097810-A2.
 PD 27-NOV-2003.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 23.16% Mismatches: 109

Query Match: 6.32% Indels: 78
 RESULT 398
 ID AD162415 standard; DNA; 1017 BP.
 DE DNA encoding nitrilase polypeptide #142.
 PN WO2003106415-A2.
 PD 24-DEC-2003.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 23.16% Mismatches: 109
 Query Match: 6.32% Indels: 78
 RESULT 399
 ID AD164536 standard; DNA; 1017 BP.
 DE DNA encoding nitrilase seq id 142.
 PN US2004014195-A1.
 PD 22-JAN-2004.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 23.16% Mismatches: 109
 Query Match: 6.32% Indels: 78
 RESULT 400
 ID ABD15610 standard; DNA; 1158 BP.
 DE Pseudomonas aeruginosa polynucleotide #14214.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.11% Mismatches: 93
 Query Match: 6.32% Indels: 84
 RESULT 401
 ID ADS45810 standard; cDNA; 1179 BP.
 DE Bacterial polynucleotide #553.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 26.23% Mismatches: 81
 Query Match: 6.32% Indels: 66
 RESULT 402
 ID ADS56767 standard; cDNA; 1248 BP.
 DE Bacterial polynucleotide #8754.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 21.52% Mismatches: 115
 Query Match: 6.32% Indels: 91
 RESULT 403
 ID AAX06863 standard; cDNA; 2105 BP.
 DE Australian banana cv. Mysore-infected badnavirus promoter pmv.
 PN WO9900492-A1.
 PD 07-JAN-1999.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.
 PA (UYQU) UNIV QUEENSLAND.
 PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
 PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 PA (UYLE-) UNIV KATHOLIEKE LEUVEN.
 Best Local Similarity: 22.33% Mismatches: 90
 Query Match: 6.32% Indels: 107
 RESULT 404
 ID AAN60591 standard; DNA; 2301 BP.
 DE Sequence encoding modified human pro-urokinase clone.
 PN WO8604351-A.
 PD 31-JUL-1986.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (MIYA/) MIYAKE T.
 PA (HODO) HODOGAYA-CHEM CO LTD.
 PA (NIPS) NIPPON SODA CO.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.

PA (NIPC) NIPPON CHEM IND CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 PA (NIPS) NIPPON SODA CO.
 Best Local Similarity: 23.81% Mismatches: 100
 Query Match: 6.32% Indels: 65
 RESULT 405
 ID ABD10127 standard; DNA; 2304 BP.
 DE Pseudomonas aeruginosa polynucleotide #8731.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.28% Mismatches: 114
 Query Match: 6.32% Indels: 118
 RESULT 406
 ID AAF93880 standard; cDNA; 2835 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0243.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 24.89% Mismatches: 61
 Query Match: 6.32% Indels: 83
 RESULT 407
 ID ABF43707 standard; cDNA; 2960 BP.
 DE Molecule for disease detection and treatment (MDDT)-15 cDNA sequence.
 PN WO2003052049-A2.
 PD 26-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 23.68% Mismatches: 94
 Query Match: 6.32% Indels: 88
 RESULT 408
 ID ABL11633 standard; cDNA; 6036 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29381.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 23.95% Mismatches: 87
 Query Match: 6.32% Indels: 76
 RESULT 409
 ID ABL18880 standard; DNA; 7441 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8113.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 22.55% Mismatches: 92
 Query Match: 6.32% Indels: 35
 RESULT 410
 ID ABU11632 standard; cDNA; 8223 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29378.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 23.95% Mismatches: 87
 Query Match: 6.32% Indels: 76
 RESULT 411
 ID ADF45448 standard; DNA; 9258 BP.
 DE Human vasodilator-responsive gene #45.
 PN JP2003310272-A.
 PD 05-NOV-2003.
 PA (TANA/) TANAKA T.
 PA (ASAH) ASAHI KASEI KK.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Best Local Similarity: 24.34% Mismatches: 91
 Query Match: 6.32% Indels: 48
 RESULT 412
 ID ADQ87183 standard; cDNA; 9260 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4060.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 24.34% Mismatches: 91

Query Match: 6.32% Indels: 48
RESULT 413
ID ADQ84906 standard; cDNA; 9260 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1720.
FN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 24.34% Mismatches: 91
Query Match: 6.32% Indels: 48
RESULT 414
ID ABX76157 standard; DNA; 9272 BP.
DE Lung cancer-associated polynucleotide #29.
FN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 24.34% Mismatches: 91
Query Match: 6.32% Indels: 48
RESULT 415
ID ADQ18965 standard; DNA; 9272 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1784.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 24.34% Mismatches: 91
Query Match: 6.32% Indels: 48
RESULT 416
ID ABK64501 standard; DNA; 9287 BP.
DE Human benign prostatic hyperplasia gene #396.
FN WO200212440-A2.
PD 14-FEB-2002.
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
Best Local Similarity: 24.34% Mismatches: 91
Query Match: 6.32% Indels: 48
RESULT 417
ID ADQ23327 standard; DNA; 9456 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6147.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 24.34% Mismatches: 91
Query Match: 6.32% Indels: 48
RESULT 418
ID ADQ91703 standard; DNA; 20256 BP.
DE Polyketide synthase ORF12, SEQ ID 26.
FN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Best Local Similarity: 27.70% Mismatches: 105
Query Match: 6.32% Indels: 85
RESULT 419
ID ADD14677 standard; cDNA; 34875 BP.
DE Human src biomarker polynucleotide SEQ ID NO:71.
FN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 21.91% Mismatches: 110
Query Match: 6.32% Indels: 109
RESULT 420
ID ADR52965 standard; DNA; 34875 BP.
DE Drug therapy altered expressed gene #316.
FN WO2004072285-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TRFP/) TRFPICCHIO W L.
Best Local Similarity: 21.91% Mismatches: 110
Query Match: 6.32% Indels: 109
RESULT 421

ID ADC00439 standard; DNA; 48423 BP.
DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 484.
FN GP2002355074-A.
PD 10-DEC-2002.
PA (UYIS-) UNIV TSUKUBA.
Best Local Similarity: 23.87% Mismatches: 75
Query Match: 6.32% Indels: 76
RESULT 422
ID ACD19124 standard; DNA; 48908 BP.
DE E. coli 0157 unique DNA sequence OZID_137.
FN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Best Local Similarity: 23.87% Mismatches: 75
Query Match: 6.32% Indels: 76
RESULT 423
ID AAA58471 standard; DNA; 58857 BP.
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
FN WO200040704-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 26.13% Mismatches: 118
Query Match: 6.32% Indels: 77
RESULT 424
ID ADU15447 standard; DNA; 85915 BP.
DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.
FN WO2004018703-A2.
PD 04-MAR-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Best Local Similarity: 26.94% Mismatches: 102
Query Match: 6.32% Indels: 86
RESULT 425
ID ADQ91695 standard; DNA; 164051 BP.
DE Polyketide synthase related DNA contig 2, SEQ ID 18.
FN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Best Local Similarity: 27.70% Mismatches: 105
Query Match: 6.32% Indels: 85
RESULT 426
ID ADP75188 standard; DNA; 276820 BP.
DE Human ADAMTS2 gene.
FN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 21.85% Mismatches: 83
Query Match: 6.32% Indels: 98
RESULT 427
ID AA96225 standard; cDNA; 1195 BP.
DE cDNA encoding a maize chitinase polypeptide designated ZmCh9.
FN WO200056908-A2.
PD 28-SEP-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Best Local Similarity: 26.09% Mismatches: 72
Query Match: 6.28% Indels: 77
RESULT 428
ID ACA23770 standard; DNA; 1212 BP.
DE Prokaryotic essential gene #5427.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 23.26% Mismatches: 146
Query Match: 6.28% Indels: 83
RESULT 429
ID ABK99935 standard; DNA; 1402 BP.
DE DNA encoding human secreted protein SCEP-18.
FN WO200248337-A2.
PD 20-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.

Best Local Similarity: 26.96% Mismatches: 92
Query Match: 6.28% Indels: 59
RESULT 430
ID ADS14792 standard; DNA; 1422 BP.
DE Pseudomonas aeruginosa quorum sensing controlled gene PA4371, SEQ ID 347.
PN WO2004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Best Local Similarity: 21.41% Mismatches: 136
Query Match: 6.28% Indels: 96
RESULT 431
ID ABD01576 standard; DNA; 1461 BP.
DE Pseudomonas aeruginosa polynucleotide #180.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.28% Mismatches: 133
Query Match: 6.28% Indels: 64
RESULT 432
ID ADQ87560 standard; cDNA; 1868 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4438.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 23.02% Mismatches: 139
Query Match: 6.28% Indels: 123
RESULT 433
ID ADS14570 standard; DNA; 2055 BP.
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2163, SEQ ID 125.
PN WO2004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Best Local Similarity: 27.92% Mismatches: 81
Query Match: 6.28% Indels: 31
RESULT 434
ID AAN71330 standard; DNA; 2304 BP.
DE Sequence encoding modified prourokinase.
PN EP236040-A.
PD 09-SEP-1987.
PA (COLB) COLLABORATIVE RES INC.
Best Local Similarity: 24.26% Mismatches: 99
Query Match: 6.28% Indels: 79
RESULT 435
ID ADT42110 standard; cDNA; 2442 BP.
DE Bacterial polynucleotide #16861.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 26.43% Mismatches: 74
Query Match: 6.28% Indels: 65
RESULT 436
ID AAD48133 standard; DNA; 2878 BP.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 437
ID ADN38941 standard; cDNA; 2878 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 438

ID ADK67783 standard; DNA; 2878 BP.
DE Human glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 439
ID ADJ80226 standard; cDNA; 3011 BP.
DE Novel human nucleic acid-associated protein coding sequence #44.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 23.91% Mismatches: 88
Query Match: 6.28% Indels: 90
RESULT 440
ID ADQ83194 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 441
ID ADQ85107 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 442
ID ACN42084 standard; cDNA; 4536 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 22.50% Mismatches: 108
Query Match: 6.28% Indels: 105
RESULT 443
ID ACC49359 standard; DNA; 7282 BP.
DE Human NR1 exons 1 and 2 DNA sequence SEQ ID NO:11.
PN WO2003018843-A1.
PD 06-MAR-2003.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Best Local Similarity: 25.12% Mismatches: 76
Query Match: 6.28% Indels: 66
RESULT 444
ID ABZ37516 standard; DNA; 59816 BP.
DE Streptomyces viridochromogenes Avi gene cluster sense strand.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Best Local Similarity: 24.02% Mismatches: 89
Query Match: 6.28% Indels: 67
RESULT 445
ID ABZ37515 standard; DNA; 59816 BP.
DE Streptomyces viridochromogenes Avi gene cluster sense strand.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Best Local Similarity: 24.02% Mismatches: 89
Query Match: 6.28% Indels: 67
RESULT 446
ID ACN44290 standard; DNA; 59856 BP.
DE Human genomic sequence hCG24994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Best Local Similarity: 24.57% Mismatches: 130
 Query Match: 6.28% Indels: 62
 RESULT 447
 ID ADJ33491 standard; DNA; 94001 BP.
 DE Human LAR related nucleotide sequence SEQ ID NO:20.
 PN WO2004010956-A2.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Best Local Similarity: 20.00% Mismatches: 98
 Query Match: 6.28% Indels: 127
 RESULT 448
 ID AAS76153 standard; cDNA; 744 BP.
 DE DNA encoding novel human diagnostic protein #11957.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 26.35% Mismatches: 74
 Query Match: 6.28% Indels: 35
 RESULT 451
 ID ADE63830 standard; DNA; 935 BP.
 DE Human gene NM_005194, SEQ ID NO 9774.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GENO-) GEN HOSPITAL CORP.
 Best Local Similarity: 24.83% Mismatches: 94
 Query Match: 6.25% Indels: 113
 RESULT 454
 ID ABX05207 standard; cDNA; 1074 BP.
 DE Human novel polynucleotide #222.
 PN WO200274961-A1.
 PD 26-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 28.45% Mismatches: 81
 Query Match: 6.25% Indels: 65
 RESULT 455
 ID AAD14511 standard; DNA; 1227 BP.
 DE Streptomyces clavuligerus ORF10 DNA downstream to pcbC gene.
 PN US6232106-B1.
 PD 15-MAY-2001.
 PA (UYAL-) UNIV ALBERTA.
 Best Local Similarity: 23.36% Mismatches: 83
 Query Match: 6.25% Indels: 91
 RESULT 456
 ID ADD26452 standard; DNA; 1227 BP.
 DE Streptomyces clavuligerus ORF10 DNA.
 PN US6589775-B1.
 PD 08-JUL-2003.
 PA (UYAL-) UNIV ALBERTA.
 Best Local Similarity: 23.36% Mismatches: 83
 Query Match: 6.25% Indels: 91
 RESULT 457
 ID ADG47797 standard; DNA; 1227 BP.
 DE Streptomyces clavuligerus 15 kb gene ORF10 DNA.
 PN US2003207411-A1.
 PD 06-NOV-2003.
 PA (UYAL-) UNIV ALBERTA.
 Best Local Similarity: 23.36% Mismatches: 83
 Query Match: 6.25% Indels: 91
 RESULT 458
 ID ACA62934 standard; DNA; 1227 BP.

DE DNA encoding clavulanic acid synthesis associated protein #10.
 PN US6514735-B1.
 PD 04-FEB-2003.
 PA (UYAL-) UNIV ALBERTA.
 Best Local Similarity: 23.36% Mismatches: 83
 Query Match: 6.25% Indels: 91
 RESULT 459
 ID ADO35847 standard; DNA; 1306 BP.
 DE Novel mouse gene sequence #520.
 PN WO2004046310-A2.
 PD 03-JUN-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 25.68% Mismatches: 81
 Query Match: 6.25% Indels: 67
 RESULT 460
 ID ADS95255 standard; DNA; 1306 BP.
 DE Murine therapeutic DNA sequence #51, SEQ ID 294.
 PN WO2004039319-A2.
 PD 13-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 25.68% Mismatches: 81
 Query Match: 6.25% Indels: 67
 RESULT 461
 ID ADS95254 standard; DNA; 1306 BP.
 DE Murine therapeutic DNA sequence #50, SEQ ID 293.
 PN WO2004039319-A2.
 PD 13-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Best Local Similarity: 25.68% Mismatches: 81
 Query Match: 6.25% Indels: 67
 RESULT 462
 ID ACC62239 standard; cDNA; 1374 BP.
 DE Human NOVI encoding cDNA SEQ ID NO:7.
 PN WO2003023001-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 21.79% Mismatches: 110
 Query Match: 6.25% Indels: 139
 RESULT 463
 ID ABD09708 standard; DNA; 1395 BP.
 DE Pseudomonas aeruginosa polynucleotide #8312.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.71% Mismatches: 80
 Query Match: 6.25% Indels: 61
 RESULT 464
 ID ABX06826 standard; DNA; 1422 BP.
 DE S. pneumoniae type 4 strain coding region #114.
 PN WO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Best Local Similarity: 23.15% Mismatches: 78
 Query Match: 6.25% Indels: 55
 RESULT 465
 ID AAS62247 standard; cDNA; 1468 BP.
 DE cDNA sequence #34 encoding novel human secreted protein.
 PN WO200177231-A2.
 PD 18-OCT-2001.
 PA (GENO-) INST GENOMIC RES.
 Best Local Similarity: 23.15% Mismatches: 78
 Query Match: 6.25% Indels: 55
 RESULT 466
 ID ABZ42437 standard; DNA; 1470 BP.
 DE Streptococcus pneumoniae polynucleotide SEQ ID NO 506.
 PN WO200283855-A2.
 PD 24-OCT-2002.
 PA (AMCY) AMERICAN CYANAMID CO.
 Best Local Similarity: 23.15% Mismatches: 78
 Query Match: 6.25% Indels: 55
 RESULT 467
 ID AAC66917 standard; cDNA; 1478 BP.

DE G-protein modulator GPMII coding sequence.
 PN WO20068249-A2.
 PD 16-NOV-2000.
 PA (MUSC-) MUSC FOUND RES DEV.
 PA (OSIP-) OSI PHARM INC.
 Best Local Similarity: 25.71% Mismatches: 53
 Query Match: 6.25% Indels: 74
 RESULT 468
 ID AAV52317 standard; DNA; 1590 BP.
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:184.
 PN WO9818931-A2.
 PD 07-MAY-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.15% Mismatches: 78
 Query Match: 6.25% Indels: 55
 RESULT 469
 ID ABD05065 standard; DNA; 1656 BP.
 DE Pseudomonas aeruginosa polynucleotide #3669.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.00% Mismatches: 95
 Query Match: 6.25% Indels: 45
 RESULT 470
 ID AAF54514 standard; DNA; 1797 BP.
 DE Fructan exohydrolase (FEH) coding sequence.
 PN WO200068402-A1.
 PD 16-NOV-2000.
 PA (LEUV-) LEUVEN RES & DEV.
 Best Local Similarity: 27.09% Mismatches: 117
 Query Match: 6.25% Indels: 73
 RESULT 471
 ID AAF565351 standard; cDNA; 1848 BP.
 DE DNA encoding novel human diagnostic protein #1155.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 27.00% Mismatches: 94
 Query Match: 6.25% Indels: 80
 RESULT 472
 ID ABV77856 standard; cDNA; 2061 BP.
 DE Human Eph receptor protein #1 coding sequence.
 PN WO200283735-A1.
 PD 24-OCT-2002.
 PA (TAKE-) TAKEDA CHEM IND LTD.
 Best Local Similarity: 27.33% Mismatches: 107
 Query Match: 6.25% Indels: 77
 RESULT 473
 ID ABD06745 standard; DNA; 2469 BP.
 DE Pseudomonas aeruginosa polynucleotide #5349.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.59% Mismatches: 99
 Query Match: 6.25% Indels: 97
 RESULT 474
 ID AAX01559 standard; cDNA to mRNA; 3003 BP.
 DE Bos taurus stialidase coding sequence.
 PN WO9853052-A1.
 PD 26-NOV-1998.
 PA (MIYA-) MIYAGI-KEN.
 Best Local Similarity: 27.83% Mismatches: 89
 Query Match: 6.25% Indels: 58
 RESULT 475
 ID ADC13560 standard; cDNA; 3117 BP.
 DE Human NOVX protein encoding cDNA sequence, SEQ ID No 39.
 PN WO2003004617-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 23.59% Mismatches: 93
 Query Match: 6.25% Indels: 105
 RESULT 476
 ID AAF74654 standard; DNA; 3186 BP.
 DE Reporter gene construct vector pTrap-Puro.

DE Mouse intracellular Na+ receptor GILT nucleotide sequence SEQ ID NO:1.
 PN WO200112805-A1.
 PD 22-FEB-2001.
 PA (UNSY) UNIV SYDNEY.
 Best Local Similarity: 25.71% Mismatches: 53
 Query Match: 6.25% Indels: 74
 RESULT 477
 ID AAD36958 standard; DNA; 3582 BP.
 DE Bacillus thuringiensis H04 hybrid toxin DNA #2.
 PN WO200215701-A2.
 PD 28-FEB-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 28.14% Mismatches: 84
 Query Match: 6.25% Indels: 51
 RESULT 478
 ID AAD36959 standard; DNA; 3582 BP.
 DE Bacillus thuringiensis H04 hybrid toxin DNA #3.
 PN WO200215701-A2.
 PD 28-FEB-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 28.14% Mismatches: 84
 Query Match: 6.25% Indels: 51
 RESULT 479
 ID ABD06588 standard; DNA; 5103 BP.
 DE Pseudomonas aeruginosa polynucleotide #5192.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.58% Mismatches: 99
 Query Match: 6.25% Indels: 97
 RESULT 480
 ID ACC44692 standard; DNA; 5192 BP.
 DE Plasmid pIRESpuo2 nucleotide sequence SEQ ID NO:88.
 PN WO200297059-A2.
 PD 05-DEC-2002.
 PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
 Best Local Similarity: 23.23% Mismatches: 97
 Query Match: 6.25% Indels: 72
 RESULT 481
 ID ADO47224 standard; DNA; 6280 BP.
 DE Nucleotide sequence of plasmid pCAR-IRES-puro (pCJ126).
 PN WO2004029249-A1.
 PD 08-APR-2004.
 PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
 Best Local Similarity: 23.23% Mismatches: 97
 Query Match: 6.25% Indels: 72
 RESULT 482
 ID ADO47201 standard; DNA; 6502 BP.
 DE Nucleotide sequence of plasmid pIRES-rtTA-puro.
 PN WO2004029249-A1.
 PD 08-APR-2004.
 PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
 Best Local Similarity: 23.23% Mismatches: 97
 Query Match: 6.25% Indels: 72
 RESULT 483
 ID AAC66821 standard; DNA; 6795 BP.
 DE Reporter gene construct vector pTrapsin-Puro3'5'.
 PN WO200061809-A2.
 PD 19-OCT-2000.
 PA (ICON-) ICONIX PHARM INC.
 Best Local Similarity: 23.23% Mismatches: 97
 Query Match: 6.25% Indels: 72
 RESULT 484
 ID AAC66822 standard; DNA; 6795 BP.
 DE Reporter gene construct vector pTrapsin-Puro 3'5'.
 PN WO200061809-A2.
 PD 19-OCT-2000.
 PA (ICON-) ICONIX PHARM INC.
 Best Local Similarity: 23.23% Mismatches: 97
 Query Match: 6.25% Indels: 72
 RESULT 485
 ID AAC66817 standard; DNA; 6795 BP.
 DE Reporter gene construct vector pTrap-Puro.

Query Match: 6.25% Indels: 89
 RESULT 505
 Best Local Similarity: 27.17% Mismatches: 90
 Query Match: 6.25% Indels: 67
 RESULT 506
 Best Local Similarity: 23.15% Mismatches: 78
 Query Match: 6.25% Indels: 55
 RESULT 507
 Best Local Similarity: 25.00% Mismatches: 92
 Query Match: 6.25% Indels: 80
 RESULT 508
 ID ABD04678 standard; DNA; 732 BP.
 DE Pseudomonas aeruginosa polynucleotide #3282.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.18% Mismatches: 68
 Query Match: 6.22% Indels: 54
 RESULT 509
 ID AAF94099 standard; DNA; 744 BP.
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 533.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 35.11% Mismatches: 41
 Query Match: 6.22% Indels: 10
 RESULT 510
 ID ABD04653 standard; DNA; 771 BP.
 DE Pseudomonas aeruginosa polynucleotide #3257.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.18% Mismatches: 68
 Query Match: 6.22% Indels: 54
 RESULT 511
 ID ADA70416 standard; DNA; 849 BP.
 DE Rice gene, SEQ ID 3739.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 22.01% Mismatches: 97
 Query Match: 6.22% Indels: 78
 RESULT 512
 ID ABD04612 standard; DNA; 939 BP.
 DE Pseudomonas aeruginosa polynucleotide #3216.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.18% Mismatches: 68
 Query Match: 6.22% Indels: 54
 RESULT 513
 ID ABD04823 standard; DNA; 945 BP.
 DE Pseudomonas aeruginosa polynucleotide #3427.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.18% Mismatches: 68
 Query Match: 6.22% Indels: 54
 RESULT 514
 ID AAJ38398 standard; DNA; 999 BP.
 DE ORF2-16 encoding Pseudomonas bto gene cluster regulator, SEQ ID NO:18.
 PN JP2000093180-A.
 PD 04-APR-2000.
 PA (TOFU) TONEN CORP.
 Best Local Similarity: 27.90% Mismatches: 90
 Query Match: 6.22% Indels: 49
 RESULT 515
 ID ABD01961 standard; DNA; 1182 BP.
 DE Pseudomonas aeruginosa polynucleotide #565.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.10% Mismatches: 97

Query Match: 6.22% Indels: 83
 RESULT 516
 ID ABD01915 standard; DNA; 1206 BP.
 DE Pseudomonas aeruginosa polynucleotide #519.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.10% Mismatches: 97
 Query Match: 6.22% Indels: 83
 RESULT 517
 ID AAQ10168 standard; DNA; 1236 BP.
 DE Encodes Pro-urokinase derivative UK-T6 with Thr at position 155.
 PN EP405285-A.
 PD 02-JAN-1991.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 25.93% Mismatches: 95
 Query Match: 6.22% Indels: 42
 RESULT 518
 ID ABD04512 standard; DNA; 1365 BP.
 DE Pseudomonas aeruginosa polynucleotide #3116.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 28.27% Mismatches: 102
 Query Match: 6.22% Indels: 43
 RESULT 519
 ID AD743155 standard; cDNA; 1407 BP.
 DE Bacterial polynucleotide #17906.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Best Local Similarity: 25.61% Mismatches: 96
 Query Match: 6.22% Indels: 64
 RESULT 520
 ID ABD10344 standard; DNA; 1746 BP.
 DE Pseudomonas aeruginosa polynucleotide #8948.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.10% Mismatches: 93
 Query Match: 6.22% Indels: 58
 RESULT 521
 ID AAD33813 standard; cDNA; 1785 BP.
 DE Human secreted protein-encoding gene 2 cDNA clone HDQF073, SEQ ID NO:12.
 PN WO200224719-A1.
 PD 28-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 26.19% Mismatches: 114
 Query Match: 6.22% Indels: 78
 RESULT 522
 ID ADA48715 standard; DNA; 1821 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 21.74% Mismatches: 112
 Query Match: 6.22% Indels: 108
 RESULT 523
 ID ADA71198 standard; DNA; 1850 BP.
 DE Rice gene, SEQ ID 4521.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 21.74% Mismatches: 112
 Query Match: 6.22% Indels: 108
 RESULT 524
 ID ABD07145 standard; DNA; 2115 BP.
 DE Pseudomonas aeruginosa polynucleotide #5749.
 PN US6551795-B1.

PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.62% Mismatches: 71
Query Match: 6.22% Indels: 52
RESULT 525
ID ABD07103 standard; DNA; 2160 BP.
DE Pseudomonas aeruginosa polynucleotide #5707.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.62% Mismatches: 71
Query Match: 6.22% Indels: 52
RESULT 526
ID ABD01889 standard; DNA; 2181 BP.
DE Pseudomonas aeruginosa polynucleotide #493.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.10% Mismatches: 97
Query Match: 6.22% Indels: 83
RESULT 527
ID ABD02005 standard; DNA; 2196 BP.
DE Pseudomonas aeruginosa polynucleotide #609.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.10% Mismatches: 97
Query Match: 6.22% Indels: 83
RESULT 528
ID ABD1680 standard; DNA; 2319 BP.
DE Pseudomonas aeruginosa polynucleotide #15284.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 22.85% Mismatches: 138
Query Match: 6.22% Indels: 88
RESULT 529
ID ABL04363 standard; cDNA; 2349 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7571.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 21.31% Mismatches: 105
Query Match: 6.22% Indels: 129
RESULT 530
ID ABD1672 standard; DNA; 2427 BP.
DE Pseudomonas aeruginosa polynucleotide #15396.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 22.85% Mismatches: 138
Query Match: 6.22% Indels: 88
RESULT 531
ID AAF93893 standard; cDNA; 2492 BP.
DE Human cDNA encoding a membrane or secretory protein clone PSEC0260.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 35.11% Mismatches: 41
Query Match: 6.22% Indels: 10
RESULT 532
ID AAAG2031 standard; DNA; 2495 BP.
DE Hydrophobic domain protein cDNA HP03140 isolated from HT-1080 cells.
PN WO20029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Best Local Similarity: 35.11% Mismatches: 41
Query Match: 6.22% Indels: 10
RESULT 533
ID ADE07431 standard; DNA; 2503 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #497.
PN WO2003054152-A2.

PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 35.11% Mismatches: 41
Query Match: 6.22% Indels: 10
RESULT 534
ID ADS10265 standard; DNA; 2531 BP.
DE Human therapeutic DNA - SEQ ID 502.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Best Local Similarity: 35.11% Mismatches: 41
Query Match: 6.22% Indels: 10
RESULT 535
ID ABD17466 standard; DNA; 2631 BP.
DE Pseudomonas aeruginosa polynucleotide #16070.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.89% Mismatches: 99
Query Match: 6.22% Indels: 45
RESULT 536
ID ADG63409 standard; cDNA; 2663 BP.
DE Novel human cDNA sequence #570.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 24.21% Mismatches: 120
Query Match: 6.22% Indels: 62
RESULT 537
ID ADL35972 standard; cDNA; 2707 BP.
DE Human NOVX cDNA #9.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY-) MALYANKAR U M.
PA (SHEN-) SHENOY S G.
PA (SPYT-) SPYTEK K A.
PA (ZERH-) ZERHUSEN B D.
PA (PATT-) PATTURAJAN M.
PA (GUOX-) GUO X.
PA (KEKU-) KEKUDA R.
PA (GANG-) GANGOLLI E A.
PA (SHIM-) SHIMKETS R A.
PA (TAUP-) TAUPIER R J.
PA (LILL-) LI L.
PA (PADI-) PADIGARU M.
Best Local Similarity: 23.91% Mismatches: 90
Query Match: 6.22% Indels: 98
RESULT 538
ID ABS71696 standard; DNA; 2713 BP.
DE DNA encoding human NOV3 protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 23.91% Mismatches: 90
Query Match: 6.22% Indels: 98
RESULT 539
ID AAS84436 standard; cDNA; 2807 BP.
DE DNA encoding novel human diagnostic protein #20240.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.55% Mismatches: 99
Query Match: 6.22% Indels: 105
RESULT 540
ID AAH18697 standard; cDNA; 2947 BP.
DE Human cDNA sequence SEQ ID NO:18960.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 23.91% Mismatches: 90
Query Match: 6.22% Indels: 98
RESULT 541
ID ACN37482 standard; cDNA; 3275 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 542
ID ABD04153 standard; DNA; 3291 BP.
DE Pseudomonas aeruginosa polynucleotide #2757.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 28.2% Mismatches: 102
Query Match: 6.22% Indels: 43
RESULT 543
ID ADT46154 standard; cDNA; 3318 BP.
DE Bacterial polynucleotide #20905.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.31% Mismatches: 86
Query Match: 6.22% Indels: 84
RESULT 544
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMCAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 545
ID AAA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 546
ID ABK69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 547
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 548
ID ADA43748 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 549
ID ADA43516 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 550
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 551
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 552
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 553
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 554
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 555
ID AD899675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 556
ID AD886958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 557
ID AD866113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 558
ID AD899791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97

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RESULT 559
ID ADB99446 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003082731-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 560
ID ADB65997 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 561
ID ADC23395 standard; cDNA; 3476 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 562
ID ADC26088 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003073194-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 563
ID ADE04915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068778-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 564
ID ADE11221 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073191-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 565
ID ADD88152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082733-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 566
ID ADD95447 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 567
ID ADE06377 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073195-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 568
ID ADE37676 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073198-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 569
ID ADD8268 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073189-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 570
ID ADD90849 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 571
ID ADF99404 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 572
ID ADG06497 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077742-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 573
ID ADG05448 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077741-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 574
ID ADG82449 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077744-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 575
ID ADE51702 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 576
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatches: 100
Indels: 97
RESULT 577
ID ADE37676 standard; cDNA; 3476 BP.
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DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 578
ID ADE37560 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 579
ID ADE95331 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 580
ID ADE38031 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 581
ID ADE76120 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 582
ID ADE39443 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 583
ID ADE04247 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 584
ID ADE39844 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 585
ID ADE19709 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 586
ID ADE77287 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 587
ID ADE65395 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 588
ID ADE76004 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 589
ID ADE37915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 590
ID ADE64525 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 591
ID ADE38860 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 592
ID ADE51934 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 593
ID ADD90965 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 594
ID ADE38744 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 595
ID ADE37444 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.

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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 596
ID ADE06261 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 597
ID ADD90120 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 598
ID ADE38628 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 599
ID ADE39559 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 600
ID ADD89164 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 601
ID ADD88931 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 602
ID ADE19825 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 603
ID ADE77403 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 604
ID ADE65279 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 605
ID ADE39327 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 606
ID ADE38512 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 607
ID ADG11065 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 608
ID ADG10949 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 609
ID ADH31477 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 610
ID ADH38725 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 611
ID ADH29360 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 612
ID ADH23663 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 22.30%
Query Match: 6.22%
Mismatch: 100
Indel: 97
RESULT 613
ID ADH26993 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 614
ID ADH38261 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 615
ID ADH26877 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 616
ID ADH38145 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 617
ID ADH38841 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 618
ID ADH23779 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 619
ID ADH40155 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 620
ID ADH40039 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 621
ID ADH31361 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 622
ID ADH29239 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97

Query Match: 6.22% Indels: 97
RESULT 623
ID ADH49454 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 624
ID ADH51918 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 625
ID ADH49773 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 626
ID ADH52374 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 627
ID ADH52490 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 628
ID ADH58487 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 629
ID ADH51802 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 630
ID ADH58363 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97
RESULT 631
ID ADH13560 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 22.30% Mismatches: 100
Query Match: 6.22% Indels: 97

AAA38389 standard; DNA; 11279 bp.
Pseudomonas sp. WF505 bto gene cluster, SEQ ID NO:1.
JP2000093180-A.

Best Local Similarity: 25.24% Mismatches: 78
 Query Match: 6.18% Indels: 61
 RESULT 652
 ID ADT45715 standard; cDNA; 918 BP.
 DE Bacterial polynucleotide #20466.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 25.65% Mismatches: 113
 Query Match: 6.18% Indels: 48
 RESULT 653
 ID AAS02050 standard; cDNA; 1100 BP.
 DE DNA encoding molecule for disease detection and treatment, mddt15.
 PN WO200123538-A2.
 PD 05-APR-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 25.24% Mismatches: 78
 Query Match: 6.18% Indels: 61
 RESULT 654
 ID AA288362 standard; cDNA; 1296 BP.
 DE Human preprouroukinase CT92 nucleotide sequence.
 PN WO200000624-A1.
 PD 06-JAN-2000.
 PA (CROP-) CROPTCH DEV CORP.
 Best Local Similarity: 23.35% Mismatches: 95
 Query Match: 6.18% Indels: 75
 RESULT 655
 ID ADS61687 standard; cDNA; 1341 BP.
 DE Bacterial polynucleotide #13674.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 26.72% Mismatches: 89
 Query Match: 6.18% Indels: 50
 RESULT 656
 ID ABD02559 standard; DNA; 1746 BP.
 DE Pseudomonas aeruginosa polynucleotide #1163.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 21.69% Mismatches: 95
 Query Match: 6.18% Indels: 84
 RESULT 657
 ID ADE61842 standard; DNA; 1795 BP.
 DE Human gene M31222, SEQ ID NO 7771.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Best Local Similarity: 26.95% Mismatches: 107
 Query Match: 6.18% Indels: 72
 RESULT 658
 ID ADG91045 standard; DNA; 1808 BP.
 DE Hepatic specific nucleic acid encoding sequence #234.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Best Local Similarity: 27.18% Mismatches: 91
 Query Match: 6.18% Indels: 30
 RESULT 659
 ID AA251001 standard; DNA; 1980 BP.
 DE X. oryzae avrExo repeat domain DNA.
 PN WO200009698-A2.
 PD 24-FEB-2000.
 PA (UNIV) UNIV KANSAS STATE RES FOUND.

Best Local Similarity: 24.15% Mismatches: 107
 Query Match: 6.18% Indels: 84
 RESULT 660
 ID AAS72743 standard; cDNA; 2130 BP.
 DE DNA encoding novel human diagnostic protein #8547.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 26.29% Mismatches: 81
 Query Match: 6.18% Indels: 24
 RESULT 661
 ID ABD07081 standard; DNA; 2190 BP.
 DE Pseudomonas aeruginosa polynucleotide #5685.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.64% Mismatches: 80
 Query Match: 6.18% Indels: 50
 RESULT 662
 ID AAN92085 standard; DNA; 2579 BP.
 DE ORF of the HCV cDNA in clones 40b, 37b 35, 36, 81, 32, 33b and 25c.
 PN EP318216-A.
 PD 31-MAY-1989.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 663
 ID AAN90315 standard; cDNA; 2579 BP.
 DE Hepatitis CDNA virus combined ORF.
 PN GB212511-A.
 PD 26-JUL-1989.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 664
 ID ABQ90126 standard; DNA; 2778 BP.
 DE M. capsulatus gene #111 for DNA array.
 PN WO200255655-A2.
 PD 18-JUL-2002.
 PA (UNIP-) UNIFOB STIFTELSEN UNIV BERGEN.
 Best Local Similarity: 24.26% Mismatches: 105
 Query Match: 6.18% Indels: 73
 RESULT 665
 ID ABD15601 standard; DNA; 2850 BP.
 DE Pseudomonas aeruginosa polynucleotide #14205.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.74% Mismatches: 77
 Query Match: 6.18% Indels: 95
 RESULT 666
 ID ACN92869 standard; DNA; 3072 BP.
 DE Breast cancer related marker, seq id 14019.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 28.51% Mismatches: 102
 Query Match: 6.18% Indels: 38
 RESULT 667
 ID ADR07958 standard; cDNA; 3329 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1464.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 24.31% Mismatches: 109
 Query Match: 6.18% Indels: 82
 RESULT 668
 ID AA251000 standard; DNA; 3720 BP.
 DE X. oryzae avrXol gene.
 PN WO200009698-A2.
 PD 24-FEB-2000.

PA (UNIV) UNIV KANSAS STATE RES FOUND.
Best Local Similarity: 24.15% Mismatches: 107
Query Match: 6.18% Indels: 84
RESULT 669
ID ABL24247 standard; DNA; 4140 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24214.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 22.50% Mismatches: 80
Query Match: 6.18% Indels: 75
RESULT 670
ID ABD07126 standard; DNA; 4647 BP.
DE Pseudomonas aeruginosa polynucleotide #5730.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 26.64% Mismatches: 80
Query Match: 6.18% Indels: 50
RESULT 671
ID AAS75115 standard; cDNA; 5232 BP.
DE DNA encoding novel human diagnostic protein #10919.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 21.24% Mismatches: 125
Query Match: 6.18% Indels: 89
RESULT 672
ID AAN92097 standard; DNA; 5300 BP.
DE Hepatitis C virus (HCV) cDNA clone.
PN EP318216-A.
PD 31-MAY-1989.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 673
ID AAN90327 standard; cDNA; 5360 BP.
DE Hepatitis C virus composite probe.
PN GB2212511-A.
PD 26-JUL-1989.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 674
ID ADI34635 standard; DNA; 5676 BP.
DE HCV modified fusion protein encoding DNA.
PN WO2004005473-A2.
PD 15-JAN-2004.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 675
ID ADO00773 standard; DNA; 5676 BP.
DE HCV NS345Core fusion protein encoding DNA SEQ ID NO:7.
PN WO2004039950-A2.
PD 13-MAY-2004.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 676
ID ADS75100 standard; DNA; 6233 BP.
DE Plasmid PCR-XL-TOPO-CMV-pur-attB.
PN WO2004080162-A2.
PD 23-SEP-2004.
PA (AVIG-) AVIGENICS INC.
Best Local Similarity: 23.27% Mismatches: 103
Query Match: 6.18% Indels: 82
RESULT 677
ID AAN92103 standard; DNA; 6905 BP.
DE Combined ORFs of the HCV cDNAs from clones 12f through 15e.
PN EP318216-A.
PD 31-MAY-1989.

PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 678
ID AAN92106 standard; DNA; 7310 BP.
DE Combined ORFs of the HCV cDNAs from clones K9-1 through 15e.
PN EP318216-A.
PD 31-MAY-1989.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 679
ID AAN90336 standard; DNA; 7310 BP.
DE Composite hepatitis C virus (HCV) cDNA.
PN GB2212511-A.
PD 26-JUL-1989.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 680
ID AAQ98221 standard; cDNA to mRNA; 7310 BP.
DE Hepatitis C virus clone genome.
PN US5443965-A.
PD 22-AUG-1995.
PA (GENE-) GENELABS INC.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 681
ID AAQ05955 standard; cDNA; 8316 BP.
DE Hepatitis C virus open reading frame.
PN EP388232-A.
PD 19-SEP-1990.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 682
ID AAA75296 standard; cDNA; 8316 BP.
DE cDNA sequence compiled Hepatitis C virus cDNA clones.
PN EP1034785-A2.
PD 13-SEP-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 683
ID ADN35977 standard; cDNA; 8316 BP.
DE HCV cDNA clone #1.
PN EP1394255-A2.
PD 03-MAR-2004.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 684
ID AAZ07656 standard; DNA; 9133 BP.
DE Nucleotide sequence of HCV-1 ORF.
PN EP939128-A2.
PD 01-SEP-1999.
PA (OYAA/) OYA A.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 685
ID AAQ05956 standard; DNA; 9185 BP.
DE Sense strand of the compiled Hepatitis C virus cDNA sequence.
PN EP388232-A.
PD 19-SEP-1990.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 22.07% Mismatches: 103
Query Match: 6.18% Indels: 45
RESULT 686
ID AAQ10566 standard; DNA; 9185 BP.
DE Hepatitis C virus strain 1 DNA.

PN EP414475-A.
 PD 27-FEB-1991.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 687
 ID AAX00459 standard; DNA; 9185 BP.
 DE Hepatitis C virus 1 ORF1.
 PN US5856437-A.
 PD 05-JAN-1999.
 PA (NAHE-) NAT INST OF HEALTH JAPAN.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 688
 ID AAX26737 standard; DNA; 9185 BP.
 DE Nucleotide sequence of the ORF of HCV1.
 PN US5871903-A.
 PD 16-FEB-1999.
 PA (NAHE-) NAT INST OF HEALTH JAPAN.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 689
 ID ADF6068 standard; DNA; 9185 BP.
 DE Hepatitis C virus 1 ORF nucleotide sequence.
 PN US5959092-A.
 PD 28-SEP-1999.
 PA (CHIR) CHIRON CORP.
 PA (NAHE-) NAT INST OF HEALTH JAPAN.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 690
 ID AAA75297 standard; cDNA; 9185 BP.
 DE Sense strand of HCV encoding a polyprotein.
 PN EP1034785-A2.
 PD 13-SEP-2000.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 691
 ID ADN35979 standard; cDNA; 9185 BP.
 DE HCV cDNA clone #2.
 PN EP1394255-A2.
 PD 03-MAR-2004.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 692
 ID AAQ36209 standard; DNA; 9379 BP.
 DE Composite cDNA for Hepatitis C virus (HCV) type 1.
 PN WO9300365-A2.
 PD 07-JAN-1993.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 693
 ID AAQ21744 standard; DNA; 9400 BP.
 DE Compiled HCV cDNA.
 PN WO9202642-A.
 PD 20-FEB-1992.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 694
 ID AAL12710 standard; cDNA; 9401 BP.
 DE Hepatitis C virus polyprotein.
 PN EP693687-A1.
 PD 24-JAN-1996.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 695

ID AAT99981 standard; DNA; 9401 BP.
 DE HCV polyprotein coding sequence.
 PN US5683864-A.
 PD 04-NOV-1997.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 696
 ID AAV09989 standard; DNA; 9401 BP.
 DE HCV polyprotein coding sequence DNA.
 PN US5712087-A.
 PD 27-JAN-1998.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 697
 ID AAD35043 standard; cDNA; 9401 BP.
 DE Hepatitis C virus (HCV) polyprotein cDNA.
 PN US6312889-B1.
 PD 06-NOV-2001.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 698
 ID ADU23106 standard; DNA; 9401 BP.
 DE Hepatitis C virus genomic DNA sequence SeqID 1.
 PN WO2004003141-A2.
 PD 08-JAN-2004.
 PA (IOWA) UNIV IOWA RES FOUND.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 699
 ID ADR29358 standard; DNA; 9401 BP.
 DE Hepatitis C virus polyprotein precursor encoding DNA SEQ ID NO:2.
 PN WO2004071414-A2.
 PD 26-AUG-2004.
 PA (GENZ) GENZYME CORP.
 PA (GSHO) GEN HOSPITAL CORP DBA MASSACHUSETTS GEN.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 700
 ID ADN33102 standard; DNA; 9618 BP.
 DE Hepatitis C virus detection method-related gene.
 PN KR2002034759-A.
 PD 09-MAY-2002.
 PA (DONG-) DONG WHA PHARM IND CO LTD.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 701
 ID AAF83667 standard; DNA; 9620 BP.
 DE HCV delNS35 ORF comprising pCMV-delNS35 nucleic acid sequence.
 PN WO200138360-A2.
 PD 31-MAY-2001.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 702
 ID AAF83666 standard; DNA; 9620 BP.
 DE HCV NS35 ORF comprising pCMV-NS35 nucleic acid sequence.
 PN WO200138360-A2.
 PD 31-MAY-2001.
 PA (CHIR) CHIRON CORP.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.18% Indels: 45
 RESULT 703
 ID ADF44493 standard; cDNA; 10655 BP.
 DE Mouse kinase protein encoding cDNA SEQ ID NO:11.
 PN WO2003084992-A1.
 PD 16-OCT-2003.
 PA (RIKE) RIKEN KK.
 PA (DNAP-) DNAFORM KK.
 PA (MITU) MITSUBISHI CHEM CORP.
 Best Local Similarity: 28.69% Mismatches: 77

Query Match:	6.18%	Indels:	69
RESULT 704			
ID AAV59364 standard; cDNA; 12980 BP.			
DE Hepatitis C virus clone p90/HCVFlong pu cDNA.			
PN WO9839031-A1.			
PD 11-SEP-1998.			
PA (UNIW) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 705			
ID ABK67286 standard; cDNA; 12980 BP.			
DE Hepatitis C virus plasmid p90/HCVFlongpu cDNA sequence.			
PN US6392028-B1.			
PD 21-MAY-2002.			
PA (UNIW) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 706			
ID ACA62469 standard; DNA; 12980 BP.			
DE DNA encoding p90/HCVFlong pu.			
PN US2003028010-A1.			
PD 06-FEB-2003.			
PA (UNIW) UNIV WASHINGTON.			
Best Local Similarity: 22.07%		Mismatches:	102
Query Match:	6.18%	Indels:	45
RESULT 707			
ID ADS75098 standard; DNA; 17402 BP.			
DE Plasmid pOMIFN-Ins-CMV-pur-attB.			
PN WO2004080162-A2.			
PD 23-SEP-2004.			
PA (AVIG-) AVIGENICS INC.			
Best Local Similarity: 23.27%		Mismatches:	103
Query Match:	6.18%	Indels:	82
RESULT 708			
ID ADS75097 standard; DNA; 18116 BP.			
DE Plasmid p12.0-lys-LSPINNM-CMV-pur-attB.			
PN WO2004080162-A2.			
PD 23-SEP-2004.			
PA (AVIG-) AVIGENICS INC.			
Best Local Similarity: 23.27%		Mismatches:	103
Query Match:	6.18%	Indels:	82
RESULT 709			
ID AAF83671 standard; DNA; 19798 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 710			
ID AAF83670 standard; DNA; 19912 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 711			
ID AAF83672 standard; DNA; 20160 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.core121.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 712			
ID AAF83674 standard; DNA; 20217 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.core140.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 713			
ID AAF83675 standard; DNA; 20247 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.core150.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 714			
ID AAF83673 standard; DNA; 20316 BP.			
DE Nucleic acid sequence of pd.deltans3NS5.pj.core173.			
PN WO200138360-A2.			
PD 31-MAY-2001.			
PA (CHIR) CHIRON CORP.			
Best Local Similarity: 22.07%		Mismatches:	103
Query Match:	6.18%	Indels:	45
RESULT 715			
ID ABO72998 standard; cDNA; 27754 BP.			
DE Human transporter protein encoding DNA SEQ ID NO:3.			
PN WO20025703-A2.			
PD 18-JUL-2002.			
PA (PEKE) PE CORP NY.			
Best Local Similarity: 24.55%		Mismatches:	81
Query Match:	6.18%	Indels:	54
RESULT 716			
ID AAQ46806 standard; DNA; 29879 BP.			
DE eryA region of S. erythraea chromosome.			
PN WO9313663-A1.			
PD 22-JUL-1993.			
PA (ABBO) ABBOTT LAB.			
Best Local Similarity: 21.58%		Mismatches:	104
Query Match:	6.18%	Indels:	47
RESULT 717			
ID ADL27113 standard; DNA; 31631 BP.			
DE Mouse genomic sequence for RORC.			
PN US2003216558-A1.			
PD 20-NOV-2003.			
PA (MORR/) MORRIS D W.			
Best Local Similarity: 26.20%		Mismatches:	91
Query Match:	6.18%	Indels:	80
RESULT 718			
ID AAX23517 standard; DNA; 50000 BP.			
DE Human kidney aminopeptidase P genomic DNA fragment 1.			
PN WO9911799-A2.			
PD 11-MAR-1999.			
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.			
Best Local Similarity: 23.39%		Mismatches:	77
Query Match:	6.18%	Indels:	88
RESULT 719			
ID ABL62723 standard; DNA; 66109 BP.			
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1060.			
PN WO200194629-A2.			
PD 13-DEC-2001.			
PA (AVAL-) AVALON PHARM.			
Best Local Similarity: 27.03%		Mismatches:	95
Query Match:	6.18%	Indels:	70
RESULT 720			
ID ABN97273 standard; DNA; 66109 BP.			
DE Gene #3771 used to diagnose liver cancer.			
PN WO200229103-A2.			
PD 11-APR-2002.			
PA (GENE-) GENE LOGIC INC.			
Best Local Similarity: 27.03%		Mismatches:	95
Query Match:	6.18%	Indels:	70
RESULT 721			
ID ADR52892 standard; DNA; 151152 BP.			
DE Drug therapy altered expressed gene #243.			
PN WO2004072265-A2.			
PD 26-AUG-2004.			
PA (AMHP) WYETH.			
PA (BURC/) BURCZYNSKI M.			
PA (TWIN/) TWINE N.			

PA (DORN/) DORNER A J.
 PA (TREP/) TREPICCHIO W L.
 Best Local Similarity: 23.3% Mismatches: 77
 Query Match: 6.1% Indels: 88
 RESULT 722
 ID ABX84699 standard; cDNA; 198285 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1270.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 27.0% Mismatches: 95
 Query Match: 6.1% Indels: 70
 RESULT 723
 ID ABN97319 standard; DNA; 198285 BP.
 DE Gene #3817 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 27.0% Mismatches: 95
 Query Match: 6.1% Indels: 70
 RESULT 724
 ID ADR52987 standard; DNA; 198285 BP.
 DE Drug therapy altered expressed gene #338.
 PN WO200407265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.
 PA (BURC) BURCZYNSKI M.
 PA (TWIN) TWINE N.
 PA (DORN/) DORNER A J.
 PA (TREP/) TREPICCHIO W L.
 Best Local Similarity: 27.0% Mismatches: 95
 Query Match: 6.1% Indels: 70
 RESULT 725
 ID ADR65058 standard; cDNA; 729 BP.
 DE Cotton cDNA sequence, SEQ ID 5839.
 PN US200418130-A1.
 PD 16-SEP-2004.
 PA (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAOY/) CAO Y.
 Best Local Similarity: 24.3% Mismatches: 104
 Query Match: 6.1% Indels: 41
 RESULT 726
 ID ACA25241 standard; DNA; 909 BP.
 DE Prokaryotic essential gene #698.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 24.5% Mismatches: 81
 Query Match: 6.1% Indels: 61
 RESULT 727
 ID AAV15072 standard; DNA; 922 BP.
 DE Hybrid DNA comprising a family 45 cellulase core region.
 PN WO9743409-A2.
 PD 20-NOV-1997.
 PA (NOVO) NOVO-NORDISK AS.
 Best Local Similarity: 21.6% Mismatches: 88
 Query Match: 6.1% Indels: 52
 RESULT 728
 ID ADE64174 standard; DNA; 981 BP.
 DE Human gene L36318, SEQ ID NO 10126.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Best Local Similarity: 26.9% Mismatches: 70
 Query Match: 6.1% Indels: 70
 RESULT 729
 ID ADE64170 standard; DNA; 981 BP.
 DE Human gene L36318, SEQ ID NO 10122.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
 Best Local Similarity: 26.9% Mismatches: 70
 Query Match: 6.1% Indels: 70
 RESULT 730
 ID ABD11890 standard; DNA; 993 BP.
 DE Pseudomonas aeruginosa polynucleotide #10494.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.1% Mismatches: 88
 Query Match: 6.1% Indels: 50
 RESULT 731
 ID AAS68339 standard; cDNA; 1128 BP.
 DE DNA encoding novel human diagnostic protein #4143.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 18.5% Mismatches: 78
 Query Match: 6.1% Indels: 88
 RESULT 732
 ID ACA43475 standard; DNA; 1140 BP.
 DE Prokaryotic essential gene #25132.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.1% Mismatches: 91
 Query Match: 6.1% Indels: 47
 RESULT 733
 ID AAZ88364 standard; cDNA; 1239 BP.
 DE Human prourokinase CT97 nucleotide sequence.
 PN WO200000624-A1.
 PD 06-JAN-2000.
 PA (CROP-) CROPTTECH DEV CORP.
 Best Local Similarity: 24.3% Mismatches: 87
 Query Match: 6.1% Indels: 62
 RESULT 734
 ID AAZ88363 standard; cDNA; 1305 BP.
 DE Patatin signal peptide and prourokinase CT111 nucleotide sequence.
 PN WO200000624-A1.
 PD 06-JAN-2000.
 PA (CROP-) CROPTTECH DEV CORP.
 Best Local Similarity: 24.3% Mismatches: 87
 Query Match: 6.1% Indels: 62
 RESULT 735
 ID ADS55918 standard; cDNA; 1488 BP.
 DE Bacterial polynucleotide #7905.
 PN US200233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 25.3% Mismatches: 100
 Query Match: 6.1% Indels: 53
 RESULT 736
 ID AAH14085 standard; cDNA; 1771 BP.
 DE Human cDNA sequence SEQ ID NO:11244.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 28.3% Mismatches: 89
 Query Match: 6.1% Indels: 55
 RESULT 737
 ID ADT44736 standard; cDNA; 1788 BP.
 DE Bacterial polynucleotide #19487.
 PN US200333675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

Best Local Similarity: 24.69% Mismatches: 67
Query Match: 6.15% Indels: 78
RESULT 738
ID AAX23753 standard; DNA; 1821 BP.
DE Rice anthranilate synthase second isozyme alpha-subunit DNA.
PD WO9511800-A1.
PD 11-MAR-1999.
PA (HOKK) HOKKO CHEM IND CO LTD.
PA (NORR) JAPAN MIN AGRIC FORESTRY & FISHERIES.
Best Local Similarity: 21.74% Mismatches: 112
Query Match: 6.15% Indels: 108
RESULT 739
ID AD50711 standard; DNA; 1821 BP.
DE Rice anthranilate synthase DNA.
PD WO200290497-A2.
PD 14-NOV-2002.
PA (RENE-) RENESSEN LLC.
PA (MONS) MONSANTO CO.
PA (WEAV-) WEAVER L M.
PA (LIAN-) LIANG J.
PA (CHEN-) CHEN R.
PA (JEON-) JEONG S S.
PA (MITS-) MITSKY T.
PA (SLAT-) SLATER S.
PA (RAPP-) RAPP W.
Best Local Similarity: 21.74% Mismatches: 112
Query Match: 6.15% Indels: 108
RESULT 740
ID ADO05512 standard; DNA; 1821 BP.
DE Rice anthranilate synthase DNA, SEQ:94.
PD WO2003092363-A2.
PD 13-NOV-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Best Local Similarity: 21.74% Mismatches: 112
Query Match: 6.15% Indels: 108
RESULT 741
ID ABD13200 standard; DNA; 1866 BP.
DE Pseudomonas aeruginosa polynucleotide #11804.
PD US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.92% Mismatches: 83
Query Match: 6.15% Indels: 114
RESULT 742
ID ADQ87560 standard; cDNA; 1868 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4438.
PD WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Best Local Similarity: 26.97% Mismatches: 75
Query Match: 6.15% Indels: 84
RESULT 743
ID ABN59958 standard; cDNA; 1915 BP.
DE Novel human coding sequence SEQ ID NO: 369.
PD WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 28.38% Mismatches: 89
Query Match: 6.15% Indels: 55
RESULT 744
ID ADG32679 standard; DNA; 1940 BP.
DE Human DNA differentially expressed in patients with SLE SeqID3.
PD WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 745
ID ADG33091 standard; DNA; 1940 BP.
DE Human DNA differentially expressed in patients with SLE SeqID415.
PD WO2003090694-A2.

PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 746
ID ADJ74893 standard; DNA; 1940 BP.
DE Marker gene SEQ ID NO:145.
PD EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 747
ID ADJ74967 standard; DNA; 1940 BP.
DE Marker gene SEQ ID NO:219.
PD EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 748
ID ADJ83069 standard; cDNA; 1940 BP.
DE Human PRO3673 cDNA, SEQ ID 271.
PD WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 749
ID ADN04326 standard; cDNA; 1940 BP.
DE Antipsoriatic cDNA sequence #363.
PD WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 750
ID ADP24097 standard; cDNA; 1940 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1275.
PD WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 751
ID ABD13031 standard; DNA; 1941 BP.
DE Pseudomonas aeruginosa polynucleotide #11635.
PD US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.92% Mismatches: 83
Query Match: 6.15% Indels: 114
RESULT 752
ID ACN41685 standard; cDNA; 2381 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:550.
PD WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.23% Mismatches: 92
Query Match: 6.15% Indels: 41
RESULT 753
ID ADQ63792 standard; cDNA; 2438 BP.
DE Novel human cDNA sequence #953.
PD EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 21.20% Mismatches: 89
Query Match: 6.15% Indels: 99
RESULT 754
ID ACN41683 standard; cDNA; 2606 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:559.
PD WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
 Best Local Similarity: 24.54% Mismatches: 110
 Query Match: 6.15% Indels: 62
 RESULT 755
 ID ACN41682 standard; cDNA; 2608 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:557.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 24.54% Mismatches: 110
 Query Match: 6.15% Indels: 62
 RESULT 756
 ID AAQ06631 standard; DNA; 2614 BP.
 DE Gene conferring teicoplanin resistance.
 PN EP393328-A.
 PD 28-NOV-1990.
 PA (LEPE) GRUPPO LEPETIT SPA.
 Best Local Similarity: 27.40% Mismatches: 82
 Query Match: 6.15% Indels: 54
 RESULT 757
 ID ADC72232 standard; DNA; 2691 BP.
 DE Human NR3B gene SEQ ID NO:9.
 PN WO2003016479-A2.
 PD 27-FEB-2003.
 PA (BURN-) BURNHAM INST.
 PA (UYVA) UNIV YALE.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 758
 ID ADN49187 standard; cDNA; 2706 BP.
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.
 PN US2004033500-A1.
 PD 19-FEB-2004.
 PA (BURN-) BURNHAM INST.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 759
 ID AAL47419 standard; cDNA; 2706 BP.
 DE Human N-methyl-D-aspartate receptor coding sequence.
 PN WO200240538-A2.
 PD 23-MAY-2002.
 PA (FARB) BAYER AG.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 760
 ID ACC47899 standard; cDNA; 2706 BP.
 DE Human NR3B subunit receptor polypeptide coding sequence.
 PN WO2003033672-A2
 PD 24-APR-2003.
 PA (RIKE) RIKEN KK.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 761
 ID ADM02343 standard; cDNA; 2715 BP.
 DE Human cDNA of the invention SEQ ID NO:1028.
 PN EPI347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 23.49% Mismatches: 99
 Query Match: 6.15% Indels: 105
 RESULT 762
 ID ADS59378 standard; cDNA; 2781 BP.
 DE Bacterial polynucleotide #11365.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Best Local Similarity: 25.00% Mismatches: 111

Query Match: 6.15% Indels: 45
 RESULT 763
 ID ADS62861 standard; cDNA; 2781 BP.
 DE Bacterial polynucleotide #14848.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Best Local Similarity: 25.00% Mismatches: 111
 Query Match: 6.15% Indels: 45
 RESULT 764
 ID ADS63051 standard; cDNA; 2781 BP.
 DE Bacterial polynucleotide #15038.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Best Local Similarity: 25.00% Mismatches: 111
 Query Match: 6.15% Indels: 45
 RESULT 765
 ID ADN49407 standard; DNA; 2898 BP.
 DE Human glutamate receptor (MEM2) DNA.
 PN US2004086931-A1.
 PD 06-MAY-2004.
 PA (SPAD) SPADERNA S K.
 PA (QUIN) QUINN K E.
 PA (SHIM) SHIMKETS R A.
 PA (PADI) PADIGARU M.
 PA (SPYT) SPYTEK K A.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 766
 ID AAS06334 standard; cDNA; 2916 BP.
 DE DNA encoding human glutamate receptor-like protein, MEM3.
 PN WO200144473-A2.
 PD 21-JUN-2001.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 767
 ID ADN49409 standard; DNA; 2916 BP.
 DE Human glutamate receptor (MEM3) DNA.
 PN US2004086931-A1.
 PD 06-MAY-2004.
 PA (SPAD) SPADERNA S K.
 PA (QUIN) QUINN K E.
 PA (SHIM) SHIMKETS R A.
 PA (PADI) PADIGARU M.
 PA (SPYT) SPYTEK K A.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 768
 ID ADC7232 standard; DNA; 3096 BP.
 DE Human NR3B gene SEQ ID NO:5.
 PN WO2003016479-A2.
 PD 27-FEB-2003.
 PA (BURN-) BURNHAM INST.
 PA (UYVA) UNIV YALE.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 769
 ID ADN49183 standard; cDNA; 3096 BP.
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.
 PN US2004033500-A1.
 PD 19-FEB-2004.
 PA (BURN-) BURNHAM INST.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 776
 ID ADC72287 standard; DNA; 3097 BP.
 DE Human NR3B gene SEQ ID NO:61.
 PN WO2003016479-A2.
 PD 27-FEB-2003.
 PA (BURN-) BURNHAM INST.
 PA (UYIA) UNIV YALE.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 777
 ID ADM49238 standard; cDNA; 3097 BP.
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.
 PN US2004033500-A1.
 PD 19-FEB-2004.
 PA (BURN-) BURNHAM INST.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 778
 ID AAS06335 standard; cDNA; 3132 BP.
 DE DNA encoding human glutamate receptor-like protein, MEM4.
 PN WO200144473-A2.
 PD 21-JUN-2001.
 PA (CURA-) CURAGEN CORP.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 779
 ID ABZ33750 standard; cDNA; 3132 BP.
 DE Human TRICH encoding cDNA SEQ ID NO 56.
 PN WO200246415-A2.
 PD 13-JUN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 780
 ID ADN49411 standard; DNA; 3132 BP.
 DE Human glutamate receptor (MEM4) DNA.
 PN US2004086931-A1.
 PD 06-MAY-2004.
 PA (SPAD-) SPADERNA S K.
 PA (QUIN-) QUINN K E.
 PA (SHIM-) SHIMKETS R A.
 PA (PADI-) PADIGARU M.
 PA (SPYT-) SPYTEK K A.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 775
 ID AAC76703 standard; cDNA; 3207 BP.
 DE Human ORFX ORF2259 polynucleotide sequence SEQ ID NO:4515.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 23.64% Mismatches: 88
 Query Match: 6.15% Indels: 96
 RESULT 776
 ID ADP98744 standard; DNA; 6051 BP.
 DE C. albicans specific gene, orf19.1084, DNA sequence.
 PN WO2004056965-A2.
 PD 08-JUL-2004.
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 Best Local Similarity: 26.06% Mismatches: 88
 Query Match: 6.15% Indels: 28
 RESULT 777
 ID ADQ24692 standard; DNA; 6961 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7512.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.

Best Local Similarity: 22.09% Mismatches: 100
 Query Match: 6.15% Indels: 139
 RESULT 778
 ID ABQ76621 standard; cDNA; 8496 BP.
 DE C. albicans BAX-associated cDNA fragment SEQ ID 667.
 PN WO200264766-A2.
 PD 22-AUG-2002.
 PA (JANC) JANSSEN PHARM NV.
 Best Local Similarity: 26.06% Mismatches: 88
 Query Match: 6.15% Indels: 28
 RESULT 779
 ID ACA37617 standard; DNA; 10232 BP.
 DE Prokaryotic essential gene #19274.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 24.68% Mismatches: 116
 Query Match: 6.15% Indels: 86
 RESULT 780
 ID ABL56921 standard; DNA; 10283 BP.
 DE Human immediate early interleukin-four induced protein genomic DNA.
 PN WO200218574-A2.
 PD 07-MAR-2002.
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
 Best Local Similarity: 22.09% Mismatches: 100
 Query Match: 6.15% Indels: 139
 RESULT 781
 ID AAK73194 standard; DNA; 12050 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28006.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 27.08% Mismatches: 72
 Query Match: 6.15% Indels: 75
 RESULT 782
 ID AAV52831 standard; DNA; 16836 BP.
 DE Acetobacter xylinum cellulose synthetase complex encoding gene.
 PN WO9839455-A1.
 PD 11-SEP-1998.
 PA (BIOP-) BIO-POLYMER RES CO LTD.
 Best Local Similarity: 20.69% Mismatches: 112
 Query Match: 6.15% Indels: 98
 RESULT 783
 ID ACC00503 standard; DNA; 23434 BP.
 DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Best Local Similarity: 24.02% Mismatches: 70
 Query Match: 6.15% Indels: 92
 RESULT 784
 ID ADL27170 standard; DNA; 29040 BP.
 DE Human genomic sequence for LFNG.
 PN US2003216558-A1.
 PD 20-NOV-2003.
 PA (MORR-) MORRIS D W.
 PA (ENGEL-) ENGELHARD E K.
 Best Local Similarity: 22.57% Mismatches: 104
 Query Match: 6.15% Indels: 76
 RESULT 785
 ID ADG59147 standard; DNA; 70782 BP.
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.
 PN DE10241152-A1.
 PD 18-MAR-2004.
 PA (GBPF) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Best Local Similarity: 23.05% Mismatches: 129
 Query Match: 6.15% Indels: 81
 RESULT 786
 ID ADO56274 standard; DNA; 99100 BP.
 DE Human cyclin-dependent kinase 10, CDK10, genomic sequence.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.

RESULT 787
 ID ABL55601 standard; DNA; 625 BP.
 DE HCV bait polypeptide 17 encoding sequence.
 PN EP1178116-A1.
 PD 06-FEB-2002.
 PA (HYBR-) HYBRIGENICS SA.
 Best Local Similarity: 21.11% Mismatches: 104
 Query Match: 6.11% Indels: 45

RESULT 788
 ID ADP99934 standard; DNA; 1220 BP.
 DE Immune Response Associated Protein, IRAP-10, coding sequence, SEQ ID 42.
 PN WO2004081157-A2.
 PD 23-SEP-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 25.68% Mismatches: 94
 Query Match: 6.11% Indels: 41

RESULT 789
 ID ABD10671 standard; DNA; 1263 BP.
 DE Pseudomonas aeruginosa polynucleotide #9275.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.73% Mismatches: 78
 Query Match: 6.11% Indels: 76

RESULT 790
 ID AAX90993 standard; cDNA; 1512 BP.
 DE cDNA encoding modified interferon regulatory factor-7 (IRF-7).
 PN WO9951737-A1.
 PD 14-OCT-1999.
 PA (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 791
 ID ABD05238 standard; DNA; 1617 BP.
 DE Pseudomonas aeruginosa polynucleotide #3842.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.47% Mismatches: 93
 Query Match: 6.11% Indels: 45

RESULT 792
 ID AAX90994 standard; cDNA; 1629 BP.
 DE cDNA encoding chimeric protein IRF-7(1-246)/IRF-3(132-427).
 PN WO9951737-A1.
 PD 14-OCT-1999.
 PA (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER B.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 793
 ID ADJ74892 standard; DNA; 1646 BP.
 DE Marker gene SEQ ID NO:144.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 25.00% Mismatches: 85
 Query Match: 6.11% Indels: 58

RESULT 794
 ID ADJ74966 standard; DNA; 1646 BP.
 DE Marker gene SEQ ID NO:218.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 25.00% Mismatches: 85
 Query Match: 6.11% Indels: 58

RESULT 795
 ID ADRI4354 standard; DNA; 1646 BP.
 DE Human NF-kappaB pathway-associated gene SeqID355.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Best Local Similarity: 25.00% Mismatches: 85
 Query Match: 6.11% Indels: 58

RESULT 796
 ID ABL68654 standard; DNA; 1816 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6991.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 797
 ID ADJ74891 standard; DNA; 1816 BP.
 DE Marker gene SEQ ID NO:143.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 798
 ID ADJ74965 standard; DNA; 1816 BP.
 DE Marker gene SEQ ID NO:217.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 799
 ID AD864449 standard; DNA; 1816 BP.
 DE Human interferon regulatory factor 7 (IRF-7) gene.
 PN US2004185489-A1.
 PD 23-SEP-2004.
 PA (CERT/) CERTA U.
 PA (FOSE/) FOSER S.
 PA (WEYE/) WEYER K.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 800
 ID ACN41686 standard; cDNA; 1843 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:561.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 801
 ID ACA56563 standard; cDNA; 1864 BP.
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1161.
 PN US6500938-B1.
 PD 31-DEC-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 802
 ID ADI56359 standard; DNA; 1864 BP.
 DE Human polynucleotide probe #1161.
 PN US2004010136-A1.
 PD 15-JAN-2004.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 803
 ID ABN96893 standard; DNA; 1890 BP.
 DE Gene #3391 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

RESULT 804
 ID ADJ74890 standard; DNA; 1890 BP.
 DE Marker gene SEQ ID NO:142.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 26.04% Mismatches: 67
 Query Match: 6.11% Indels: 37

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RESULT 805
ID ADJ74964 standard; DNA; 1890 BP.
DE Marker gene SEQ ID NO:216.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 26.04%
Query Match: 6.11%
Mismatches: 67
Indels: 37

RESULT 806
ID ADB90126 standard; DNA; 1956 BP.
DE Mycobacterium tuberculosis nutrient starvation-inducible gene #82.
PN WO2003004520-A2.
PD 16-JAN-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Best Local Similarity: 20.68%
Query Match: 6.11%
Mismatches: 103
Indels: 126

RESULT 807
ID ABX56503 standard; cDNA; 2102 BP.
DE Human protein modification and maintenance molecule (PMOD) cDNA #5.
PN WO200281636-A2.
PD 17-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 24.42%
Query Match: 6.11%
Mismatches: 86
Indels: 121

RESULT 808
ID ADG77055 standard; cDNA; 2286 BP.
DE Human nucleic acid associated polypeptide (NAAP) 30 cDNA sequence.
PN WO2003076586-A2.
PD 18-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 26.04%
Query Match: 6.11%
Mismatches: 67
Indels: 37

RESULT 809
ID ADR99935 standard; DNA; 2418 BP.
DE Immune Response Associated Protein, IRAP-11, coding sequence, SEQ ID 43.
PN WO2004081197-A2.
PD 23-SEP-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 26.04%
Query Match: 6.11%
Mismatches: 67
Indels: 37

RESULT 810
ID ACN41684 standard; cDNA; 2436 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:559.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.68%
Query Match: 6.11%
Mismatches: 94
Indels: 41

RESULT 811
ID ACN41681 standard; cDNA; 2609 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:556.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 26.04%
Query Match: 6.11%
Mismatches: 67
Indels: 37

RESULT 812
ID ABD17785 standard; DNA; 3744 BP.
DE Pseudomonas aeruginosa polynucleotide #16389.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 23.67%
Query Match: 6.11%
Mismatches: 92
Indels: 97

RESULT 813
ID ADD78275 standard; DNA; 4801 BP.
DE Human CGDD-17 coding sequence.
PN WO2003077875-A2.
PD 25-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 25.72%
Query Match: 6.11%
Mismatches: 110
Indels: 64

RESULT 814
ID ADJ74964 standard; DNA; 1890 BP.
DE Marker gene SEQ ID NO:216.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 26.04%
Query Match: 6.11%
Mismatches: 67
Indels: 37

RESULT 815
ID ACD13338 standard; cDNA; 4933 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 7.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Best Local Similarity: 25.72%
Query Match: 6.11%
Mismatches: 110
Indels: 64

RESULT 816
ID ADP13275 standard; DNA; 5047 BP.
DE Renal cell carcinoma differentially expressed gene #11.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN) TWINE N C.
PA (BURC) BURCZYNSKI M E.
PA (TREP) TREPICCHIO W L.
PA (DORN) DORNER A.
PA (STOV) STOVER J A.
PA (SLON) SLONI D K.
Best Local Similarity: 24.23%
Query Match: 6.11%
Mismatches: 66
Indels: 90

RESULT 817
ID ADQ84256 standard; cDNA; 5047 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1070.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD) WU T D.
PA (ZHOU) ZHOU Y.
Best Local Similarity: 24.23%
Query Match: 6.11%
Mismatches: 66
Indels: 90

RESULT 818
ID ADQ85638 standard; cDNA; 5047 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2452.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD) WU T D.
PA (ZHOU) ZHOU Y.
Best Local Similarity: 24.23%
Query Match: 6.11%
Mismatches: 66
Indels: 90

RESULT 819
ID ADQ86737 standard; cDNA; 5047 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3612.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD) WU T D.
PA (ZHOU) ZHOU Y.
Best Local Similarity: 24.23%
Query Match: 6.11%
Mismatches: 66
Indels: 90

RESULT 820
ID AAD57243 standard; cDNA; 4884 BP.
DE Human CGDD-24 cDNA.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 25.72%
Query Match: 6.11%
Mismatches: 110
Indels: 64

RESULT 821
ID ABV72514 standard; cDNA; 5139 BP.
DE Nucleotide sequence of a human intracellular signalling molecule.
PN WO200277235-A2.
PD 03-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.

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Best Local Similarity: 25.72% Mismatches: 110
 Query Match: 6.11% Indels: 64
 RESULT 822
 ID ADO34015 standard; cDNA; 5153 BP.
 DE Human MBCTAT (modifier of beta-catenin) SCRIB cDNA, SEQ ID NO:5.
 PN WO2004047761-A2.
 PD 10-JUN-2004.
 PA (EXEL-) EXELIXIS INC.
 Best Local Similarity: 25.72% Mismatches: 110
 Query Match: 6.11% Indels: 64
 RESULT 823
 ID ABS78655 standard; DNA; 5811 BP.
 DE S. macromyceticus DNA encoding PKSE protein macromomycin.
 PN CA2387401-A1.
 PD 04-SEP-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 26.48% Mismatches: 91
 Query Match: 6.11% Indels: 73
 RESULT 824
 ID AAL54423 standard; DNA; 6609 BP.
 DE Hepatitis C virus DNA, SEQ ID NO 1.
 PN FR2824072-A1.
 PD 31-OCT-2002.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 825
 ID ADD93727 standard; DNA; 7983 BP.
 DE Hepatitis C virus genotype 1a replicon.
 PN WO2003085084-A2.
 PD 16-OCT-2003.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 826
 ID ADD93722 standard; DNA; 7989 BP.
 DE Hepatitis C virus strain H77 (BB7-F1) replicon.
 PN WO2003085084-A2.
 PD 16-OCT-2003.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 827
 ID ADR38453 standard; DNA; 7990 BP.
 DE DNA encoding Hepatitis C virus strain H77 NS3-NS5B polyprotein Seq 4.
 PN WO2004074507-A2.
 PD 02-SEP-2004.
 PA (MERI) MERCK & CO INC.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 828
 ID ADD93723 standard; DNA; 7992 BP.
 DE Hepatitis C virus strain H77 (BB7-F1/F2) replicon.
 PN WO2003085084-A2.
 PD 16-OCT-2003.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 829
 ID AAL54425 standard; DNA; 8451 BP.
 DE Hepatitis C virus DNA, SEQ ID NO 3.
 PN FR2824072-A1.
 PD 31-OCT-2002.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 830
 ID AAT41882 standard; cDNA; 9401 BP.
 DE Hepatitis C virus protease NS3-NS4 cDNA.
 PN WO9634976-A1.
 PD 07-NOV-1996.
 PA (VERT-) VERTEX PHARM INC.
 Best Local Similarity: 22.07% Mismatches: 103

Query Match: 6.11% Indels: 45
 RESULT 831
 ID AAV59378 standard; cDNA; 9416 BP.
 DE Hepatitis C virus H-CMR cDNA.
 PN WO9839031-A1.
 PD 11-SEP-1998.
 PA (UNIW) UNIV WASHINGTON.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 832
 ID ABK87300 standard; cDNA; 9416 BP.
 DE cDNA encoding hepatitis C virus (HCV) HCV protein.
 PN US6392028-B1.
 PD 21-MAY-2002.
 PA (UNIW) UNIV WASHINGTON.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 833
 ID ACA62483 standard; cDNA; 9416 BP.
 DE HEV-H cDNA.
 PN US2003028010-A1.
 PD 06-FEB-2003.
 PA (UNIW) UNIV WASHINGTON.
 Best Local Similarity: 22.07% Mismatches: 103
 Query Match: 6.11% Indels: 45
 RESULT 834
 ID AAD03778 standard; cDNA; 9518 BP.
 DE Hepatitis C virus envelope 2 protein lacking hypervariable region 1 cDNA.
 PN WO200121807-A1.
 PD 29-MAR-2001.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 835
 ID AAD03808 standard; cDNA; 9518 BP.
 DE Hepatitis C virus H77C cDNA lacking HVRI region from chimpanzee #96A008.
 PN WO200121807-A1.
 PD 29-MAR-2001.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 836
 ID AAD03807 standard; cDNA; 9518 BP.
 DE Hepatitis C virus H77C cDNA lacking HVRI region from chimpanzee 1590.
 PN WO200121807-A1.
 PD 29-MAR-2001.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 837
 ID AAX24833 standard; DNA; 9599 BP.
 DE Infectious hepatitis C virus genotype 1a/1b chimera genome.
 PN WO9904008-A2.
 PD 28-JAN-1999.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 838
 ID AAX24832 standard; DNA; 9599 BP.
 DE Infectious hepatitis C virus genotype 1a strain H77C genome.
 PN WO9904008-A2.
 PD 28-JAN-1999.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45
 RESULT 839
 ID AAF23491 standard; DNA; 9599 BP.
 DE Infectious Hepatitis C virus 1a genotype.
 PN WO200075337-A1.
 PD 14-DEC-2000.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Best Local Similarity: 21.17% Mismatches: 104
 Query Match: 6.11% Indels: 45

RESULT 840
ID AAC86638 standard; DNA; 9599 BP.
DE Nucleotide sequence of a hepatitis C virus (HCV) clone genotype 1a.
PN WO200075352-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID ADJ56743 standard; DNA; 9599 BP.
DE Hepatitis C virus DNA SeqID 13.
PN WO2004005498-A1.
PD 15-JAN-2004.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (INSP) INST PASTEUR.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID ADJ64255 standard; DNA; 9599 BP.
DE Hepatitis C virus polynucleotide.
PN US2004039187-A1.
PD 26-FEB-2004.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (INSP) INST PASTEUR.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAC86646 standard; DNA; 9611 BP.
DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77(p7)-CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAC86645 standard; DNA; 9611 BP.
DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAC86647 standard; DNA; 9611 BP.
DE Nucleotide sequence of chimeric Hepatitis C virus clone J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAC86648 standard; DNA; 9611 BP.
DE Nucleotide sequence of chimeric Hepatitis C virus clone pH77(p7)-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAL54424 standard; DNA; 9622 BP.
DE Hepatitis C virus DNA, SEQ ID No 2.
PN FR2824072-A1.
PD 31-OCT-2002.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 22.07% Mismatches: 103
Indels: 45
Query Match:
Query Match:
Query Match:
ID AAV59361 standard; cDNA; 9646 BP.
DE Hepatitis C virus H77 consensus sequence.
PN WO9839031-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 22.07% Mismatches: 103

Query Match: 6.11% Indels: 45
RESULT 849
ID ABK87285 standard; cDNA; 9646 BP.
DE cDNA encoding hepatitis C virus (HCV) H77 consensus protein.
PN US6392028-B1.
PD 21-MAY-2002.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 22.07% Mismatches: 103
Indels: 45
Query Match:
Query Match:
Query Match:
ID ACA62466 standard; cDNA; 9646 BP.
DE HCV H77 consensus sequence cDNA.
PN US2003028010-A1.
PD 06-FEB-2003.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 22.07% Mismatches: 103
Indels: 45
Query Match:
Query Match:
Query Match:
ID ADD67945 standard; DNA; 10803 BP.
DE Modified hepatitis C virus (HCV) RNA seqid 17.
PN US2003125541-A1.
PD 03-JUL-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID ABX10617 standard; DNA; 10803 BP.
DE MO-Z nucleotide sequence encoding viral polypeptides.
PN US2002155582-A1.
PD 24-OCT-2002.
PA (LEMO) LEMON S M.
PA (YIMM) YI M.
Best Local Similarity: 21.17% Mismatches: 104
Indels: 45
Query Match:
Query Match:
Query Match:
ID ACD19239 standard; DNA; 12848 BP.
DE E. coli 0157 unique DNA sequence OZID_252.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT) BLATTNER F R.
PA (BURL) BURLAND V D.
PA (PERN) PERNA N T.
PA (PLON) PLUNKETT G.
PA (WELC) WELCH R.
Best Local Similarity: 23.20% Mismatches: 111
Indels: 87
Query Match:
Query Match:
Query Match:
ID ABZ28892 standard; DNA; 21407 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38149.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.45% Mismatches: 103
Indels: 141
Query Match:
Query Match:
Query Match:
ID ADC00831 standard; DNA; 39824 BP.
DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 876.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS) UNIV TSUKUBA.
Best Local Similarity: 23.20% Mismatches: 111
Indels: 87
Query Match:
Query Match:
Query Match:
ID AAT80413 standard; DNA; 43280 BP.
DE Tyactone synthase gene cluster.
PN EP791655-A2.
PD 27-AUG-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 24.08% Mismatches: 102
Indels: 101
Query Match:
Query Match:
Query Match:
ID AAZ23902 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 4.

PN WO9950284-A2.
 PA (ROSE/) ROSENTHAL A.
 Best Local Similarity: 22.97% Mismatches: 114
 Query Match: 6.11% Indels: 86
 RESULT 858
 ID AA223904 standard; DNA; 49999 BP.
 DE Human LOBO homologue genomic DNA fragment 6.
 PN WO9950284-A2.
 PA (ROSE/) ROSENTHAL A.
 Best Local Similarity: 28.85% Mismatches: 78
 Query Match: 6.11% Indels: 51
 RESULT 859
 ID ACN44438 standard; DNA; 73967 BP.
 DE Human genomic sequence hCG27607.
 PN WO2003073826-A2.
 PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity: 22.18% Mismatches: 105
 Query Match: 6.11% Indels: 87
 RESULT 860
 ID ADP64454 standard; DNA; 76994 BP.
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
 PN WO2004053065-A2.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Best Local Similarity: 26.81% Mismatches: 118
 Query Match: 6.11% Indels: 75
 RESULT 861
 ID AAL50814 standard; DNA; 79528 BP.
 DE Human cancer status prediction method-related DNA sequence #6.
 PN WO200272828-A1.
 PA (DNAC-) DNA CHIP RES INC.
 Best Local Similarity: 24.51% Mismatches: 119
 Query Match: 6.11% Indels: 74
 RESULT 862
 ID ADQ19802 standard; DNA; 79528 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2621.
 PN WO2004048938-A2.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity: 24.51% Mismatches: 119
 Query Match: 6.11% Indels: 74
 RESULT 863
 ID ADQ56274 standard; DNA; 99100 BP.
 DE Human cyclin-dependent kinase 10, CDK10, genomic sequence.
 Best Local Similarity: 28.31% Mismatches: 74
 Query Match: 6.11% Indels: 58
 RESULT 864
 Best Local Similarity: 20.68% Mismatches: 103
 Query Match: 6.11% Indels: 126
 RESULT 865
 Best Local Similarity: 20.68% Mismatches: 103
 Query Match: 6.11% Indels: 126
 RESULT 866
 ID AAC42335 standard; DNA; 816 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35161.
 PN EP1033405-A2.
 Best Local Similarity: 24.31% Mismatches: 80
 Query Match: 6.08% Indels: 103
 RESULT 867
 ID ABR65240 standard; cDNA; 1037 BP.
 DE Arabidopsis cDNA encoding a transcription factor #92.
 PN WO200215675-A1.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Best Local Similarity: 25.78% Mismatches: 93
 Query Match: 6.08% Indels: 72
 RESULT 875
 ID ADS56770 standard; cDNA; 1383 BP.
 DE Bacterial polynucleotide #8757.
 PN US2003233675-A1.

PA (HEAR/) HEARD J.
 PA (JIAN/) JIANG C.
 PA (KEDD/) KEDDIE J.
 PA (ADAM/) ADAM L.
 PA (RATC/) RATCLIFF O.
 PA (REUB/) REUBER J L.
 PA (RIEC/) RIECHMANN J L.
 PA (YUGG/) YU G.
 PA (PINE/) PINEDA O.
 Best Local Similarity: 24.31% Mismatches: 80
 Query Match: 6.08% Indels: 103
 RESULT 868
 ID ADO61718 standard; DNA; 1037 BP.
 DE Transcription factor G1142 coding sequence, SEQ ID 185.
 PN WO2004031349-A2.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Best Local Similarity: 24.31% Mismatches: 80
 Query Match: 6.08% Indels: 103
 RESULT 869
 ID ADF57640 standard; cDNA; 1041 BP.
 DE Human polynucleotide sequence SEQ ID NO:7.
 PN WO2003080795-A2.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 25.00% Mismatches: 81
 Query Match: 6.08% Indels: 107
 RESULT 870
 ID ADM80103 standard; DNA; 1179 BP.
 DE Spiramycin biosynthesis orf18, SEQ ID 70.
 PN FR2845394-A1.
 PA (AVET) AVENTIS PHARMA SA.
 Best Local Similarity: 25.91% Mismatches: 106
 Query Match: 6.08% Indels: 97
 RESULT 871
 ID ADN97619 standard; DNA; 1179 BP.
 DE S ambofaciens spiramycin biosynthetic gene ORF18.
 PN WO2004033689-A2.
 PA (AVET) AVENTIS PHARMA SA.
 Best Local Similarity: 25.91% Mismatches: 106
 Query Match: 6.08% Indels: 97
 RESULT 872
 ID ABD17265 standard; DNA; 1366 BP.
 DE Pseudomonas aeruginosa polynucleotide #15869.
 PN US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.87% Mismatches: 124
 Query Match: 6.08% Indels: 100
 RESULT 873
 ID ABD04654 standard; DNA; 1362 BP.
 DE Pseudomonas aeruginosa polynucleotide #3258.
 PN US6551795-B1.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.95% Mismatches: 75
 Query Match: 6.08% Indels: 108
 RESULT 874
 ID ADG33747 standard; DNA; 1383 BP.
 DE Actinomycetes dual condensation/epimerisation NRPS domain DNA ID 6.
 PN WO2003089641-A2.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 25.78% Mismatches: 93
 Query Match: 6.08% Indels: 72
 RESULT 875
 ID ADS56770 standard; cDNA; 1383 BP.
 DE Bacterial polynucleotide #8757.
 PN US2003233675-A1.

PA (HYSE-) HYSEQ INC.	102	PA (UYOV-) UNIV OVIEDO.	78
Best Local Similarity: 26.64%	Mismatches:	Best Local Similarity: 25.69%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 893	57	RESULT 902	50
ID ADP10534 standard; DNA; 4239 BP.		ID ADM80034 standard; DNA; 30943 BP.	
DE Reference mRNA sequences for marker probe #211.		DE Spiramycin biosynthesis related DNA, SEQ ID 1.	
PN WO2000402346-A2.		PN FR2845394-A1.	
PD 21-MAY-2004.		PD 09-APR-2004.	
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.	102	PA (AVET) AVENTIS PHARMA SA.	106
Best Local Similarity: 26.64%	Mismatches:	Best Local Similarity: 25.91%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 894	57	RESULT 903	97
ID ADQ64705 standard; cDNA; 4293 BP.		ID ADN97550 standard; DNA; 30943 BP.	
DE Novel human cDNA sequence #1866.		DE S ambofaciens spiramycin biosynthetic enzyme genomic region.	
PN EP1440981-A2.		PN WO2004033689-A2.	
PD 28-JUL-2004.		PD 22-APR-2004.	
PA (REAS-) RES ASSOC BIOTECHNOLOGY.	102	PA (AVET) AVENTIS PHARMA SA.	106
Best Local Similarity: 26.64%	Mismatches:	Best Local Similarity: 25.91%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 895	57	RESULT 904	97
ID ACF04824 standard; DNA; 5244 BP.		ID ADA03020 standard; DNA; 38764 BP.	
DE M lichenicola melithiazol synthesis gene Mel G.		DE Human RAC2 carcinoma associated gene, SEQ ID NO:1538.	
PN WO2003080828-A2.		PN WO2003057146-A2.	
PD 02-OCT-2003.		PD 17-JUL-2003.	
PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.	83	PA (SAGR-) SAGRES DISCOVERY.	117
Best Local Similarity: 26.79%	Mismatches:	Best Local Similarity: 24.75%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 896	56	RESULT 905	73
ID ABX72552 standard; cDNA; 5465 BP.		ID ADB72758 standard; DNA; 38764 BP.	
DE Human CA125 cDNA encoding the amino terminal domain.		DE Human RAC2 gene.	
PN WO200283866-A2.		PN WO2003008583-A2.	
PD 24-OCT-2002.		PD 30-JAN-2003.	
PA (UYAR-) UNIV ARKANSAS.	119	PA (SAGR-) SAGRES DISCOVERY.	117
Best Local Similarity: 21.92%	Mismatches:	Best Local Similarity: 24.75%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 897	72	RESULT 906	73
ID ABS78696 standard; DNA; 5802 BP.		ID ADC85500 standard; DNA; 38764 BP.	
DE S. kaniharaensis DNA encoding PKSE.		DE Human Rac2 genomic sequence.	
PN CA2387401-A1.		PN WO2003045230-A2.	
PD 04-SEP-2002.		PD 03-JUN-2003.	
PA (ECOP-) ECOPIA BIOSCIENCES INC.	122	PA (SAGR-) SAGRES DISCOVERY.	117
Best Local Similarity: 21.82%	Mismatches:	Best Local Similarity: 24.75%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 898	88	RESULT 907	73
ID AAV45225 standard; DNA; 5960 BP.		ID ADM74615 standard; DNA; 38764 BP.	
DE Human nerve growth factor promoter plasmid pGL3-neo.		DE Human carcinoma associated (CA) nucleic acid #142.	
PN WO9835027-A2.		PN US2004072154-A1.	
PD 13-AUG-1998.		PD 15-APR-2004.	
PA (HMRI) HOECHST MARION ROUSSEL INC.	97	PA (MORR/) MORRIS D W.	117
Best Local Similarity: 20.62%	Mismatches:	Best Local Similarity: 24.75%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 899	118	RESULT 908	73
ID ABX71177 standard; cDNA; 5967 BP.		ID ABQ88150 standard; cDNA; 40668 BP.	
DE Novel human cDNA sequence #402.		DE Human osteoblast differentiation related cDNA SEQ ID NO 57.	
PN WO200281731-A2.		PN WO200250301-A2.	
PD 17-OCT-2002.		PD 27-JUN-2002.	
PA (HYSE-) HYSEQ INC.	112	PA (GENE-) GENE LOGIC INC.	59
PA (GOOD/) GOODRICH R W.	101	PA (PROC) PROCTER & GAMBLE CO.	78
Best Local Similarity: 23.25%	Mismatches:	Best Local Similarity: 32.57%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 900	101	RESULT 909	59
ID AAV62154 standard; DNA; 21034 BP.		ID ACF04818 standard; DNA; 51855 BP.	
DE HSV-2 strain SB5 Contig ID 10 DNA sequence.		DE Melithiazol biosynthetic gene cluster.	
PN WO9820016-A1.		PN WO2003080828-A2.	
PD 14-MAY-1998.		PD 02-OCT-2003.	
PA (SMIK) SMITHKLINE BEECHAM CORP.	111	PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.	95
Best Local Similarity: 22.59%	Mismatches:	Best Local Similarity: 26.61%	Mismatches:
Query Match: 6.08%	Indels:	Query Match: 6.08%	Indels:
RESULT 901	121	RESULT 910	63
ID ADJ53165 standard; DNA; 25681 BP.		ID ADP84151 standard; DNA; 57082 BP.	
DE Saccharothrix aerocolonigenes rebeccamycin biosynthetic gene cluster.			
PN WO200303706-A1.			
PD 24-APR-2003.			

DE	Human CA125 genomic DNA amino terminal sequence SeqID 1.		
PN	WO2004045553-A2.		
PD	03-JUN-2004.		
PA	(UYAR-) UNIV ARKANSAS.		
Best Local Similarity:	21.92%	Mismatches:	119
Query Match:	6.08%	Indels:	72
RESULT 911			
ID	ADP84154 standard; cDNA; 66765 BP.		
DE	Human CA125 cDNA SeqID 4.		
PN	WO2004045553-A2.		
PD	03-JUN-2004.		
PA	(UYAR-) UNIV ARKANSAS.		
Best Local Similarity:	21.92%	Mismatches:	119
Query Match:	6.08%	Indels:	72
RESULT 912			
ID	ADR72872 standard; DNA; 66765 BP.		
DE	Human ovarian cancer-related tumour marker CA125 DNA.		
PN	WO2004075713-A2.		
PD	10-SEP-2004.		
PA	(MOUN) MOUNT SINAI HOSPITAL.		
Best Local Similarity:	21.92%	Mismatches:	119
Query Match:	6.08%	Indels:	72
RESULT 913			
Best Local Similarity:	23.38%	Mismatches:	82
Query Match:	6.08%	Indels:	60
RESULT 914			
Best Local Similarity:	22.46%	Mismatches:	108
Query Match:	6.08%	Indels:	66
RESULT 915			
Best Local Similarity:	23.38%	Mismatches:	82
Query Match:	6.08%	Indels:	60
RESULT 916			
Best Local Similarity:	22.46%	Mismatches:	108
Query Match:	6.08%	Indels:	66
RESULT 917			
Best Local Similarity:	24.32%	Mismatches:	74
Query Match:	6.08%	Indels:	42
RESULT 918			
ID	AAV62176 standard; DNA; 117213 BP.		
DE	HSV-2 strain SB5 Contig ID 15 DNA sequence.		
PN	US2004023306-A1.		
PD	05-FEB-2004.		
PA	(ISIS-) ISIS PHARM INC.		
Best Local Similarity:	23.13%	Mismatches:	105
Query Match:	6.08%	Indels:	71
RESULT 920			
ID	ADL13780 standard; DNA; 190117 BP.		
DE	Osteoarthritis-associated polymorphic nucleotide #312.		
PN	WO2003054166-A2.		
PD	03-JUL-2003.		
PA	(INCY-) INCYTE GENOMICS INC.		
Best Local Similarity:	21.86%	Mismatches:	95
Query Match:	6.08%	Indels:	123
RESULT 921			
ID	ADO25291 standard; cDNA; 191010 BP.		
DE	Human protein kinase C zeta I/zeta II genomic sequence.		
PN	WO2004041212-A2.		
PD	21-MAY-2004.		
PA	(SACK/) SACKTOR T C.		
PA	(CRAR/) CRARY J F.		
PA	(HERN/) HERNANDEZ A I.		
PA	(MIRR/) MIRRA S.		
PA	(SHAO/) SHAO C.		
Best Local Similarity:	27.75%	Mismatches:	74
Query Match:	6.08%	Indels:	57
RESULT 922			
ID	ABD05109 standard; DNA; 612 BP.		
DE	Pseudomonas aeruginosa polynucleotide #3713.		

PN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	27.51%	Mismatches:	87	
Query Match:	6.04%	Indels:	53	
RESULT 923				
ID	ACA90158 standard; cDNA; 717 BP.			
DE	cDNA encoding novel human protein NOV1b.			
PN	WO2003031571-A2.			
PD	17-APR-2003.			
PA	(CURA-) CURAGEN CORP.			
Best Local Similarity:	25.54%	Mismatches:	73	
Query Match:	6.04%	Indels:	77	
RESULT 924				
ID	ABD05881 standard; DNA; 963 BP.			
DE	Pseudomonas aeruginosa polynucleotide #4485.			
PN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	25.23%	Mismatches:	58	
Query Match:	6.04%	Indels:	82	
RESULT 925				
ID	ADS14617 standard; DNA; 1023 BP.			
DE	Pseudomonas aeruginosa quorum sensing controlled gene PA2514, SEQ ID 172.			
PN	WO2004083385-A2.			
PD	30-SEP-2004.			
PA	(IOWA) UNIV IOWA RES FOUND.			
Best Local Similarity:	27.85%	Mismatches:	100	
Query Match:	6.04%	Indels:	42	
RESULT 926				
ID	ACA53049 standard; DNA; 1086 BP.			
DE	Prokaryotic essential gene #34706.			
PN	WO200277183-A2.			
PD	03-OCT-2002.			
PA	(ELIT-) ELITRA PHARM INC.			
Best Local Similarity:	28.43%	Mismatches:	55	
Query Match:	6.04%	Indels:	51	
RESULT 927				
ID	ACA37717 standard; DNA; 1098 BP.			
DE	Prokaryotic essential gene #19374.			
PN	WO200277183-A2.			
PD	03-OCT-2002.			
PA	(ELIT-) ELITRA PHARM INC.			
Best Local Similarity:	25.76%	Mismatches:	70	
Query Match:	6.04%	Indels:	48	
RESULT 928				
ID	ABD02700 standard; DNA; 1098 BP.			
DE	Pseudomonas aeruginosa polynucleotide #1304.			
PN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	21.76%	Mismatches:	93	
Query Match:	6.04%	Indels:	80	
RESULT 929				
ID	ABD10087 standard; DNA; 1149 BP.			
DE	Pseudomonas aeruginosa polynucleotide #8691.			
PN	US6551795-B1.			
PD	22-APR-2003.			
PA	(GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity:	24.24%	Mismatches:	97	
Query Match:	6.04%	Indels:	107	
RESULT 930				
ID	ADT42293 standard; cDNA; 1191 BP.			
DE	Bacterial polynucleotide #17044.			
PN	US2003233675-A1.			
PD	18-DEC-2003.			
PA	(CAOY/) CAO Y.			
PA	(HINK/) HINKLE G J.			
PA	(SLAT/) SLATER S C.			
PA	(CHEN/) CHEN X.			
PA	(GOLD/) GOLDMAN B S.			
Best Local Similarity:	23.70%	Mismatches:	86	
Query Match:	6.04%	Indels:	86	

RESULT 931
 ID ADH77842 standard; DNA; 1218 BP.
 DE Hepatitis B virus surface antigen, HBsAgL coding sequence, SEQ ID 1.
 PN WO2004002459-A1.
 PD 08-JAN-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 932
 ID ADO48158 standard; DNA; 1218 BP.
 DE Hepatitis B virus pre-S1 protein gene SeqID1.
 PN WO2004047812-A1.
 PD 10-JUN-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 933
 ID ADS91503 standard; DNA; 1218 BP.
 DE Nucleotide sequence of a HBV surface antigen protein.
 PN WO2004082720-A1.
 PD 30-SEP-2004.
 PA (BEAC-) BEACLE INC.
 PA (VIBV-) VIB VLAAMS INTERUNIVERSITAIR INST BIOTEC.
 PA (COLL-) COLLEN RES FOUND VZW ONDERWIJZEN NAVORSI.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 934
 ID ABL08663 standard; cDNA; 1235 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20471.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Best Local Similarity: 27.05% Mismatches: 100
 Query Match: 6.04% Indels: 55
 RESULT 935
 ID AAC40581 standard; DNA; 1270 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 28826.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 26.40% Mismatches: 54
 Query Match: 6.04% Indels: 25
 RESULT 936
 ID AAQ06049 standard; DNA; 1296 BP.
 DE plasmid pUK1 pro-Urokinase sequence.
 PN EP390592-A.
 PD 03-OCT-1990.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (EXPE-) CENT INST EXPER ANIMALS.
 PA (JIKK-) JIKKEN DOBUTSU CHUO KENK.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 937
 ID AAQ55772 standard; cDNA to mRNA; 1296 BP.
 DE Pro-urokinase derivative.
 PN JP05336965-A.
 PD 21-DEC-1993.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 938
 ID ABK86598 standard; cDNA; 1296 BP.
 DE Human plasminogen activator, urokinase (PLAU) cDNA.
 PN WO200240503-A2.
 PD 23-MAY-2002.
 PA (GENA-) GENAISSANCE PHARM INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 939
 ID ABA00207 standard; cDNA; 1296 BP.
 DE sc-UPA coding sequence.
 PN EP1232755-A2.
 PD 21-AUG-2002.
 PA (JCRP-) JCR PHARM CO LTD.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 940
 ID ADF28768 standard; cDNA; 1296 BP.
 DE Human urokinase-type plasminogen activator (uPA) encoding cDNA.
 PN WO2003082072-A2.
 PD 09-OCT-2003.
 PA (HARB/) HARBECK N.
 PA (KATE/) KATES R E.
 PA (SCHM/) SCHMITT M.
 PA (FOEK/) FOEKENS J A.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 941
 ID ABD03649 standard; DNA; 1323 BP.
 DE Pseudomonas aeruginosa polynucleotide #2253.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.14% Mismatches: 100
 Query Match: 6.04% Indels: 90
 RESULT 942
 ID ABD03827 standard; DNA; 1389 BP.
 DE Pseudomonas aeruginosa polynucleotide #2431.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.14% Mismatches: 100
 Query Match: 6.04% Indels: 90
 RESULT 943
 ID ABD05663 standard; DNA; 1428 BP.
 DE Pseudomonas aeruginosa polynucleotide #4267.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.23% Mismatches: 58
 Query Match: 6.04% Indels: 82
 RESULT 944
 ID AAS67372 standard; cDNA; 1470 BP.
 DE DNA encoding novel human diagnostic protein #3176.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 25.10% Mismatches: 70
 Query Match: 6.04% Indels: 89
 RESULT 945
 ID AAN92037 standard; DNA; 1473 BP.
 DE Sequence of variant human prourokinase.
 PN JP01252283-A.
 PD 06-OCT-1989.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 946
 ID AAN50138 standard; DNA; 1474 BP.
 DE Sequence of the signal sequence and noncoding region of the pro-UK
 DE structural gene (Sequence II).
 PN EP154272-A.
 PD 11-SEP-1985.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 947
 ID AAN81558 standard; DNA; 1475 BP.
 DE Pro-UK structural gene, signal sequence and non-coding region.
 PN EP265874-A.
 PD 04-MAY-1988.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 948
 ID AA224619 standard; cDNA; 1475 BP.
 DE Human lung tumor associated polynucleotide.

PN WO9947674-A2.
 PD 23-SEP-1999.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 949
 ID AAC65858 standard; cDNA; 1475 BP.
 DE Human lung cancer-associated cDNA for contig 10.
 PN WO200061612-A2.
 PD 19-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 950
 ID AB235047 standard; cDNA; 1475 BP.
 DE Human gene expression profile polynucleotide SEQ ID NO 159.
 PN WO200274979-A2.
 PD 26-SEP-2002.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 951
 ID AB149077 standard; cDNA; 1475 BP.
 DE Human lung tumour cDNA sequence for contig 10 SEQ ID NO:122.
 PN WO200200174-A2.
 PD 03-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 952
 ID ABO92263 standard; cDNA; 1475 BP.
 DE Human lung cancer associated cDNA sequence SEQ ID NO:122.
 PN WO200247534-A2.
 PD 20-JUN-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 953
 ID ADA28212 standard; cDNA; 1475 BP.
 DE Human lung tumour associated cDNA contig 10.
 PN US2003064947-A1.
 PD 03-APR-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 954
 ID ADE53417 standard; cDNA; 1475 BP.
 DE Human lung tumour protein cDNA sequence #119.
 PN US2003119763-A1.
 PD 26-JUN-2003.
 PA (WANG/) WANG T.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 955
 ID ADH36776 standard; cDNA; 1475 BP.
 DE Human lung cancer-related cDNA sequence #119.
 PN WO2003086175-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 956
 ID ACCT7885 standard; DNA; 1475 BP.
 DE Human urokinase encoding DNA.
 PN WO2003031464-A2.
 PD 17-APR-2003.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 957
 ID ADM56579 standard; cDNA; 1475 BP.
 DE Human lung tumour cDNA #119.
 PN US2003138438-A1.

PD 24-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 958
 ID ADN89623 standard; cDNA; 1475 BP.
 DE Human lung squamous cell carcinoma cDNA seqid 122.
 PN US6660838-B1.
 PD 09-DEC-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 959
 ID ADN49705 standard; DNA; 1475 BP.
 DE Human urokinase DNA SeqID 33.
 PN WO2004033651-A2.
 PD 22-APR-2004.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 960
 ID AAN91617 standard; DNA; 1500 BP.
 DE Sequence of entire prourokinase (PKU) gene from PKU-producing tumour cell line ATCC CCL138 clone PUC20.
 PN EP312941-A.
 PD 26-APR-1989.
 PA (BADI) BASF AG.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 961
 ID AAN91618 standard; cDNA to mRNA; 1500 BP.
 DE Human pro-urokinase coding sequence plus untranslated regions.
 PN EP312942-A.
 PD 26-APR-1989.
 PA (BADI) BASF AG.
 Best Local Similarity: 23.05% Mismatches: 96
 Indels: 73
 Query Match:
 RESULT 962
 ID ABD16344 standard; DNA; 1713 BP.
 DE Pseudomonas aeruginosa polynucleotide #14948.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.01% Mismatches: 127
 Indels: 56
 Query Match:
 RESULT 963
 ID ADQ83498 standard; cDNA; 1740 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #312.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 23.00% Mismatches: 103
 Indels: 80
 Query Match:
 RESULT 964
 ID ADQ85633 standard; cDNA; 1740 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2447.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 23.00% Mismatches: 103
 Indels: 80
 Query Match:
 RESULT 965
 ID ADD69669 standard; DNA; 1779 BP.
 DE Chimeric IFN beta/HBsAg L DNA - SEQ ID 17.
 PN WO2003082345-A1.
 PD 09-OCT-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Best Local Similarity: 27.54% Mismatches: 41
 Indels: 68
 Query Match:

RESULT 966
 ID ADF81657 standard; DNA; 1781 BP.
 DE Leukaemia-related DNA sequence #2213.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DRUT KREBSFORSCHUNGSZENTRUM.
 PA (UYIU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAPE-) HAFERLACH T.
 PA (SCHO-) SCHOCH C.
 PA (KERN-) KERN W.
 Best Local Similarity: 23.00% Mismatches: 103
 Query Match: 6.04% Indels: 80
 RESULT 967
 ID ABD17236 standard; DNA; 1782 BP.
 DE Pseudomonas aeruginosa polynucleotide #15840.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.56% Mismatches: 139
 Query Match: 6.04% Indels: 58
 RESULT 968
 ID ADD69667 standard; DNA; 1803 BP.
 DE Chimeric IFN omega/HBsAg L DNA - SEQ ID 15.
 PN WO2003082345-A1.
 PD 09-OCT-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 969
 ID ABD05993 standard; DNA; 1836 BP.
 DE Pseudomonas aeruginosa polynucleotide #4587.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.23% Mismatches: 58
 Query Match: 6.04% Indels: 82
 RESULT 970
 ID ADM98693 standard; DNA; 1884 BP.
 DE HMG-CoA reductase DNA #28.
 PN US2004072323-A1.
 PD 15-APR-2004.
 PA (MATS-) MATSUDA S P T.
 PA (HART-) HART E A.
 Best Local Similarity: 23.15% Mismatches: 107
 Query Match: 6.04% Indels: 87
 RESULT 971
 ID AAH48560 standard; DNA; 1896 BP.
 DE Human fascin DNA fragment SEQ ID 10.
 PN WO200151631-A2.
 PD 19-JUL-2001.
 PA (RESK-) RESKE-KUNZ A.
 PA (ROSS-) ROSS X.
 PA (ROSS-) ROSS R.
 PA (BROS-) BROS M.
 Best Local Similarity: 27.65% Mismatches: 91
 Query Match: 6.04% Indels: 42
 RESULT 972
 ID AAH28220 standard; DNA; 1964 BP.
 DE Nucleotide sequence of urokinase plasminogen activator.
 PN WO200149309-A2.
 PD 12-JUL-2001.
 PA (PFIZ-) PFIZER LTD.
 PA (PFIZ-) PFIZER INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 973
 ID AAD27855 standard; cDNA; 1964 BP.
 DE Human uPA cDNA.
 PN WO200196606-A2.
 PD 20-DEC-2001.
 PA (NYXI-) NYXIS NEURO THERAPIES INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73

RESULT 974
 ID ADD69687 standard; DNA; 2013 BP.
 DE Chimeric GFP/HBsAg L DNA - SEQ ID 13.
 PN WO2003082345-A1.
 PD 09-OCT-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 975
 ID ADS45868 standard; cDNA; 2058 BP.
 DE Bacterial polynucleotide #611.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY-) CAO Y.
 PA (HINK-) HINKLE G J.
 PA (SLAT-) SLATER S C.
 PA (CHEN-) CHEN X.
 PA (GOLD-) GOLDMAN B S.
 Best Local Similarity: 27.20% Mismatches: 103
 Query Match: 6.04% Indels: 46
 RESULT 976
 ID ABD17273 standard; DNA; 2121 BP.
 DE Pseudomonas aeruginosa polynucleotide #15877.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.56% Mismatches: 139
 Query Match: 6.04% Indels: 58
 RESULT 977
 ID ABZ18317 standard; cDNA; 2161 BP.
 DE Group III cDNA cancer related clone SEQ ID NO:743.
 PN WO200278516-A2.
 PD 10-OCT-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 24.74% Mismatches: 97
 Query Match: 6.04% Indels: 89
 RESULT 978
 ID AAN93079 standard; DNA; 2266 BP.
 DE Sequence encoding prourokinase.
 PN EP299706-A.
 PD 18-JAN-1989.
 PA (COLB-) COLLABORATIVE RES INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 979
 ID AA224620 standard; cDNA; 2281 BP.
 DE Human lung tumor associated polynucleotide.
 PN WO9947674-A2.
 PD 23-SEP-1999.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 980
 ID AAC65859 standard; cDNA; 2294 BP.
 DE Human lung cancer-associated cDNA for contig 12.
 PN WO200061612-A2.
 PD 19-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 981
 ID ABL49078 standard; cDNA; 2294 BP.
 DE Human lung tumour cDNA sequence for contig 12 SEQ ID NO:123.
 PN WO200200174-A2.
 PD 03-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 982
 ID ABQ92264 standard; cDNA; 2294 BP.
 DE Human lung cancer associated cDNA sequence SEQ ID NO:123.
 PN WO200247534-A2.
 PD 20-JUN-2002.

PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 983
 ID ADA28213 standard; cDNA; 2294 BP.
 DE Human lung tumour associated cDNA contig 12.
 PN US2003064947-A1.
 PD 03-APR-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 984
 ID ADE53418 standard; cDNA; 2294 BP.
 DE Human lung tumour protein cDNA sequence #120.
 PN US2003119763-A1.
 PD 26-JUN-2003.
 PA (WANG/) WANG T.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 985
 ID ADH36777 standard; cDNA; 2294 BP.
 DE Human lung cancer-related cDNA sequence #120.
 PN WO2003086175-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 986
 ID ADK61310 standard; DNA; 2294 BP.
 DE Ovarian cancer-related DNA #465 with altered ovarian cancer expression.
 PN WO2003068054-A2.
 PD 21-AUG-2003.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 987
 ID ADI31891 standard; cDNA; 2294 BP.
 DE Human cDNA #1217.
 PN US6607879-B1.
 PD 19-AUG-2003.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 988
 ID ADM56580 standard; cDNA; 2294 BP.
 DE Human lung tumour cDNA #120.
 PN US2003138438-A1.
 PD 24-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 989
 ID ADN89624 standard; cDNA; 2294 BP.
 DE Human lung squamous cell carcinoma cDNA seqid 123.
 PN US6660838-B1.
 PD 09-DEC-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 990
 ID ACN44243 standard; cDNA; 2297 BP.
 DE Human mRNA sequence hCT11616.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 991
 ID AAN80981 standard; DNA; 2298 BP.
 DE Sequence of the single chain urokinase plasminogen activator (SCU-PA)
 DE cDNA insert prepared from human Hep3 cells.
 PN EP288435-A.

PD 26-OCT-1988.
 PA (CIBA) CIBA GEIGY AG.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 992
 ID AAN60703 standard; DNA; 2299 BP.
 DE Sequence encoding human urokinase.
 PN JP61181377-A.
 PD 14-AUG-1986.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (HODO) HODOGAYA CHEM IND CO LTD.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (NIPS) NIPPON SODA CO.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 993
 ID AAN70390 standard; DNA; 2301 BP.
 DE cDNA encoding human prourokinase in plasmid pKU22.
 PN EP231883-A.
 PD 12-AUG-1987.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (NIPS) NIPPON SODA CO.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (TOYJ) TOYO SODA MFG CO LTD.
 PA (NISC) NISSAN CHEM IND LTD.
 PA (NISC) NISSAN CHEMICAL INDS KK.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 994
 ID AAN91075 standard; DNA; 2301 BP.
 DE cDNA encoding natural human prourokinase and 5' UTR and 3' UTR.
 PN WO9901513-A.
 PD 23-FEB-1989.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (CENG) CENTRAL GLASS CO LTD.
 PA (HODO) HODOGAYA CHEM KK.
 PA (NIPS) NIPPON SODA CO.
 PA (NISC) NISSAN CHEM IND LTD.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 995
 ID AAN91740 standard; DNA; 2303 BP.
 DE Sequence of prourokinase cDNA.
 PN EP316068-A.
 PD 17-MAY-1989.
 PA (COLB) COLLABORATIVE RES INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 996
 ID AAQ73483 standard; cDNA; 2303 BP.
 DE Full length human urokinase protein cDNA.
 PN EP620279-A1.
 PD 19-OCT-1994.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 997
 ID AAN30030 standard; cDNA; 2304 BP.
 DE Sequence encoding full length urokinase.
 PN EP92182-A.
 PD 26-OCT-1983.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 998
 ID ABL59543 standard; cDNA; 2304 BP.
 DE Human pro-urokinase (uPA) cDNA SEQ ID NO:43.
 PN WO200227028-A1.
 PD 04-APR-2002.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Best Local Similarity: 23.05% Mismatches: 96

Query Match:	6.04%	Indels:	73
RESULT 999			
ID ABX76437 standard; DNA; 2304 BP.			
DE Lung cancer-associated polynucleotide #301.			
PN WO200286443-A2.			
PD 31-OCT-2002.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1000			
ID ABX76275 standard; DNA; 2304 BP.			
DE Lung cancer-associated polynucleotide #140.			
PN WO200286443-A2.			
PD 31-OCT-2002.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1001			
ID ABX17681 standard; DNA; 2304 BP.			
DE DNA encoding Human urokinase plasminogen activator #1.			
PN WO200279515-A1.			
PD 10-OCT-2002.			
PA (ISIS-) ISIS PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1002			
ID ACF12920 standard; cDNA; 2304 BP.			
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:183.			
PN WO2002101075-A2.			
PD 19-DEC-2002.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1003			
ID ADG89387 standard; DNA; 2304 BP.			
DE Cancer detection method related gene #50.			
PN WO2003078662-A1.			
PD 25-SEP-2003.			
PA (GENO-) GENOMIC HEALTH INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1004			
ID ADN39095 standard; cDNA; 2304 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:413.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1005			
ID ADN39740 standard; cDNA; 2304 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:CI12.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1006			
ID ADN95543 standard; DNA; 2304 BP.			
DE Human BEC/LEC-related gene sequence SeqID466.			
PN WO2003080640-A1.			
PD 02-OCT-2003.			
PA (LUDW-) LUDWIG INST CANCER RES.			
PA (LICN) LICENTIA LTD.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1007			
ID ADL70594 standard; cDNA; 2304 BP.			
DE Cervical cancer marker M58, urokinase, cDNA.			
PN WO2004018999-A2.			
PD 04-MAR-2004.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1008			
ID ADP07333 standard; DNA; 2304 BP.			
DE Human UPA DNA.			
PN DE10255104-A1.			
PD 11-MAR-2004.			
PA (BFIG-) EPIGENOMICS AG.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1009			
ID ADP23870 standard; cDNA; 2304 BP.			
DE PRO polypeptide encoding cDNA SEQ ID NO:1048.			
PN WO2004041170-A2.			
PD 21-MAY-2004.			
PA (GETH) GENENTECH INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1010			
ID AD825630 standard; cDNA; 2328 BP.			
DE Human gene expression profile polynucleotide SEQ ID NO 458.			
PN US2003194721-A1.			
PD 16-OCT-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1011			
ID AB235347 standard; cDNA; 2336 BP.			
DE Human gene expression profile polynucleotide SEQ ID NO 46.			
PN WO200274979-A2.			
PD 26-SEP-2002.			
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1012			
ID AD847346 standard; cDNA; 2336 BP.			
DE Human cDNA upregulated in dendritic cells SEQ ID NO 46.			
PN US2003134283-A1.			
PD 17-JUL-2003.			
PA (PETE/) PETERSON D P.			
PA (PEAR/) PEARSON C I.			
PA (COCK/) COCKS B G.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1013			
ID ADE54011 standard; cDNA; 2336 BP.			
DE Human prostate cancer cDNA #358.			
PN US2003190640-A1.			
PD 09-OCT-2003.			
PA (FARI/) FARIS M.			
PA (PEAR/) PEARSON C I.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1014			
ID ACH03958 standard; cDNA; 2341 BP.			
DE Human cDNA differentially expressed in lung cancer #163.			
PN US2003065157-A1.			
PD 03-APR-2003.			
PA (LASE/) LASEK A W.			
Best Local Similarity: 23.05%		Mismatches:	96
Query Match: 6.04%		Indels:	73
RESULT 1015			
ID ADO62846 standard; cDNA; 2352 BP.			
DE Novel human cDNA sequence #7.			
PN EPI440981-A2.			
PD 28-JUL-2004.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 24.79%		Mismatches:	110
Query Match: 6.04%		Indels:	44
RESULT 1016			
ID AAQ20360 standard; cDNA; 2377 BP.			
DE Human pro-urokinase cDNA.			
PN DE4122688-A.			
PD 16-JAN-1992.			

PA (FARM) FARMITALIA ERBA SRL CARLO.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 1017
 ID AAQ04107 standard; cDNA; 2427 BP.
 DE Human pro-urokinase cDNA of clone pcUK176.
 PN EP365894-A.
 PD 02-MAY-1990.
 PA (FARM) FARMITALIA ERBA SPA CARLO.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 1018
 ID ABQ54872 standard; cDNA; 2484 BP.
 DE Human ovarian antigen HVCB79 cDNA, SEQ ID NO:752.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 1019
 ID AAH34897 standard; cDNA; 2486 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1979.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 1020
 ID AAS75261 standard; cDNA; 2511 BP.
 DE DNA encoding novel human diagnostic protein #11065.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 25.84% Mismatches: 68
 Query Match: 6.04% Indels: 42
 RESULT 1021
 ID ADN61537 standard; cDNA; 2554 BP.
 DE Human KPP-47 encoding cDNA SEQ ID NO:103.
 PN WO2004042022-A2.
 PD 21-MAY-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 27.33% Mismatches: 107
 Query Match: 6.04% Indels: 77
 RESULT 1022
 ID ADQ22641 standard; DNA; 2655 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5461.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity: 23.05% Mismatches: 96
 Query Match: 6.04% Indels: 73
 RESULT 1023
 ID ADS6316 standard; cDNA; 2855 BP.
 DE Bacterial polynucleotide #8303.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAQY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 27.44% Mismatches: 89
 Query Match: 6.04% Indels: 79
 RESULT 1024
 ID AAK53269 standard; cDNA; 2976 BP.
 DE Human polynucleotide SEQ ID NO 2798.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 25.96% Mismatches: 81
 Query Match: 6.04% Indels: 68
 RESULT 1025
 ID ABD11116 standard; DNA; 3006 BP.

DE Pseudomonas aeruginosa polynucleotide #9720.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.38% Mismatches: 93
 Query Match: 6.04% Indels: 70
 RESULT 1026
 ID AAC98992 standard; cDNA; 3094 BP.
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:220.
 PN WO200055320-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.19% Mismatches: 117
 Query Match: 6.04% Indels: 47
 RESULT 1027
 ID ABD16084 standard; DNA; 3144 BP.
 DE Pseudomonas aeruginosa polynucleotide #14688.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.01% Mismatches: 127
 Query Match: 6.04% Indels: 56
 RESULT 1028
 ID AAS1474 standard; DNA; 3189 BP.
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #59.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.01% Mismatches: 127
 Query Match: 6.04% Indels: 56
 RESULT 1029
 ID ACA19473 standard; DNA; 3189 BP.
 DE Prokaryotic essential gene #1130.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.01% Mismatches: 127
 Query Match: 6.04% Indels: 56
 RESULT 1030
 ID ABD16462 standard; DNA; 3198 BP.
 DE Pseudomonas aeruginosa polynucleotide #15066.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.01% Mismatches: 127
 Query Match: 6.04% Indels: 56
 RESULT 1031
 ID AAS34856 standard; cDNA; 3220 BP.
 DE cDNA encoding novel human neoplastic disease associated polypeptide #90.
 PN WO200155163-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.96% Mismatches: 81
 Query Match: 6.04% Indels: 68
 RESULT 1032
 ID ADC46014 standard; cDNA; 3220 BP.
 DE Human neoplastic disease-associated gene 90 cDNA #1.
 PN US2003082758-A1.
 PD 01-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.96% Mismatches: 81
 Query Match: 6.04% Indels: 68
 RESULT 1033
 ID ADD69671 standard; DNA; 3359 BP.
 DE Chimeric HGP/HBSng L DNA - SEQ ID 19.
 PN WO2003082345-A1.
 PD 09-OCT-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Best Local Similarity: 27.54% Mismatches: 41
 Query Match: 6.04% Indels: 68
 RESULT 1034
 ID ABV21315 standard; cDNA; 3440 BP.
 DE Human prostate expression marker cDNA 21306.

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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1035
ID ABV27134 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 27125.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1036
ID ABV22159 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 22150.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1037
ID ABV27998 standard; cDNA; 3440 BP.
DE Human prostate expression marker cDNA 27989.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1038
ID ADS9759 standard; cDNA; 3462 BP.
DE Bacterial polynucleotide #11746.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.32% Mismatches: 84
Query Match: 6.04% Indels: 61
RESULT 1039
ID AAA97456 standard; cDNA; 3585 BP.
DE Human RalGDS (hralGDS) cDNA.
PN CN1257923-A.
PD 28-JUN-2000.
PA (UYFU-) UNIV FUDAN.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1040
ID ABN67289 standard; DNA; 3632 BP.
DE Streptococcus polynucleotide SEQ ID NO 2491.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 23.66% Mismatches: 123
Query Match: 6.04% Indels: 41
RESULT 1041
ID ADR07359 standard; cDNA; 3690 BP.
DE Full length human cDNA useful for treating neurological disease Seq 865.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 25.96% Mismatches: 81
Query Match: 6.04% Indels: 68
RESULT 1042
ID ABX93554 standard; cDNA; 3691 BP.
DE Human cDNA encoding GTP releasing factor 15368.
PN US2002187138-A1.
PD 12-DEC-2002.
PA (MEYE/) MEYERS R.
Best Local Similarity: 25.96% Mismatches: 81

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Query Match: 6.04% Indels: 68
RESULT 1043
ID ADJ67856 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038289-A1.
PD 26-FEB-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1044
ID ADJ68068 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038290-A1.
PD 26-FEB-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1045
ID ADK01146 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme subunit DNA #6.
PN US2004043415-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1046
ID ADJ79365 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004043414-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1047
ID ADJ84805 standard; DNA; 3729 BP.
DE T. thermophilus DNA polymerase III alpha subunit gene.
PN US2004048309-A1.
PD 11-MAR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60% Mismatches: 97
Query Match: 6.04% Indels: 63
RESULT 1048
ID ADM77593 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme related polynucleotide #4.
PN US2004077012-A1.
PD 22-APR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.

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PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60%
Query Match: 6.04%
Mismatch: 97
Indels: 63
RESULT 1049
ID ADM66260 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
FN US2004081995-A1.
PD 29-APR-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60%
Query Match: 6.04%
Mismatch: 97
Indels: 63
RESULT 1050
ID ADO04313 standard; DNA; 3729 BP.
DE T. thermophilus DNA polymerase III dnaE gene.
FN US2004106137-A1.
PD 03-JUN-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60%
Query Match: 6.04%
Mismatch: 97
Indels: 63
RESULT 1051
ID ADP82390 standard; DNA; 3729 BP.
DE Thermus thermophilus dnaE gene.
FN US2004110210-A1.
PD 10-JUN-2004.
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
Best Local Similarity: 24.60%
Query Match: 6.04%
Mismatch: 97
Indels: 63
RESULT 1052
ID ABD14910 standard; DNA; 4401 BP.
DE Pseudomonas aeruginosa polynucleotide #13514.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.77%
Query Match: 6.04%
Mismatch: 82
Indels: 66
RESULT 1053
ID ABL22547 standard; DNA; 4674 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 19114.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 22.14%
Query Match: 6.04%
Mismatch: 93
Indels: 87
RESULT 1054
ID AAK52952 standard; cDNA; 5537 BP.
DE Human polynucleotide SEQ ID NO 2481.
FN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.52%
Query Match: 6.04%
Mismatch: 97
Indels: 86
RESULT 1055
ID AAD28151 standard; DNA; 5628 BP.
DE Human secretion and trafficking DNA-6 (SAT-6).
FN WO200202610-A2.

PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 25.52%
Query Match: 6.04%
Mismatch: 97
Indels: 86
RESULT 1056
ID ABS78666 standard; DNA; 5871 BP.
DE S. ghanaensis DNA encoding PKSE.
FN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Best Local Similarity: 25.85%
Query Match: 6.04%
Mismatch: 87
Indels: 39
RESULT 1057
ID ADM06776 standard; cDNA; 10011 BP.
DE Human pericentrin-B cDNA, SEQ ID NO:3.
FN WO2004024887-A2.
PD 25-MAR-2004.
PA (UYMA-) UNIV MASSACHUSETTS.
Best Local Similarity: 23.97%
Query Match: 6.04%
Mismatch: 104
Indels: 52
RESULT 1058
ID AAS74106 standard; cDNA; 10438 BP.
DE DNA encoding novel human diagnostic protein #9910.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 23.97%
Query Match: 6.04%
Mismatch: 104
Indels: 52
RESULT 1059
ID ADQ24969 standard; DNA; 10725 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7789.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 23.97%
Query Match: 6.04%
Mismatch: 104
Indels: 52
RESULT 1060
ID AAZ55620 standard; DNA; 10877 BP.
DE Human BMP-7 gene 5' upstream region.
FN WO9957293-A1.
PD 11-NOV-1999.
PA (HMRI) HOECHST MARION ROUSSEL LTD.
Best Local Similarity: 23.34%
Query Match: 6.04%
Mismatch: 110
Indels: 78
RESULT 1061
ID ADH50604 standard; DNA; 13000 BP.
DE Human IRAK-1 associated DNA sequence #1.
FN US2003228690-A1.
PD 11-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Best Local Similarity: 24.56%
Query Match: 6.04%
Mismatch: 103
Indels: 84
RESULT 1062
ID AAH48621 standard; DNA; 13055 BP.
DE Human fascin DNA fragment #1.
FN WO200151631-A2.
PD 19-JUL-2001.
PA (RESK/) RESKE-KUNZ A.
PA (ROSS/) ROSS X.
PA (ROSS/) ROSS R.
PA (BROS/) BROS M.
Best Local Similarity: 27.65%
Query Match: 6.04%
Mismatch: 91
Indels: 42
RESULT 1063
ID AAH48620 standard; DNA; 16951 BP.
DE Human fascin DNA fragment SEQ ID 72.
FN WO200151631-A2.
PD 19-JUL-2001.
PA (RESK/) RESKE-KUNZ A.
PA (ROSS/) ROSS X.
PA (ROSS/) ROSS R.
PA (BROS/) BROS M.
Best Local Similarity: 27.65%
Query Match: 6.04%
Mismatch: 91
Indels: 42

Query Match:	6.04%	Indels:	42
RESULT 1064			
ID AAH48622 standard; DNA; 16951 BP.			
DE Human fascin DNA fragment #2.			
PN WO200151631-A2.			
PA (RESK/) RESK-KUNZ A.			
PA (ROSS/) ROSS X.			
PA (ROSS/) ROSS R.			
PA (BROS/) BROS M.			
Best Local Similarity: 27.65%		Mismatches:	91
Query Match:	6.04%	Indels:	42
RESULT 1065			
ID ADI23928 standard; DNA; 18876 BP.			
DE Streptomyces refuineus 024A locus ORF4.			
PN US200319891-A1.			
PA (ECOP-) ECOPIA BIOSCIENCES INC.			
Best Local Similarity: 23.26%		Mismatches:	118
Query Match:	6.04%	Indels:	67
RESULT 1066			
ID ABZ75344 standard; DNA; 23673 BP.			
DE Human R1128 gene cluster.			
PN US6340774-B1.			
PD 22-JAN-2002.			
PA (STRD) UNIV LELAND STANFORD JUNIOR.			
Best Local Similarity: 26.69%		Mismatches:	80
Query Match:	6.04%	Indels:	77
RESULT 1067			
ID AAA11992 standard; DNA; 37856 BP.			
DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.			
PN DE19846493-A1.			
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.			
Best Local Similarity: 25.94%		Mismatches:	92
Query Match:	6.04%	Indels:	83
RESULT 1068			
ID ADI23920 standard; DNA; 61944 BP.			
DE Streptomyces refuineus 024A locus (NRRL 3143).			
PN US200319891-A1.			
PD 23-OCT-2003.			
PA (ECOP-) ECOPIA BIOSCIENCES INC.			
Best Local Similarity: 23.26%		Mismatches:	118
Query Match:	6.04%	Indels:	67
RESULT 1069			
ID ADQ74672 standard; DNA; 74787 BP.			
DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.			
Best Local Similarity: 21.74%		Mismatches:	87
Query Match:	6.04%	Indels:	119
RESULT 1070			
ID ADL15447 standard; DNA; 85915 BP.			
DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.			
PN WO2004018703-A2.			
PD 04-MAR-2004.			
PA (KOSA-) KOSAN BIOSCIENCES INC.			
Best Local Similarity: 23.87%		Mismatches:	101
Query Match:	6.04%	Indels:	112
RESULT 1071			
ID ADP65471 standard; DNA; 92794 BP.			
DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.			
PN WO2003072827-A1.			
PD 04-SEP-2003.			
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.			
Best Local Similarity: 22.02%		Mismatches:	97
Query Match:	6.04%	Indels:	90
RESULT 1072			
ID ABD33009 standard; DNA; 99918 BP.			
DE Human cancer-associated genomic DNA HD21-032.			
PN WO2004074320-A2.			
PD 02-SEP-2004.			
PA (SAGR-) SAGRES DISCOVERY INC.			
Best Local Similarity: 25.90%		Mismatches:	73
Query Match:	6.04%	Indels:	90
RESULT 1073			
ID ABL68122 standard; DNA; 174424 BP.			
DE Ovary cancer related gene sequence SEQ ID NO:6459.			
PN WO200194629-A2.			
PD 13-DEC-2001.			
PA (AVAL-) AVALON PHARM.			
Best Local Similarity: 24.56%		Mismatches:	103
Query Match:	6.04%	Indels:	84
RESULT 1074			
ID ADQ19573 standard; DNA; 181343 BP.			
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.			
PN WO2004048938-A2.			
PD 10-JUN-2004.			
PA (PROT-) PROTEIN DESIGN LABS INC.			
Best Local Similarity: 24.56%		Mismatches:	103
Query Match:	6.04%	Indels:	84
RESULT 1075			
ID ABD07796 standard; DNA; 636 BP.			
DE Pseudomonas aeruginosa polynucleotide #6400.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 25.84%		Mismatches:	59
Query Match:	6.01%	Indels:	55
RESULT 1076			
ID ACA23440 standard; DNA; 864 BP.			
DE Prokaryotic essential gene #5097.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITPA PHARM INC.			
Best Local Similarity: 24.80%		Mismatches:	96
Query Match:	6.01%	Indels:	59
RESULT 1077			
ID ABZ38524 standard; DNA; 933 BP.			
DE N. gonorrhoeae nucleotide sequence SEQ ID 1637.			
PN WO200279243-A2.			
PD 10-OCT-2002.			
PA (CHIR-) CHIRON SPA.			
Best Local Similarity: 22.02%		Mismatches:	67
Query Match:	6.01%	Indels:	46
RESULT 1080			
ID ABD06399 standard; DNA; 981 BP.			
DE Pseudomonas aeruginosa polynucleotide #5003.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 23.57%		Mismatches:	100
Query Match:	6.01%	Indels:	86
RESULT 1081			
ID ABD09462 standard; DNA; 993 BP.			
DE Pseudomonas aeruginosa polynucleotide #8066.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 19.57%		Mismatches:	84
Query Match:	6.01%	Indels:	106
RESULT 1082			
ID ABD15086 standard; DNA; 1014 BP.			
DE Pseudomonas aeruginosa polynucleotide #13690.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 25.58%		Mismatches:	108
Query Match:	6.01%	Indels:	82
RESULT 1083			
ID ABD10877 standard; DNA; 1083 BP.			
DE Pseudomonas aeruginosa polynucleotide #9481.			

PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.27% Mismatches: 64
 Query Match: 6.01% Indels: 57
 RESULT 1084
 ID ABI07351 standard; cDNA; 1142 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16535.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Best Local Similarity: 21.15% Mismatches: 97
 Query Match: 6.01% Indels: 89
 RESULT 1085
 ID AD32623 standard; cDNA; 1160 BP.
 DE Human novel cDNA contig sequence, SEQ ID NO:2705.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 28.52% Mismatches: 85
 Query Match: 6.01% Indels: 79
 RESULT 1086
 ID AAS67936 standard; cDNA; 1164 BP.
 DE DNA encoding novel human diagnostic protein #3740.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 23.53% Mismatches: 113
 Query Match: 6.01% Indels: 79
 RESULT 1087
 ID ABD03878 standard; DNA; 1179 BP.
 DE Pseudomonas aeruginosa polynucleotide #2482.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.20% Mismatches: 95
 Query Match: 6.01% Indels: 66
 RESULT 1088
 ID AAT18237 standard; DNA; 1233 BP.
 DE Pro-urokinase gene.
 PN WO9604004-A1.
 PD 15-FEB-1996.
 PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1089
 ID AAT68797 standard; DNA; 1233 BP.
 DE Coding sequence for pro-urokinase.
 PN US5626841-A.
 PD 06-MAY-1997.
 PA (GURE/) GUREWICH V.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1090
 ID AAT61671 standard; cDNA; 1236 BP.
 DE Human native prourokinase cDNA.
 PN EP398361-A.
 PD 22-NOV-1990.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1091
 ID AA041450 standard; DNA; 1236 BP.
 DE Mutant human prourokinase gene.
 PN EP541952-A1.
 PD 19-MAY-1993.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1092
 ID AAQ48228 standard; DNA; 1236 BP.
 DE FUK gene.
 PN JP05192142-A.
 PD 03-AUG-1993.
 PA (GREC) GREEN CROSS CORP.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1093
 ID AAD27077 standard; DNA; 1236 BP.
 DE Human urokinase-type plasminogen activator tcuPA and scuPA DNA.
 PN WO200197752-A2.
 PD 27-DEC-2001.
 PA (UYPE-) UNIV PENNSYLVANIA.
 Best Local Similarity: 24.00% Mismatches: 88
 Query Match: 6.01% Indels: 60
 RESULT 1094
 ID ABD03749 standard; DNA; 1341 BP.
 DE Pseudomonas aeruginosa polynucleotide #2353.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.20% Mismatches: 95
 Query Match: 6.01% Indels: 66
 RESULT 1095
 ID AD747038 standard; cDNA; 1365 BP.
 DE Bacterial polynucleotide #21789.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 28.17% Mismatches: 70
 Query Match: 6.01% Indels: 84
 RESULT 1096
 ID ABD03960 standard; DNA; 1398 BP.
 DE Pseudomonas aeruginosa polynucleotide #2564.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.20% Mismatches: 95
 Query Match: 6.01% Indels: 66
 RESULT 1097
 ID ABD11805 standard; DNA; 1398 BP.
 DE Pseudomonas aeruginosa polynucleotide #10409.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.84% Mismatches: 109
 Query Match: 6.01% Indels: 51
 RESULT 1098
 ID ACA43969 standard; DNA; 1407 BP.
 DE Prokaryotic essential gene #25626.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 22.84% Mismatches: 97
 Query Match: 6.01% Indels: 95
 RESULT 1099
 ID ACA45499 standard; DNA; 1413 BP.
 DE Prokaryotic essential gene #27156.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 21.15% Mismatches: 102
 Query Match: 6.01% Indels: 82
 RESULT 1100
 ID ABD12148 standard; DNA; 1446 BP.
 DE Pseudomonas aeruginosa polynucleotide #10752.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.84% Mismatches: 109
 Query Match: 6.01% Indels: 51
 RESULT 1101

ID ACA42073 standard; DNA; 1480 BP.
 DE Prokaryotic essential gene #23730.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.27% Mismatches: 107
 Query Match: 6.01% Indels: 43
 RESULT 1102

ID AAC43474 standard; DNA; 1491 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 39370.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 25.00% Mismatches: 104
 Query Match: 6.01% Indels: 20
 RESULT 1103

ID AB214815 standard; DNA; 1491 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2620.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 25.00% Mismatches: 104
 Query Match: 6.01% Indels: 20
 RESULT 1104

ID ADN73354 standard; cDNA; 1491 BP.
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1249.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDISEIGN NV.
 Best Local Similarity: 25.00% Mismatches: 104
 Query Match: 6.01% Indels: 20
 RESULT 1105

ID AAA09191 standard; DNA; 1500 BP.
 DE Trametes versicolor laccase coding sequence.
 PN WO200020615-A2.
 PD 13-APR-2000.
 PA (PROD-) PRODIGENE INC.
 Best Local Similarity: 22.40% Mismatches: 117
 Query Match: 6.01% Indels: 83
 RESULT 1106

ID ABA92910 standard; cDNA; 1500 BP.
 DE Trametes versicolor laccase I gene.
 PN WO200196543-A2.
 PD 20-DEC-2001.
 PA (PROD-) PRODIGENE INC.
 PA (GENV) GENENCOR INC.
 Best Local Similarity: 22.40% Mismatches: 117
 Query Match: 6.01% Indels: 83
 RESULT 1107

ID ABQ94267 standard; DNA; 1728 BP.
 DE lovf gene expression regulator At240 coding sequence.
 PN WO200257456-A2.
 PD 25-JUL-2002.
 PA (MICR-) MICROBIA.
 Best Local Similarity: 19.81% Mismatches: 101
 Query Match: 6.01% Indels: 110
 RESULT 1108

ID ABN79911 standard; DNA; 1728 BP.
 DE Fungal ZBC gene sequence #148.
 PN WO200224865-A2.
 PD 28-MAR-2002.
 PA (MICR-) MICROBIA INC.
 Best Local Similarity: 19.81% Mismatches: 101
 Query Match: 6.01% Indels: 110
 RESULT 1109

ID ADA69634 standard; DNA; 1845 BP.
 DE Rice gene, SEQ ID 2957.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 22.60% Mismatches: 83
 Query Match: 6.01% Indels: 125
 RESULT 1110

ID ABD08028 standard; DNA; 1848 BP.
 DE Pseudomonas aeruginosa polynucleotide #6632.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 26.27% Mismatches: 107
 Query Match: 6.01% Indels: 43
 RESULT 1111

ID AAC49857 standard; DNA; 1883 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62696.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 25.00% Mismatches: 104
 Query Match: 6.01% Indels: 20
 RESULT 1112

ID ADG55901 standard; cDNA; 1923 BP.
 DE Bacterial polynucleotide #7888.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 24.69% Mismatches: 86
 Query Match: 6.01% Indels: 73
 RESULT 1113

ID ABD08626 standard; DNA; 1932 BP.
 DE Pseudomonas aeruginosa polynucleotide #7230.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.77% Mismatches: 97
 Query Match: 6.01% Indels: 125
 RESULT 1114

ID AB030350 standard; DNA; 1986 BP.
 DE Pseudomonas aeruginosa polynucleotide #1654.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.51% Mismatches: 98
 Query Match: 6.01% Indels: 123
 RESULT 1115

ID ADS14561 standard; DNA; 1995 BP.
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA1251, SEQ ID 116.
 PN WO2004083385-A2.
 PD 30-SEP-2004.
 PA (IOWA) UNIV IOWA RES FOUND.
 Best Local Similarity: 19.57% Mismatches: 84
 Query Match: 6.01% Indels: 106
 RESULT 1116

ID AQ032857 standard; DNA; 2027 BP.
 DE Mutant bovine herpes virus type 1 - deletion in gE gene.
 PN WO9221751-A1.
 PD 10-DEC-1992.
 PA (DIER-) STICHTING CENT DIERGENEESKUNDIG INST.
 Best Local Similarity: 25.93% Mismatches: 120
 Query Match: 6.01% Indels: 49
 RESULT 1117

ID AAQ36769 standard; DNA; 2040 BP.
 DE Sequence of the IBR glycoprotein E gene.
 PN WO9302104-A1.
 PD 04-FEB-1993.
 PA (SVTR) SYNTRO CORP.
 Best Local Similarity: 23.34% Mismatches: 115
 Query Match: 6.01% Indels: 93
 RESULT 1118

ID AAQ97671 standard; DNA; 2040 BP.
 DE Infectious bovine rhinotracheitis virus glycoprotein E gene.
 PN WO9521261-A1.
 PD 10-AUG-1995.
 PA (SVTR) SYNTRO CORP.
 Best Local Similarity: 23.34% Mismatches: 115
 Query Match: 6.01% Indels: 93
 RESULT 1119

Query Match:	6.01%	Indels:	93
RESULT 1119			
ID ABD09392 standard; DNA; 2046 BP.			
DE Pseudomonas aeruginosa polynucleotide #7996.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 25.71%	Mismatches:		78
Query Match: 6.01%	Indels:		57
RESULT 1120			
ID ABD09454 standard; DNA; 2046 BP.			
DE Pseudomonas aeruginosa polynucleotide #8058.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 25.71%	Mismatches:		78
Query Match: 6.01%	Indels:		57
RESULT 1121			
ID ABD09591 standard; DNA; 2121 BP.			
DE Pseudomonas aeruginosa polynucleotide #8195.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 19.57%	Mismatches:		84
Query Match: 6.01%	Indels:		106
RESULT 1122			
ID AAT03824 standard; DNA; 2336 BP.			
DE Bovine herpesvirus-1 FM gII glycoprotein gene.			
PN EP668356-A2.			
PD 23-AUG-1995.			
PA (HPR-) LAB HIPRA SA.			
Best Local Similarity: 25.93%	Mismatches:		120
Query Match: 6.01%	Indels:		49
RESULT 1123			
ID AAH1671 standard; cDNA; 2348 BP.			
DE Human cDNA sequence SEQ ID NO:17236.			
PN EP1074617-A2.			
PD 07-FEB-2001.			
PA (HELI-) HELIX RES INST.			
Best Local Similarity: 24.51%	Mismatches:		86
Query Match: 6.01%	Indels:		74
RESULT 1124			
ID ABD08027 standard; DNA; 2715 BP.			
DE Pseudomonas aeruginosa polynucleotide #6631.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 26.27%	Mismatches:		107
Query Match: 6.01%	Indels:		43
RESULT 1125			
ID ABD09507 standard; DNA; 2727 BP.			
DE Pseudomonas aeruginosa polynucleotide #8111.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 19.57%	Mismatches:		84
Query Match: 6.01%	Indels:		106
RESULT 1126			
ID ADR07670 standard; cDNA; 2732 BP.			
DE Full length human cDNA useful for treating neurological			
PN EP1447413-A2.			
PD 18-AUG-2004.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Best Local Similarity: 25.89%	Mismatches:		112
Query Match: 6.01%	Indels:		80
RESULT 1127			
ID ABD08863 standard; DNA; 2898 BP.			
DE Pseudomonas aeruginosa polynucleotide #7467.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 22.77%	Mismatches:		97
Query Match: 6.01%	Indels:		125

RESULT 1128					
ID	ABF743728 standard; cDNA; 3181 BP.				
DE	Molecule for disease detection and treatment (MDDT)-36 cDNA sequence.				
FN	W02003052049-A2.				
PD	26-JUN-2003.				
PA	(INCY-) INCYTE GENOMICS INC.				
Best Local Similarity:	23.16%	Mismatches:	90		
Query Match:	6.01%	Indels:	99		
RESULT 1129					
ID	ADM87438 standard; cDNA; 3376 BP.				
DE	Human EST derived nucleotide sequence SEQ ID NO:531.				
FN	W02004009834-A2.				
PD	29-JAN-2004.				
PA	(NUVE-) NUVELO INC.				
Best Local Similarity:	25.40%	Mismatches:	80		
Query Match:	6.01%	Indels:	76		
RESULT 1130					
ID	ADC59315 standard; DNA; 3399 BP.				
DE	DNA encoding human polypeptide #4.				
FN	JP2002360268-A.				
PD	17-DEC-2002.				
PA	(KAZU-) ZH KAZUSA DNA KENKYUSHO.				
PA	(DAUC) DAIICHI PHARM CO LTD.				
Best Local Similarity:	20.23%	Mismatches:	103		
Query Match:	6.01%	Indels:	58		
RESULT 1131					
ID	ACA43576 standard; DNA; 3636 BP.				
DE	Prokaryotic essential gene #24233.				
FN	WO200277183-A2.				
PD	03-OCT-2002.				
PA	(ELIT-) ELITRA PHARM INC.				
Best Local Similarity:	26.27%	Mismatches:	107		
Query Match:	6.01%	Indels:	43		
RESULT 1132					
ID	ABD08062 standard; DNA; 3702 BP.				
DE	Pseudomonas aeruginosa polynucleotide #6666.				
FN	US6551795-B1.				
PD	22-APR-2003.				
PA	(GENO-) GENOME THERAPEUTICS CORP.				
Best Local Similarity:	26.27%	Mismatches:	107		
Query Match:	6.01%	Indels:	43		
RESULT 1133					
ID	AAS5350 standard; DNA; 4190 BP.				
DE	Sequence of the unique short (Us) region of bovine herpes virus (BHV)				
DE	which forms the insertion region and comprises 3 open reading frames.				
FN	W09400586-A2.				
PD	06-JAN-1994.				
PA	(INMR) RHONE MERIEUX SA.				
Best Local Similarity:	25.93%	Mismatches:	120		
Query Match:	6.01%	Indels:	49		
RESULT 1134					
ID	AAD54622 standard; DNA; 4989 BP.				
DE	Human Mastermind (Mam) homologue DNA, MAML2.				
FN	WO2002102987-A2.				
PD	27-DEC-2002.				
PA	(GHEO) GEN HOSPITAL CORP.				
Best Local Similarity:	20.23%	Mismatches:	103		
Query Match:	6.01%	Indels:	58		
RESULT 1135					
ID	ABA91314 standard; DNA; 6650 BP.				
DE	Human colon specific gene 203640.				
FN	WO200192528-A2.				
PD	06-DEC-2001.				
PA	(DIAD-) DIADEXUS INC.				
Best Local Similarity:	22.11%	Mismatches:	104		
Query Match:	6.01%	Indels:	114		
RESULT 1136					
ID	AAK70210 standard; DNA; 7885 BP.				
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25022.				
FN	WO200157182-A2.				
PD	09-AUG-2001.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Best Local Similarity:	25.48%	Mismatches:	69		

Query Match: 6.01% Indels: 60

RESULT 1137
ID ABT07614 standard; cDNA; 8156 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 93.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 24.10% Mismatches: 65
Query Match: 6.01% Indels: 66

RESULT 1138
ID AAS32754 standard; DNA; 9134 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 708.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 26.57% Mismatches: 101
Query Match: 6.01% Indels: 70

RESULT 1139
ID ABZ22017 standard; cDNA; 9646 BP.
DE Human leukaemia associated CML nucleotide sequence SEQ ID NO:2.
PN CN1356390-A.
PD 03-JUL-2002.
PA (UYHO-) UNIV HOSPITAL NO 2 ATTACHED TO MEDICAL C.
Best Local Similarity: 26.67% Mismatches: 69
Query Match: 6.01% Indels: 50

RESULT 1140
ID AAL61173 standard; DNA; 9975 BP.
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW-) UNIV WASHINGTON.
Best Local Similarity: 24.50% Mismatches: 94
Query Match: 6.01% Indels: 74

RESULT 1141
ID AB150560 standard; DNA; 14071 BP.
DE Micromonospora carbonacea everninomicin locus nucleotide contig 6.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Best Local Similarity: 24.92% Mismatches: 121
Query Match: 6.01% Indels: 69

RESULT 1142
ID ACA19579 standard; DNA; 15450 BP.
DE Prokaryotic essential gene #1236.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Best Local Similarity: 26.46% Mismatches: 89
Query Match: 6.01% Indels: 79

RESULT 1143
ID AAV23494 standard; DNA; 17612 BP.
DE Pseudomonas Xpc, OrfV, OrfX operon.
PN WO9806836-A2.
PD 19-FEB-1998.
PA (GENV) GENENCOR INT INC.
Best Local Similarity: 24.34% Mismatches: 105
Query Match: 6.01% Indels: 77

RESULT 1144
ID AAL13905 standard; DNA; 17612 BP.
DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:29.
PN US6048710-A.
PD 11-APR-2000.
PA (GENV) GENENCOR INT INC.
Best Local Similarity: 24.34% Mismatches: 105
Query Match: 6.01% Indels: 77

RESULT 1145
ID AAP30870 standard; DNA; 17612 BP.
DE Pseudomonas alcaligenes secretion factor gene region.
PN US6225106-B1.
PD 01-MAY-2001.
PA (GENV) GENENCOR INT INC.
Best Local Similarity: 24.34% Mismatches: 105

Query Match: 6.01% Indels: 77

RESULT 1146
ID AAD22882 standard; DNA; 17612 BP.
DE Pseudomonas alcaligenes 17.612 bp DNA from the insert on cosmid #600.
PN US6313283-B1.
PD 06-NOV-2001.
PA (GENV) GENENCOR INT INC.
Best Local Similarity: 24.34% Mismatches: 105
Query Match: 6.01% Indels: 77

RESULT 1147
ID ADA03092 standard; DNA; 29322 BP.
DE Human LFNG carcinoma associated gene, SEQ ID NO:1610.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 22.57% Mismatches: 104
Query Match: 6.01% Indels: 76

RESULT 1148
ID ADA66376 standard; DNA; 29322 BP.
DE Human LFNG gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 22.57% Mismatches: 104
Query Match: 6.01% Indels: 76

RESULT 1149
ID ADB72830 standard; DNA; 29322 BP.
DE Human LFNG gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 22.57% Mismatches: 104
Query Match: 6.01% Indels: 76

RESULT 1150
ID ABZ66811 standard; DNA; 48221 BP.
DE Orthomyxovirus biosynthetic gene cluster SEQ ID NO 280.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Best Local Similarity: 24.92% Mismatches: 121
Query Match: 6.01% Indels: 69

RESULT 1151
ID AAD55810 standard; DNA; 60196 BP.
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.
PN CA2391131-A1.
PD 19-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Best Local Similarity: 23.56% Mismatches: 96
Query Match: 6.01% Indels: 47

RESULT 1152
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.19% Mismatches: 94
Query Match: 6.01% Indels: 87

RESULT 1153
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.19% Mismatches: 94
Query Match: 6.01% Indels: 87

RESULT 1154
ID AAL61224 standard; DNA; 82746 BP.
DE Actinosynnema pretiosum aneamitocin biosynthetic gene cluster I.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 27.95% Mismatches: 96
Query Match: 6.01% Indels: 43

RESULT 1155
 Best Local Similarity: 26.98% Mismatches: 99
 Query Match: 6.01% Indels: 76
 RESULT 1156
 Best Local Similarity: 29.17% Mismatches: 64
 Query Match: 6.01% Indels: 44
 RESULT 1157
 Best Local Similarity: 29.17% Mismatches: 64
 Query Match: 6.01% Indels: 44
 RESULT 1158
 ID ABS5655 standard; DNA; 171936 BP.
 DE Human SULF2 genomic DNA sequence.
 PN WO200259327-A2.
 PD 01-AUG-2002.
 PA (REGC) UNIV CALIFORNIA.
 Best Local Similarity: 23.08% Mismatches: 69
 Query Match: 6.01% Indels: 79
 RESULT 1159
 ID ADN16205 standard; DNA; 171936 BP.
 DE Mouse sulfatase SULF2 gene.
 PN WO2004011365-A2.
 PD 15-APR-2004.
 PA (REGC) UNIV CALIFORNIA.
 PA (THIO-) THIOS PHARM INC.
 Best Local Similarity: 23.08% Mismatches: 69
 Query Match: 6.01% Indels: 79
 RESULT 1160
 ID A468534 standard; DNA; 309400 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 7069.
 PN EP108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 25.35% Mismatches: 91
 Query Match: 6.01% Indels: 42
 RESULT 1161
 ID ABQ81842 standard; DNA; 349980 BP.
 DE Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.
 PN EP127152-A1.
 PD 31-JUL-2002.
 PA (NEST) SOC PROD NESTLE SA.
 Best Local Similarity: 23.84% Mismatches: 105
 Query Match: 6.01% Indels: 80
 RESULT 1162
 ID ADK56808 standard; DNA; 651 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #4191.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Best Local Similarity: 22.03% Mismatches: 74
 Query Match: 5.97% Indels: 37
 RESULT 1163
 ID ADA70766 standard; DNA; 783 BP.
 DE Rice gene, SEQ ID 4089.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 29.45% Mismatches: 54
 Query Match: 5.97% Indels: 48
 RESULT 1164
 ID ABZ11237 standard; cDNA; 866 BP.
 DE Human polynucleotide SEQ ID NO 119.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.76% Mismatches: 113
 Query Match: 5.97% Indels: 90
 RESULT 1165
 ID ADM43755 standard; cDNA; 866 BP.
 DE Novel human arginine-rich protein cDNA #119.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.

PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Best Local Similarity: 24.76% Mismatches: 113
 Query Match: 5.97% Indels: 90
 RESULT 1166
 ID ABL55081 standard; DNA; 1015 BP.
 DE Human cDNA sequence #1 from clone HVARW53.
 PN WO200222638-A1.
 PD 21-MAR-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.26% Mismatches: 113
 Query Match: 5.97% Indels: 84
 RESULT 1167
 ID ADA40227 standard; cDNA; 1015 BP.
 DE Human secreted protein encoding cDNA.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.26% Mismatches: 113
 Query Match: 5.97% Indels: 84
 RESULT 1168
 ID ADC73753 standard; DNA; 1015 BP.
 DE Human secreted protein-related DNA - SEQ ID 386.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 23.26% Mismatches: 113
 Query Match: 5.97% Indels: 84
 RESULT 1169
 ID AAS66980 standard; cDNA; 1026 BP.
 DE DNA encoding novel human diagnostic protein #2784.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.87% Mismatches: 80
 Query Match: 5.97% Indels: 41
 RESULT 1170
 ID AAT41786 standard; DNA; 1047 BP.
 DE Fusion peptide #1 having G-CSF and TPO activity.
 PN WO9634016-A1.
 PD 31-OCT-1996.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 28.38% Mismatches: 97
 Query Match: 5.97% Indels: 42
 RESULT 1171
 ID ABZ14593 standard; DNA; 1062 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2398.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 20.96% Mismatches: 99
 Query Match: 5.97% Indels: 85
 RESULT 1172
 ID ADG87742 standard; cDNA; 1062 BP.
 DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #184.
 PN WO200222675-A2.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UNYC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANG J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Best Local Similarity: 20.96% Mismatches: 99
 Query Match: 5.97% Indels: 85
 RESULT 1173
 ID ADA68341 standard; DNA; 1062 BP.
 DE Arabidopsis thaliana gene, SEQ ID 793.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Best Local Similarity: 20.96%	Mismatches: 99	Query Match: 5.97%	Indels: 86
Query Match: 5.97%	Indels: 85	RESULT 1174	
ID AAS78523 standard; cDNA; 1218 BP.		ID ABD10565 standard; DNA; 1470 BP.	
DE DNA encoding novel human diagnostic protein #14327.		DE Pseudomonas aeruginosa polynucleotide #9169.	
PN WO200175067-A2.		PN US6551795-B1.	
PD 11-OCT-2001.		PD 22-APR-2003.	
PA (HYSE-) HYSEQ INC.		PA (GENO-) GENOME THERAPEUTICS CORP.	
Best Local Similarity: 22.83%	Mismatches: 81	Best Local Similarity: 24.62%	Mismatches: 118
Query Match: 5.97%	Indels: 90	Query Match: 5.97%	Indels: 50
RESULT 1175		RESULT 1184	
ID ABD04990 standard; DNA; 1254 BP.		ID ADS60780 standard; cDNA; 1473 BP.	
DE Pseudomonas aeruginosa polynucleotide #3594.		DE Bacterial polynucleotide #12767.	
PN US6551795-B1.		PN US2003233675-A1.	
PD 22-APR-2003.		PD 18-DEC-2003.	
PA (GENO-) GENOME THERAPEUTICS CORP.		PA (CAOY/) CAO Y.	
Best Local Similarity: 24.83%	Mismatches: 100	PA (HINK/) HINKLE G J.	
Query Match: 5.97%	Indels: 96	PA (SLAT/) SLATER S C.	
RESULT 1176		PA (CHEN/) CHEN X.	
ID AAC47583 standard; DNA; 1267 BP.		PA (GOLD/) GOLDMAN B S.	
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54355.		Best Local Similarity: 23.63%	Mismatches: 100
PN EPI033405-A2.		Query Match: 5.97%	Indels: 57
PD 06-SEP-2000.		RESULT 1185	
Best Local Similarity: 20.96%	Mismatches: 99	ID AAN70356 standard; cDNA to mRNA; 1475 BP.	
Query Match: 5.97%	Indels: 85	DE Human urine-derived high molecular weight type urokinase A and B-chain	
RESULT 1177		DE pre-structural gene.	
ID ACA41158 standard; DNA; 1296 BP.		PN EP232544-A.	
DE Prokaryotic essential gene #22815.		PD 19-AUG-1987.	
PN WO200277183-A2.		PA (GREC) GREEN CROSS CORP.	
PD 03-OCT-2002.		Best Local Similarity: 23.05%	Mismatches: 96
PA (ELIT-) ELITRA PHARM INC.		Query Match: 5.97%	Indels: 73
Best Local Similarity: 20.54%	Mismatches: 91	RESULT 1186	
Query Match: 5.97%	Indels: 113	ID AD744663 standard; cDNA; 1487 BP.	
RESULT 1178		DE Bacterial polynucleotide #19414.	
ID AB239320 standard; DNA; 1302 BP.		PN US2003233675-A1.	
DE N. gonorrhoeae nucleotide sequence SEQ ID 3229.		PD 18-DEC-2003.	
PN WO200279243-A2.		PA (CAOY/) CAO Y.	
PD 10-OCT-2002.		PA (HINK/) HINKLE G J.	
PA (CHIR-) CHIRON SPA.		PA (SLAT/) SLATER S C.	
Best Local Similarity: 20.54%	Mismatches: 91	PA (CHEN/) CHEN X.	
Query Match: 5.97%	Indels: 113	PA (GOLD/) GOLDMAN B S.	
RESULT 1179		Best Local Similarity: 21.14%	Mismatches: 86
ID AAQ13898 standard; DNA; 1307 BP.		Query Match: 5.97%	Indels: 78
DE aroA gene.		RESULT 1187	
PN WO9113978-A.		ID AAS89540 standard; cDNA; 1569 BP.	
PD 19-SEP-1991.		DE DNA encoding novel human diagnostic protein #25344.	
PA (TRIN-) TRINITY COLLEGE DUB.		PN WO200175067-A2.	
Best Local Similarity: 25.79%	Mismatches: 94	PD 11-OCT-2001.	
Query Match: 5.97%	Indels: 50	PA (HYSE-) HYSEQ INC.	
RESULT 1180		Best Local Similarity: 22.94%	Mismatches: 91
ID AA254386 standard; DNA; 1311 BP.		Query Match: 5.97%	Indels: 57
DE Neisseria gonorrhoeae ORF 904 partial DNA sequence SEQ ID NO:2721.		RESULT 1188	
PN WO9957280-A2.		ID AAS77802 standard; cDNA; 1569 BP.	
PD 11-NOV-1999.		DE DNA encoding novel human diagnostic protein #13606.	
PA (CHIR-) CHIRON CORP.		PN WO200175067-A2.	
PA (GENO-) INST GENOMIC RES.		PD 11-OCT-2001.	
Best Local Similarity: 20.54%	Mismatches: 91	PA (HYSE-) HYSEQ INC.	
Query Match: 5.97%	Indels: 113	Best Local Similarity: 22.94%	Mismatches: 91
RESULT 1181		Query Match: 5.97%	Indels: 57
ID AAS54377 standard; DNA; 1365 BP.		RESULT 1189	
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #508.		ID ADK12502 standard; DNA; 1584 BP.	
PN WO200170955-A2.		DE Human NAC-1 coding sequence #2.	
PD 27-SEP-2001.		PN US2003100495-A1.	
PA (ELIT-) ELITRA PHARM INC.		PD 29-MAY-2003.	
Best Local Similarity: 25.35%	Mismatches: 99	PA (ZHAN/) ZHANG J.	
Query Match: 5.97%	Indels: 86	Best Local Similarity: 25.33%	Mismatches: 94
RESULT 1182		Query Match: 5.97%	Indels: 44
ID ACA42795 standard; DNA; 1365 BP.		RESULT 1190	
DE Prokaryotic essential gene #24452.		ID ADK12501 standard; DNA; 1589 BP.	
PN WO200277183-A2.		DE Human NAC-1 coding sequence #1.	
PD 03-OCT-2002.		PN US2003100495-A1.	
PA (ELIT-) ELITRA PHARM INC.		PD 29-MAY-2003.	
Best Local Similarity: 25.35%	Mismatches: 99	PA (ZHAN/) ZHANG J.	
Query Match: 5.97%	Indels: 86	Best Local Similarity: 25.33%	Mismatches: 94

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Query Match: 5.97% Indels: 44
RESULT 1191
ID ADS60286 standard; cDNA; 1746 BP.
DE Bacterial polynucleotide #12273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Best Local Similarity: 23.41% Mismatches: 94
Query Match: 5.97% Indels: 140
RESULT 1192
ID ABD10193 standard; DNA; 1764 BP.
DE Pseudomonas aeruginosa polynucleotide #8797.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.62% Mismatches: 118
Query Match: 5.97% Indels: 50
RESULT 1193
ID ABD05170 standard; DNA; 1785 BP.
DE Pseudomonas aeruginosa polynucleotide #3774.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.83% Mismatches: 100
Query Match: 5.97% Indels: 96
RESULT 1194
ID ADQ83596 standard; cDNA; 1804 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #410.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD//) WU T D.
PA (ZHOU//) ZHOU Y.
Best Local Similarity: 25.33% Mismatches: 94
Query Match: 5.97% Indels: 44
RESULT 1195
ID ABS55879 standard; cDNA; 1881 BP.
DE Human polynucleotide #5.
PN US2002127199-A1.
PD 12-SEP-2002.
PA (TANG//) TANG Y T.
PA (ZHOU//) ZHOU P.
PA (GOOD//) GOODRICH R.
PA (ASUN//) ASUNDI V.
PA (YANG//) YANG Y.
PA (ZHAN//) ZHANG J.
PA (WEHR//) WEHRMAN T.
PA (DRNA//) DRMANAC R T.
Best Local Similarity: 25.33% Mismatches: 94
Query Match: 5.97% Indels: 44
RESULT 1196
ID ADJ92543 standard; DNA; 1881 BP.
DE Human DNA #5 of the invention.
PN US2004013657-A1.
PD 22-JAN-2004.
PA (TANG//) TANG Y T.
PA (ASUN//) ASUNDI V.
PA (WEHR//) WEHRMAN T.
PA (ZHAN//) ZHANG Y.
PA (ZHOU//) ZHOU P.
PA (DRNA//) DRMANAC R T.
PA (GOOD//) GOODRICH R.
Best Local Similarity: 25.33% Mismatches: 94
Query Match: 5.97% Indels: 44
RESULT 1197
ID ADB61949 standard; cDNA; 1904 BP.
DE Human cDNA encoding clone BRACE20061620.
PN EP1308459-A2.

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PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 27.20% Mismatches: 82
Query Match: 5.97% Indels: 75
RESULT 1198
ID ABO6145 standard; DNA; 2004 BP.
DE Novel human gene. SEQ ID 16.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 24.30% Mismatches: 93
Query Match: 5.97% Indels: 91
RESULT 1199
ID ADO67473 standard; cDNA; 2098 BP.
DE Novel human cDNA sequence #2446.
PN EP140981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 27.20% Mismatches: 82
Query Match: 5.97% Indels: 75
RESULT 1200
ID ABX97046 standard; cDNA; 2214 BP.
DE Human NOV22a cDNA.
PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.33% Mismatches: 94
Query Match: 5.97% Indels: 44
RESULT 1201
ID ADN61808 standard; cDNA; 2214 BP.
DE Human cDNA encoding NOV22a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI//) PADIGARU M.
PA (SPVT//) SPYTEK K A.
PA (SHEN//) SHENOY S G.
PA (TAUP//) TAUPIER R J.
PA (PENA//) PENA C E A.
PA (LILL//) LI L.
PA (ZERH//) ZERHUSEN B D.
PA (GUSE//) GUSEV V Y.
PA (JIW//) JI W.
PA (GORM//) GORMAN L.
PA (MILL//) MILLER C E.
PA (KEKU//) KEKUDA R.
PA (PATT//) PATTURAJAN M.
PA (GANG//) GANGOLLI E A.
PA (VERN//) VERNET C A M.
PA (GUOX//) GUO X S.
PA (TCHER//) TCHERNEV V T.
PA (FERN//) FERNANDES E R.
PA (CASM//) CASMAN S J.
PA (MALY//) MALYANKAR U M.
PA (GERL//) GERLACH V.
PA (LIUY//) LIU Y.
PA (ANDE//) ANDERSON D W.
PA (SPAD//) SPADERNA S K.
PA (CATT//) CATTERTON E.
PA (LEIT//) LEITE M W.
PA (ZHON//) ZHONG H.
PA (ALSO//) ALSOBROOK J P.
PA (LEPL//) LEFLEY D M.
PA (RIEG//) RIEGER D K.
PA (BURG//) BURGESS C E.
Best Local Similarity: 25.33% Mismatches: 94
Query Match: 5.97% Indels: 44
RESULT 1202
ID ABD10306 standard; DNA; 2256 BP.
DE Pseudomonas aeruginosa polynucleotide #8910.
PN US6551795-B1.

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PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.62% Mismatches: 118
 Query Match: 5.97% Indels: 50
 RESULT 1203
 ID ADA53079 standard; cDNA; 2304 BP.
 DE Human coding sequence, SEQ ID 647.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 22.29% Mismatches: 110
 Query Match: 5.97% Indels: 104
 RESULT 1204
 ID ACA43839 standard; DNA; 2313 BP.
 DE Prokaryotic essential gene #25496.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 24.79% Mismatches: 124
 Query Match: 5.97% Indels: 94
 RESULT 1205
 ID ADG91055 standard; DNA; 2321 BP.
 DE Hepatic specific nucleic acid encoding sequence #244.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Best Local Similarity: 30.00% Mismatches: 58
 Query Match: 5.97% Indels: 15
 RESULT 1206
 ID ADJ39295 standard; cDNA; 2322 BP.
 DE Plant cDNA #295.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW-) BUDWORTH P.
 PA (MOUG-) MOUGHAMER T.
 PA (BRIG-) BRIGGS S P.
 PA (COOP-) COOPER B.
 PA (GLAZ-) GLAZEBROOK J.
 PA (GOFF-) GOFF S A.
 PA (KATA-) KATAGIRI P.
 PA (KREP-) KREPS J.
 PA (PROV-) PROVART N.
 PA (RICK-) RIQUE D.
 PA (ZHUT-) ZHU T.
 Best Local Similarity: 24.37% Mismatches: 95
 Query Match: 5.97% Indels: 68
 RESULT 1207
 ID AAF81369 standard; DNA; 2334 BP.
 DE Quorum sensing controlled gene qsc112 ORF.
 PN WO200118248-A2.
 PD 15-MAR-2001.
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (QUOR-) QUORUM SCI INC.
 Best Local Similarity: 25.10% Mismatches: 90
 Query Match: 5.97% Indels: 58
 RESULT 1208
 ID AAC75904 standard; cDNA; 2636 BP.
 DE Human ORF1459 polynucleotide sequence SEQ ID NO:2917.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 25.31% Mismatches: 127
 Query Match: 5.97% Indels: 93
 RESULT 1209
 ID AAS66988 standard; cDNA; 2778 BP.
 DE DNA encoding novel human diagnostic protein #2792.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.87% Mismatches: 80
 Query Match: 5.97% Indels: 41
 RESULT 1210

ID AAC44728 standard; DNA; 2868 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43911.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 26.04% Mismatches: 74
 Query Match: 5.97% Indels: 29
 RESULT 1211
 ID ADN73322 standard; cDNA; 3012 BP.
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1217.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPPDESIGN NV.
 Best Local Similarity: 26.04% Mismatches: 74
 Query Match: 5.97% Indels: 29
 RESULT 1212
 ID ABT42814 standard; DNA; 3049 BP.
 DE Human neuroblastoma-related DNA sequence, SEQ ID NO:95.
 PN WO2002103017-A1.
 PD 27-DEC-2002.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Best Local Similarity: 23.33% Mismatches: 79
 Query Match: 5.97% Indels: 80
 RESULT 1213
 ID ACA42098 standard; DNA; 3099 BP.
 DE Prokaryotic essential gene #23755.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.80% Mismatches: 95
 Query Match: 5.97% Indels: 60
 RESULT 1214
 ID ADJ27260 standard; DNA; 3174 BP.
 DE Human TRICH-44 coding sequence, SEQ ID 92.
 PN WO2004013293-A2.
 PD 12-FEB-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 23.91% Mismatches: 118
 Query Match: 5.97% Indels: 58
 RESULT 1215
 ID ADA70995 standard; DNA; 3189 BP.
 DE Rice gene, SEQ ID 4318.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 21.73% Mismatches: 138
 Query Match: 5.97% Indels: 87
 RESULT 1216
 ID AAS18239 standard; cDNA; 3273 BP.
 DE Human cDNA encoding hunc-2.
 PN WO200196561-A1.
 PD 20-DEC-2001.
 PA (MERE) MERCK PATENT GMBH.
 Best Local Similarity: 25.94% Mismatches: 78
 Query Match: 5.97% Indels: 63
 RESULT 1217
 ID AAC50900 standard; DNA; 3294 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66548.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Best Local Similarity: 26.04% Mismatches: 74
 Query Match: 5.97% Indels: 29
 RESULT 1218
 ID ADT45733 standard; cDNA; 3435 BP.
 DE Bacterial polynucleotide #20484.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY) CAO Y.
 PA (HINK) HINKLE G J.
 PA (SLAT) SLATER S C.
 PA (CHEN) CHEN X.
 PA (GOLD) GOLDMAN B S.
 Best Local Similarity: 24.65% Mismatches: 105

Query Match: 5.97% Indels: 84
 RESULT 1219
 ID ADR07512 standard; cDNA; 3652 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1018.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 25.59% Mismatches: 126
 Query Match: 5.97% Indels: 69
 RESULT 1220
 ID ADQ81352 standard; DNA; 3711 BP.
 DE Human Notch-like polypeptide coding sequence.
 PN WO2004063223-A2.
 PD 29-JUL-2004.
 PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 Best Local Similarity: 25.59% Mismatches: 126
 Query Match: 5.97% Indels: 69
 RESULT 1221
 ID AAD60684 standard; DNA; 3786 BP.
 DE Human CRUMBS (CRB) DNA #7 that modify branching morphogenesis.
 PN US2003100005-A1.
 PD 29-MAY-2003.
 PA (KARI/) KARIM F D.
 PA (KEYE/) KEYES L N.
 PA (PLOW/) PLOWMAN G D.
 PA (OLIM/) OLIMANN M M.
 PA (MAXW/) MAXWELL M E.
 PA (DIAG/) DIAGANA T T.
 Best Local Similarity: 25.59% Mismatches: 126
 Query Match: 5.97% Indels: 69
 RESULT 1222
 ID ADH22633 standard; cDNA; 3850 BP.
 DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID131.
 PN WO2003093444-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 23.91% Mismatches: 118
 Query Match: 5.97% Indels: 58
 RESULT 1223
 ID ADS48637 standard; cDNA; 4135 BP.
 DE Bacterial polynucleotide #3380.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 24.84% Mismatches: 55
 Query Match: 5.97% Indels: 42
 RESULT 1224
 ID ADR08444 standard; cDNA; 4319 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1950.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 21.82% Mismatches: 101
 Query Match: 5.97% Indels: 130
 RESULT 1225
 ID ACA42414 standard; DNA; 4347 BP.
 DE Prokaryotic essential gene #24071.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 26.56% Mismatches: 102
 Query Match: 5.97% Indels: 51
 RESULT 1226
 ID ADB80394 standard; DNA; 4387 BP.
 DE Human MDDT gene Seq ID NO:81.
 PN WO2003016497-A2.
 PD 27-FEB-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 26.27% Mismatches: 82

Query Match: 5.97% Indels: 57
 RESULT 1227
 ID ADC78227 standard; cDNA; 4476 BP.
 DE Human secreted protein encoding cDNA Seq ID NO:34.
 PN WO2003072761-A1.
 PD 04-SEP-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.36% Mismatches: 112
 Query Match: 5.97% Indels: 72
 RESULT 1228
 ID ABX72242 standard; cDNA; 4483 BP.
 DE Human NOVX polynucleotide #73.
 PN WO200281498-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 25.31% Mismatches: 127
 Query Match: 5.97% Indels: 93
 RESULT 1229
 ID ABK46137 standard; cDNA; 4932 BP.
 DE cDNA encoding colon tumour protein, SEQ ID NO 1688.
 PN WO200212328-A2.
 PD 14-FEB-2002.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 23.62% Mismatches: 86
 Query Match: 5.97% Indels: 97
 RESULT 1230
 ID ACC50996 standard; cDNA; 5352 BP.
 DE Human bladder cancer associated cDNA sequence SEQ ID NO:85.
 PN WO2003003906-A2.
 PD 16-JAN-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Best Local Similarity: 21.64% Mismatches: 106
 Query Match: 5.97% Indels: 69
 RESULT 1231
 ID ABZ24581 standard; cDNA; 7564 BP.
 DE Human cell adhesion and extracellular matrix protein 4 cDNA.
 PN WO200288322-A2.
 PD 07-NOV-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 25.70% Mismatches: 88
 Query Match: 5.97% Indels: 68
 RESULT 1232
 ID AAK79820 standard; DNA; 8308 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34632.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.63% Mismatches: 69
 Query Match: 5.97% Indels: 62
 RESULT 1233
 ID AAX68091 standard; DNA; 8308 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22903.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 25.63% Mismatches: 69
 Query Match: 5.97% Indels: 62
 RESULT 1234
 ID AAS18100 standard; DNA; 10210 BP.
 DE Human angiotensin receptor-like 1 (AGTRL1) DNA.
 PN WO200190123-A2.
 PD 29-NOV-2001.
 PA (GENA-) GENAISSANCE PHARM INC.
 Best Local Similarity: 22.14% Mismatches: 84
 Query Match: 5.97% Indels: 95
 RESULT 1235
 ID AAD03809 standard; DNA; 14806 BP.
 DE Streptomyces galilaeus gene cluster for actinomycin biosynthesis.
 PN WO200123578-A1.
 PD 05-APR-2001.
 PA (GALI-) GALILAEUS OY.
 Best Local Similarity: 23.84% Mismatches: 111
 Query Match: 5.97% Indels: 68

RESULT 1236
ID ABA97921 standard; DNA; 23668 BP.
DE Human transporter protein encoding genomic DNA SEQ ID NO 2.
FN WO200190360-A2.
PD 29-NOV-2001.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 20.28% Mismatches: 115
Query Match: 5.97% Indels: 124
RESULT 1237
ID ADR86701 standard; DNA; 26000 BP.
DE Human Ephrin B4 (EphB4) genomic DNA.
FN WO2004080425-A2.
PD 23-SEP-2004.
PA (VASG-) VASGENE THERAPEUTICS INC.
Best Local Similarity: 23.84% Mismatches: 132
Query Match: 5.97% Indels: 59
RESULT 1238
ID ADR82648 standard; DNA; 26000 BP.
DE Human EphA4 gene.
FN WO2004080418-A2.
PD 23-SEP-2004.
PA (VASG-) VASGENE THERAPEUTICS INC.
Best Local Similarity: 23.84% Mismatches: 132
Query Match: 5.97% Indels: 59
RESULT 1239
ID AAD56075 standard; DNA; 32767 BP.
DE Human SNL carcinoma associated (CA) gene.
FN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 27.48% Mismatches: 84
Query Match: 5.97% Indels: 53
RESULT 1240
ID ADA02437 standard; DNA; 32767 BP.
DE Human SNL carcinoma associated gene, SEQ ID NO:956.
FN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 27.48% Mismatches: 84
Query Match: 5.97% Indels: 53
RESULT 1241
ID ADB72176 standard; DNA; 32767 BP.
DE Human SNL gene.
FN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 27.48% Mismatches: 84
Query Match: 5.97% Indels: 53
RESULT 1242
ID ADE82920 standard; DNA; 32767 BP.
DE Human SNL genomic DNA sequence.
FN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 27.48% Mismatches: 84
Query Match: 5.97% Indels: 53
RESULT 1243
ID ACC58251 standard; DNA; 35359 BP.
DE Coumermycin A1 biosynthetic gene cluster.
FN WO2003014352-A2.
PD 20-FEB-2003.
PA (UYTU-) UNIV TUEBINGEN.
Best Local Similarity: 26.39% Mismatches: 106
Query Match: 5.97% Indels: 62
RESULT 1244
ID AAF88313 standard; DNA; 50000 BP.
DE S. spinosa DNA fragment SEQ ID 2.
FN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Best Local Similarity: 19.95% Mismatches: 114
Query Match: 5.97% Indels: 146
RESULT 1245

ID AAF88316 standard; DNA; 50000 BP.
DE S. spinosa DNA fragment SEQ ID 5.
FN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Best Local Similarity: 19.95% Mismatches: 114
Query Match: 5.97% Indels: 146
RESULT 1246
ID ADD71050 standard; DNA; 75270 BP.
DE Human secretory carrier membrane protein 3 gene SEQ ID NO:54.
FN WO2003061564-A2.
PD 31-JUL-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.21% Mismatches: 96
Query Match: 5.97% Indels: 50
RESULT 1247
ID ACA63030 standard; DNA; 75270 BP.
DE Human chromosome 1q21 region surrounding the glucocerebrosidase gene.
FN US2003013178-A1.
PD 16-JAN-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 23.21% Mismatches: 96
Query Match: 5.97% Indels: 50
RESULT 1248
ID ADQ19735 standard; DNA; 75270 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2554.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 23.21% Mismatches: 96
Query Match: 5.97% Indels: 50
RESULT 1249
ID AA221501 standard; DNA; 80161 BP.
DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.
FN WO200297082-A2.
PD 05-DEC-2002.
PA (UYDU-) UNIV COLLEGE DUBLIN.
Best Local Similarity: 27.71% Mismatches: 80
Query Match: 5.97% Indels: 63
RESULT 1251
ID AAD54480 standard; DNA; 117962 BP.
DE Human CIP DNA #1.
FN WO200299055-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Best Local Similarity: 23.84% Mismatches: 132
Query Match: 5.97% Indels: 59
RESULT 1252
ID ADQ20606 standard; DNA; 195917 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 23.62% Mismatches: 86
Query Match: 5.97% Indels: 97
RESULT 1253
ID ABZ72040 standard; DNA; 207433 BP.
DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.
FN WO200178894-A2.
PD 25-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 22.02% Mismatches: 97
Query Match: 5.97% Indels: 90
RESULT 1254
ID ABE74891 standard; DNA; 207433 BP.
DE BAC1098L22 DNA sequence.
FN WO200283077-A2.

PD 24-OCT-2002.
 PA (SCHE) SCHERING CORP.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.02% Mismatches: 97
 Query Match: 5.97% Indels: 90
 RESULT 1255
 ID ADJ36614 standard; DNA; 207433 BP.
 DE Bacterial artificial chromosome RPCI-11.
 PN US2004002470-A1.
 PD 01-JAN-2004.
 PA (KEIT) KEITH T.
 PA (LITT) LITTLE R. D.
 PA (VEER) VAN EERDEWEGH P.
 PA (DUPU) DUPUIS J.
 PA (DNAS) DEL MASTRO R. G.
 PA (SIMO) SIMON J.
 PA (ALLE) ALLEN K.
 PA (PAND) PANDIT S.
 Best Local Similarity: 22.02% Mismatches: 97
 Query Match: 5.97% Indels: 90
 RESULT 1256
 ID ADL81193 standard; DNA; 207433 BP.
 DE BAC1098L22 DNA sequence.
 PN US2004023215-A1.
 PD 05-FEB-2004.
 PA (KEIT) KEITH T.
 PA (LITT) LITTLE R. D.
 PA (EERD) EERDEWEGH P. V.
 PA (DUPU) DUPUIS J.
 PA (DNAS) DEL MASTRO R. G.
 PA (SIMO) SIMON J.
 PA (ALLE) ALLEN K.
 PA (PAND) PANDIT S.
 Best Local Similarity: 22.02% Mismatches: 97
 Query Match: 5.97% Indels: 90
 RESULT 1257
 ID ABR84349 standard; cDNA; 222930 BP.
 DE Human cDNA differentially expressed in granulocytic cells #920.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE) GENE LOGIC INC.
 Best Local Similarity: 22.36% Mismatches: 99
 Query Match: 5.97% Indels: 117
 RESULT 1258
 ID ADI73714 standard; DNA; 401 BP.
 DE Human ovarian cancer DNA marker #6456.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
 Best Local Similarity: 35.96% Mismatches: 37
 Query Match: 5.94% Indels: 10
 RESULT 1259
 ID ADI67317 standard; DNA; 401 BP.
 DE Human ovarian cancer DNA marker #59.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
 Best Local Similarity: 35.96% Mismatches: 37
 Query Match: 5.94% Indels: 10
 RESULT 1260
 ID ADK14113 standard; cDNA; 455 BP.
 DE Human autoimmune disorder gene #17.
 PN US2003228617-A1.
 PD 11-DEC-2003.
 PA (UYVA) UNIV VANDERBILT.
 Best Local Similarity: 25.00% Mismatches: 51
 Query Match: 5.94% Indels: 81
 RESULT 1261
 ID ADL38951 standard; DNA; 458 BP.
 DE Human ovarian cancer DNA marker #12841.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.

Best Local Similarity: 35.96% Mismatches: 37
 Query Match: 5.94% Indels: 10
 RESULT 1262
 ID ABA57564 standard; DNA; 460 BP.
 DE Human foetal liver single exon nucleic acid probe #5869.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1263
 ID AAI37122 standard; DNA; 460 BP.
 DE Probe #5808 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1264
 ID AAK31218 standard; DNA; 460 BP.
 DE Human bone marrow expressed single exon probe SEQ ID NO: 5775.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1265
 ID AAK05613 standard; DNA; 460 BP.
 DE Human brain expressed single exon probe SEQ ID NO: 5604.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1266
 ID ABS30899 standard; DNA; 460 BP.
 DE Human liver single exon probe, SEQ ID No 5889.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1267
 ID ABS05970 standard; DNA; 460 BP.
 DE Human genome-derived single exon probe from lung SEQ ID No 5961.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Best Local Similarity: 30.48% Mismatches: 37
 Query Match: 5.94% Indels: 19
 RESULT 1268
 ID ACH91710 standard; DNA; 567 BP.
 DE Human genome derived single exon probe #24905.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN) PENN S. G.
 PA (RANK) RANK D. R.
 PA (HANZ) HANZEL D. K.
 Best Local Similarity: 26.70% Mismatches: 69
 Query Match: 5.94% Indels: 76
 RESULT 1269
 ID ADR01427 standard; DNA; 606 BP.
 DE A. gossypii genomic DNA PAG104411.
 PN US6239264-B1.
 PD 29-MAY-2001.
 PA (SYNG) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 30.85% Mismatches: 31
 Query Match: 5.94% Indels: 26
 RESULT 1270
 ID AAS78418 standard; cDNA; 645 BP.
 DE DNA encoding novel human diagnostic protein #14222.
 PN WO200175067-A2.
 PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC. Mismatches: 78
 Query Match: 5.94% Indels: 56
 RESULT 1271
 ID ABT19178 standard; DNA; 825 BP.
 DE Aspergillus fumigatus essential gene #1536.
 PN WO200286090-A2.
 PD 31-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 86
 Best Local Similarity: 24.18% Indels: 69
 Query Match: 5.94%
 RESULT 1272
 ID ADK54727 standard; DNA; 855 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #2110.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO. Mismatches: 82
 Best Local Similarity: 22.81% Indels: 70
 Query Match: 5.94%
 RESULT 1273
 ID ADK58741 standard; DNA; 879 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #6124.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO. Mismatches: 82
 Best Local Similarity: 22.81% Indels: 70
 Query Match: 5.94%
 RESULT 1274
 ID ABD09128 standard; DNA; 996 BP.
 DE Pseudomonas aeruginosa polynucleotide #7732.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 109
 Best Local Similarity: 22.68% Indels: 91
 Query Match: 5.94%
 RESULT 1275
 ID ACA45839 standard; DNA; 1047 BP.
 DE Prokaryotic essential gene #27496.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 83
 Best Local Similarity: 26.17% Indels: 54
 Query Match: 5.94%
 RESULT 1276
 ID ADA70982 standard; DNA; 1113 BP.
 DE Rice gene, SEQ ID 4305.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG. Mismatches: 95
 Best Local Similarity: 25.00% Indels: 91
 Query Match: 5.94%
 RESULT 1277
 ID ACD27929 standard; cDNA; 1127 BP.
 DE Human S100 protein S100P2 cDNA.
 PN US2003096337-A1.
 PD 22-MAY-2003.
 PA (HILL/) HILLMAN J L. Mismatches: 82
 Best Local Similarity: 22.77% Indels: 64
 Query Match: 5.94%
 RESULT 1278
 ID AAV73499 standard; DNA; 1141 BP.
 DE Human S100P2 DNA.
 PN US5849528-A.
 PD 15-DEC-1998.
 PA (INCY-) INCYTE PHARM INC. Mismatches: 54
 Best Local Similarity: 29.66% Indels: 30
 Query Match: 5.94%

RESULT 1279
 ID AA59691 standard; cDNA; 1141 BP.
 DE cDNA encoding a human S100 polypeptide.
 PN US6103497-A.
 PD 15-AUG-2000.
 PA (INCY-) INCYTE PHARM INC. Mismatches: 54
 Best Local Similarity: 29.66% Indels: 30
 Query Match: 5.94%
 RESULT 1280
 ID ACA38612 standard; DNA; 1215 BP.
 DE Prokaryotic essential gene #20269.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 89
 Best Local Similarity: 22.26% Indels: 103
 Query Match: 5.94%
 RESULT 1281
 ID ADS80144 standard; DNA; 1215 BP.
 DE Mycobacterium tuberculosis nutrient starvation-inducible gene #91.
 PN WO2003004520-A2.
 PD 16-JAN-2003.
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY. Mismatches: 89
 Best Local Similarity: 22.26% Indels: 103
 Query Match: 5.94%
 RESULT 1282
 ID ACA40730 standard; DNA; 1218 BP.
 DE Prokaryotic essential gene #22387.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. Mismatches: 89
 Best Local Similarity: 22.26% Indels: 103
 Query Match: 5.94%
 RESULT 1283
 ID AAV60558 standard; DNA; 1224 BP.
 DE GtFD gene from Amycolatopsis orientalis A82846.
 PN US5821098-A.
 PD 13-OCT-1998.
 PA (ELIL) LILLY & CO ELI. Mismatches: 84
 Best Local Similarity: 23.04% Indels: 65
 Query Match: 5.94%
 RESULT 1284
 ID AA257050 standard; DNA; 1224 BP.
 DE A. orientalis glycosyltransferase protein GtFD encoding DNA.
 PN US6025174-A.
 PD 15-FEB-2000.
 PA (ELIL) LILLY & CO ELI. Mismatches: 84
 Best Local Similarity: 23.04% Indels: 65
 Query Match: 5.94%
 RESULT 1285
 ID AA257051 standard; mRNA; 1224 BP.
 DE A. orientalis glycosyltransferase protein GtFD mRNA.
 PN US6025174-A.
 PD 15-FEB-2000.
 PA (ELIL) LILLY & CO ELI. Mismatches: 84
 Best Local Similarity: 23.04% Indels: 65
 Query Match: 5.94%
 RESULT 1286
 ID ABD08963 standard; DNA; 1224 BP.
 DE Pseudomonas aeruginosa polynucleotide #7567.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 110
 Best Local Similarity: 23.42% Indels: 72
 Query Match: 5.94%
 RESULT 1287
 ID ABD08018 standard; DNA; 1239 BP.
 DE Pseudomonas aeruginosa polynucleotide #6622.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 96
 Best Local Similarity: 27.11% Indels: 40
 Query Match: 5.94%
 RESULT 1288

ID ACA24586 standard; DNA; 1248 BP.
 DE Prokaryotic essential gene #6243.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 22.50% Mismatches: 75
 Query Match: 5.94% Indels: 49
 RESULT 1289

ID AAS54328 standard; DNA; 1350 BP.
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #459.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 27.64% Mismatches: 109
 Query Match: 5.94% Indels: 51
 RESULT 1290

ID ACA42686 standard; DNA; 1350 BP.
 DE Prokaryotic essential gene #24343.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 27.64% Mismatches: 109
 Query Match: 5.94% Indels: 51
 RESULT 1291

ID ADH13098 standard; DNA; 1350 BP.
 DE P aeruginosa biotin carboxylase gene SeqID49.
 PN WO2003084986-A2.
 PD 16-OCT-2003.
 PA (AFFI-) AFFINIUM PHARM INC.
 Best Local Similarity: 27.64% Mismatches: 109
 Query Match: 5.94% Indels: 51
 RESULT 1292

ID ADH13100 standard; DNA; 1350 BP.
 DE P aeruginosa biotin carboxylase gene SeqID51.
 PN WO2003084986-A2.
 PD 16-OCT-2003.
 PA (AFFI-) AFFINIUM PHARM INC.
 Best Local Similarity: 27.64% Mismatches: 109
 Query Match: 5.94% Indels: 51
 RESULT 1293

ID AAS54344 standard; DNA; 1425 BP.
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #475.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 31.22% Mismatches: 87
 Query Match: 5.94% Indels: 47
 RESULT 1294

ID ACA42715 standard; DNA; 1425 BP.
 DE Prokaryotic essential gene #24372.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 31.22% Mismatches: 87
 Query Match: 5.94% Indels: 47
 RESULT 1295

ID ABD08038 standard; DNA; 1449 BP.
 DE Pseudomonas aeruginosa polynucleotide #6642.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.11% Mismatches: 96
 Query Match: 5.94% Indels: 40
 RESULT 1296

ID ABD15356 standard; DNA; 1467 BP.
 DE Pseudomonas aeruginosa polynucleotide #13960.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.75% Mismatches: 103
 Query Match: 5.94% Indels: 41
 RESULT 1297

ID AB211285 standard; cDNA; 1643 BP.

DE Human polynucleotide SEQ ID NO 167.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 26.70% Mismatches: 69
 Query Match: 5.94% Indels: 76
 RESULT 1298

ID ADM43803 standard; cDNA; 1643 BP.
 DE Novel human arginine-rich protein cDNA #167.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Best Local Similarity: 26.70% Mismatches: 69
 Query Match: 5.94% Indels: 76
 RESULT 1299

ID ABD07972 standard; DNA; 1647 BP.
 DE Pseudomonas aeruginosa polynucleotide #6576.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 27.11% Mismatches: 96
 Query Match: 5.94% Indels: 40
 RESULT 1300

ID AAD5811 standard; DNA; 1683 BP.
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.
 PN CA2391131-A1.
 PD 19-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Best Local Similarity: 21.64% Mismatches: 120
 Query Match: 5.94% Indels: 86
 RESULT 1301

ID ADA47975 standard; DNA; 1770 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Best Local Similarity: 22.05% Mismatches: 103
 Query Match: 5.94% Indels: 123
 RESULT 1302

ID AAU51471 standard; DNA; 1916 BP.
 DE Human epithelial cell sodium channel delta subunit coding sequence.
 PN WO200287306-A2.
 PD 07-NOV-2002.
 PA (SENO-) SENOMYX INC.
 Best Local Similarity: 23.72% Mismatches: 102
 Query Match: 5.94% Indels: 68
 RESULT 1303

ID ADS60101 standard; cDNA; 1917 BP.
 DE Bacterial polynucleotide #12088.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 25.66% Mismatches: 80
 Query Match: 5.94% Indels: 93
 RESULT 1304

ID ABO90272 standard; DNA; 1974 BP.
 DE M. capcutatus gene #257 for DNA array.
 PN WO200255655-A2.
 PD 18-JUL-2002.
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
 PA (TIGR-) TIGR.
 Best Local Similarity: 25.73% Mismatches: 85
 Query Match: 5.94% Indels: 67
 RESULT 1305

ID ABD15246 standard; DNA; 2049 BP.
 DE Pseudomonas aeruginosa polynucleotide #13850.
 PN US6551795-B1.

PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.75% Mismatches: 103
Query Match: 5.94% Indels: 41
RESULT 1306
ID AAS26071 standard; cDNA; 2131 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 250.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 22.07% Mismatches: 110
Query Match: 5.94% Indels: 93
RESULT 1307
ID ABX73412 standard; DNA; 2131 BP.
DE Human novel polynucleotide #240.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 22.07% Mismatches: 110
Query Match: 5.94% Indels: 93
RESULT 1308
ID ADQ83852 standard; cDNA; 2166 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #666.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH/) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 26.70% Mismatches: 69
Query Match: 5.94% Indels: 76
RESULT 1309
ID ADQ87301 standard; cDNA; 2166 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4178.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH/) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 26.70% Mismatches: 69
Query Match: 5.94% Indels: 76
RESULT 1310
ID ACN41498 standard; cDNA; 2198 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:373.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.72% Mismatches: 102
Query Match: 5.94% Indels: 68
RESULT 1311
ID ADC68527 standard; cDNA; 2231 BP.
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:19.
PN WO2003040306-A2.
PD 15-MAY-2003.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Best Local Similarity: 22.65% Mismatches: 105
Query Match: 5.94% Indels: 122
RESULT 1312
ID ADA52873 standard; cDNA; 2262 BP.
DE Human coding sequence, SEQ ID 441.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 35.96% Mismatches: 37
Query Match: 5.94% Indels: 10
RESULT 1313
ID ACN41496 standard; cDNA; 2275 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:371.
PN WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.72% Mismatches: 102
Query Match: 5.94% Indels: 68
RESULT 1314
ID AAD24009 standard; cDNA; 2305 BP.
DE Human drug metabolising enzyme (DME) -4 cDNA.
PN WO200190334-A2.
PD 29-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 19.57% Mismatches: 88
Query Match: 5.94% Indels: 97
RESULT 1315
ID ADO63961 standard; cDNA; 2381 BP.
DE Novel human cDNA sequence #1122.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.64% Mismatches: 106
Query Match: 5.94% Indels: 96
RESULT 1316
ID AA223939 standard; DNA; 2387 BP.
DE T. versicolor GAPDH promoter DNA.
PN WO9951757-A1.
PD 14-OCT-1999.
PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
Best Local Similarity: 24.69% Mismatches: 111
Query Match: 5.94% Indels: 38
RESULT 1317
ID ABO77426 standard; cDNA; 2535 BP.
DE Human CGDD cDNA 914113B1 SEQ ID 40.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 24.80% Mismatches: 80
Query Match: 5.94% Indels: 90
RESULT 1318
ID ADB63377 standard; cDNA; 2679 BP.
DE Human cDNA encoding clone TESTI20105910.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.72% Mismatches: 102
Query Match: 5.94% Indels: 68
RESULT 1319
ID AAD17479 standard; cDNA; 2714 BP.
DE Human transporter and ion channel-12 (TRICH-12) cDNA.
PN WO200162923-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 23.72% Mismatches: 102
Query Match: 5.94% Indels: 68
RESULT 1320
ID ADJ27222 standard; DNA; 2757 BP.
DE Human TRICH-6 coding sequence, SEQ ID 54.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.87% Mismatches: 80
Query Match: 5.94% Indels: 78
RESULT 1321
ID ADA53699 standard; cDNA; 2758 BP.
DE Human coding sequence, SEQ ID 1267.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 27.39% Mismatches: 92
Query Match: 5.94% Indels: 49
RESULT 1322
ID AAQ79921 standard; DNA; 2760 BP.
DE P. aeruginosa accB and accC genes.
PN WO9429467-A2.

PD 22-DEC-1994.
PA (CALJ) CALGENE INC. Mismatches: 109
Best Local Similarity: 27.64% Indels: 51
Query Match: 5.94%
RESULT 1323
ID ABT07915 standard; DNA; 2848 BP.
DE Human lung specific gene SEQ ID NO 60.
PN WO200262945-A2.
PD 15-AUG-2002.
PA (DIAD-) DIADEXUS INC. Mismatches: 93
Best Local Similarity: 25.59% Indels: 41
Query Match: 5.94%
RESULT 1324
ID AA232001 standard; cDNA; 3008 BP.
DE Human METH2 encoding cDNA.
PN WO9937660-A1.
PD 29-JUL-1999.
PA (IRUE/) IRUELA-ARISPE L. Mismatches: 93
PA (HAST/) HASTINGS G A. Indels: 41
PA (RUBE/) RUBEN S M.
Best Local Similarity: 21.23% Mismatches: 104
Query Match: 5.94% Indels: 147
RESULT 1325
ID AAC90058 standard; DNA; 3008 BP.
DE Human METH2 coding sequence.
PN WO200071577-A1.
PD 30-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA (IRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
PA (JONA-) JONAK Z L.
PA (TRUL/) TRULLI S H.
PA (FORN/) FORNWALD J A.
PA (TERR/) TERRETT J A.
Best Local Similarity: 21.23% Mismatches: 104
Query Match: 5.94% Indels: 147
RESULT 1326
ID AAS78943 standard; cDNA; 3093 BP.
DE DNA encoding novel human diagnostic protein #14747.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. Mismatches: 69
Best Local Similarity: 26.70% Indels: 76
Query Match: 5.94%
RESULT 1327
ID AAL61181 standard; DNA; 3354 BP.
DE Actinobryonema pretiosum transcriptional regulator gene #1.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Best Local Similarity: 24.03% Mismatches: 89
Query Match: 5.94% Indels: 82
RESULT 1328
ID ADR10432 standard; cDNA; 3370 BP.
DE Full length human cDNA useful for treating neurological disease Seq 3938.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.72% Mismatches: 102
Query Match: 5.94% Indels: 68
RESULT 1329
ID ACM43323 standard; cDNA; 3443 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2198.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 22.07% Mismatches: 84
Query Match: 5.94% Indels: 114
RESULT 1330
ID ADE85181 standard; DNA; 3711 BP.

DE Farnesyl transferase inhibitor modulated leukemia associated gene #400.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC. Mismatches: 104
Best Local Similarity: 21.23% Indels: 147
Query Match: 5.94%
RESULT 1331
ID ADR83445 standard; DNA; 3711 BP.
DE Human METH2 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Best Local Similarity: 21.23% Mismatches: 104
Query Match: 5.94% Indels: 147
RESULT 1332
ID ACN92835 standard; DNA; 3937 BP.
DE Breast cancer related marker, seq id 13985.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC. Mismatches: 133
Best Local Similarity: 24.92% Indels: 79
Query Match: 5.94%
RESULT 1333
ID AAA30567 standard; DNA; 4145 BP.
DE Genomic DNA encoding C. tropicalis cytochrome P450 oxidoreductase CPRB.
PN WO20020566-A2.
PD 13-APR-2000.
PA (HENK) HENKEL CORP. Mismatches: 111
Best Local Similarity: 19.36% Indels: 121
Query Match: 5.94%
RESULT 1334
ID ABK31886 standard; DNA; 4145 BP.
DE Candida tropicalis CPRB gene.
PN US6331420-B1.
PD 18-DEC-2001.
PA (WILS) WILSON C R.
PA (CRAF) CRAFT D L.
PA (EIRI) EIRICH L D.
PA (ESHO) ESHOO M.
PA (MADD) MADDURI K M.
PA (CORN) CORNETT C A.
PA (BREN) BRENNER A A.
PA (TANG) TANG M.
PA (LOPE) LOPER J C.
PA (GLEE) GLEESON M.
Best Local Similarity: 19.36% Mismatches: 111
Query Match: 5.94% Indels: 121
RESULT 1335
ID ABU55695 standard; DNA; 4145 BP.
DE Candida tropicalis cytochrome P450 reductase B gene.
PN WO200208413-A2.
PD 31-JAN-2002.
PA (COGN-) COGNIS CORP. Mismatches: 111
Best Local Similarity: 19.36% Indels: 121
Query Match: 5.94%
RESULT 1336
ID ADG31765 standard; DNA; 4145 BP.
DE Candida tropicalis CPRB DNA encoding a heterologous protein SeqID 3.
PN WO200208412-A2.
PD 31-JAN-2002.
PA (COGN-) COGNIS CORP. Mismatches: 111
Best Local Similarity: 19.36% Indels: 121
Query Match: 5.94%
RESULT 1337
ID ADC45081 standard; DNA; 4145 BP.
DE Yeast CPRB DNA.
PN US2003049821-A1.
PD 13-MAR-2003.
PA (WILS) WILSON C R.
PA (CRAF) CRAFT D L.
PA (EIRI) EIRICH L D.
PA (ESHO) ESHOO M.
PA (MADD) MADDURI K M.

PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1338
ID ADC45651 standard; DNA; 4145 BP.
DE Yeast CPRB DNA.
PN US2003049822-A1.
PD 13-MAR-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1339
ID ADE52162 standard; DNA; 4145 BP.
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.
PN US2003073220-A1.
PD 17-APR-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1340
ID ADF72469 standard; DNA; 4145 BP.
DE NADPH cytochrome P450 oxidoreductase CPRB DNA seq id 82.
PN US2003077795-A1.
PD 24-APR-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1341
ID ADF11909 standard; DNA; 4145 BP.
DE C. tropicalis CPRB DNA.
PN US2003153060-A1.
PD 14-AUG-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1342
ID ADF11791 standard; DNA; 4145 BP.
DE C. tropicalis CPRB DNA.
PN US2003148486-A1.
PD 07-AUG-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1343
ID ADE64326 standard; DNA; 4145 BP.
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.
PN US2003068800-A1.
PD 10-APR-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1344
ID ADJ26707 standard; DNA; 4145 BP.
DE Candida tropicalis CPRB protein coding sequence.
PN US2003186411-A1.
PD 02-OCT-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1345
ID AAZ30081 standard; CDNA; 4509 BP.
DE CDNA encoding a human MPR-related ABC transporter designated MOAT-B.
PN WO9949735-A1.
PD 07-OCT-1999.
PA (FOXC-) FOX CHASE CANCER CENT.
Best Local Similarity: 24.67%
Query Match: 5.94%
RESULT 1346
ID AAD16259 standard; CDNA; 4511 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant CDNA #4.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67%
Query Match: 5.94%
RESULT 1347
ID AAD16262 standard; CDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant CDNA #7.

Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1342
ID ADF11791 standard; DNA; 4145 BP.
DE C. tropicalis CPRB DNA.
PN US2003148486-A1.
PD 07-AUG-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1343
ID ADE64326 standard; DNA; 4145 BP.
DE C. tropicalis NADPH-cytochrome P450 reductase, CPRB DNA.
PN US2003068800-A1.
PD 10-APR-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1344
ID ADJ26707 standard; DNA; 4145 BP.
DE Candida tropicalis CPRB protein coding sequence.
PN US2003186411-A1.
PD 02-OCT-2003.
PA (WILS//) WILSON C R.
PA (CRAF//) CRAFT D L.
PA (EIRI//) EIRICH L D.
PA (ESHO//) ESHOO M.
PA (MADD//) MADDURI K M.
PA (CORN//) CORNETT C A.
PA (BREN//) BRENNER A A.
PA (TANG//) TANG M.
PA (LOPE//) LOPER J C.
PA (GLEE//) GLEESON M.
Best Local Similarity: 19.36%
Query Match: 5.94%
RESULT 1345
ID AAZ30081 standard; CDNA; 4509 BP.
DE CDNA encoding a human MPR-related ABC transporter designated MOAT-B.
PN WO9949735-A1.
PD 07-OCT-1999.
PA (FOXC-) FOX CHASE CANCER CENT.
Best Local Similarity: 24.67%
Query Match: 5.94%
RESULT 1346
ID AAD16259 standard; CDNA; 4511 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant CDNA #4.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67%
Query Match: 5.94%
RESULT 1347
ID AAD16262 standard; CDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant CDNA #7.

PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1348
ID AAD16231 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) cDNA coding sequence.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1349
ID AAD16264 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #9.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1350
ID AAD16260 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #5.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1351
ID AAD16257 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #2.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1352
ID AAD16258 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #3.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1353
ID AAD16263 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #8.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1354
ID AAD16256 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #1.
PN WO200162977-A2.
PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1355
ID AAD16261 standard; cDNA; 4512 BP.
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #6.
PN WO200162977-A2.

PD 30-AUG-2001.
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1356
ID ADO39092 standard; DNA; 4535 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 755.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 24.67% Mismatches: 98
Query Match: 5.94% Indels: 98
RESULT 1357
ID ABN59902 standard; cDNA; 4866 BP.
DE Novel human coding sequence SEQ ID NO: 313.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 23.91% Mismatches: 113
Query Match: 5.94% Indels: 71
RESULT 1358
ID ACN39307 standard; cDNA; 4943 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325546, SEQ ID NO:3367.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 23.91% Mismatches: 113
Query Match: 5.94% Indels: 71
RESULT 1359
ID ADR08306 standard; cDNA; 5266 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1812.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.00% Mismatches: 102
Query Match: 5.94% Indels: 87
RESULT 1360
ID ADR32243 standard; cDNA; 5360 BP.
DE Human tumour suppressor BNO208 cDNA, SEQ ID NO:13.
PN WO200264780-A1.
PD 22-AUG-2002.
PA (BION-) BIONOMICS LTD.
Best Local Similarity: 22.12% Mismatches: 123
Query Match: 5.94% Indels: 95
RESULT 1361
ID ADN95876 standard; DNA; 5449 BP.
DE Human BEC/LEC-related gene sequence SeqID800.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Best Local Similarity: 23.91% Mismatches: 113
Query Match: 5.94% Indels: 71
RESULT 1362
ID ADF81982 standard; DNA; 5456 BP.
DE Leukaemia-related DNA sequence #2538.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Best Local Similarity: 24.90% Mismatches: 77
Query Match: 5.94% Indels: 86
RESULT 1363
ID ADO23094 standard; DNA; 5491 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5914.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 22.12% Mismatches: 123

Query Match: 5.94% Indels: 95
 RESULT 1364
 ID ADC99116 standard; cDNA; 5973 BP.
 DE Human KPP cDNA - SEQ ID 69.
 PN WO2003033680-A2.
 PD 24-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 23.38%
 Query Match: 5.94% Mismatches: 64
 Indels: 64
 RESULT 1365
 ID ABX34702 standard; cDNA; 5999 BP.
 DE Human mddt cDNA SEQ ID 263.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 28.57%
 Query Match: 5.94% Mismatches: 30
 Indels: 38
 RESULT 1366
 ID ABX34526 standard; cDNA; 6001 BP.
 DE Human mddt cDNA SEQ ID 87.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 28.57%
 Query Match: 5.94% Mismatches: 30
 Indels: 38
 RESULT 1367
 ID AAS91791 standard; cDNA; 6258 BP.
 DE DNA encoding novel human diagnostic protein #27595.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.40%
 Query Match: 5.94% Mismatches: 114
 Indels: 114
 RESULT 1368
 ID AAS86371 standard; cDNA; 6306 BP.
 DE DNA encoding novel human diagnostic protein #22175.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 24.40%
 Query Match: 5.94% Mismatches: 114
 Indels: 114
 RESULT 1369
 ID AAQ20186 standard; DNA; 7076 BP.
 DE HLVA gene with ctxB and mer gene inserted.
 PN WO9118979-A.
 PD 12-DEC-1991.
 PA (UYMA-) UNIV MARYLAND BALTI.
 Best Local Similarity: 23.93%
 Query Match: 5.94% Mismatches: 118
 Indels: 96
 RESULT 1370
 ID AB856664 standard; DNA; 9320 BP.
 DE Plasmid p5-Puro-CMV-(N'-EGFP)-CMV-Red (EGFP-BJ) DNA.
 PN WO200270740-A2.
 PD 12-SEP-2002.
 PA (WIES/) WIESMUELLER L.
 Best Local Similarity: 23.88%
 Query Match: 5.94% Mismatches: 88
 Indels: 104
 RESULT 1371
 ID ADG75175 standard; DNA; 9369 BP.
 DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.
 PN WO2003086308-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 22.94%
 Query Match: 5.94% Mismatches: 115
 Indels: 111
 RESULT 1372
 ID ADG75118 standard; DNA; 9369 BP.
 DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.
 PN WO2003086308-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Best Local Similarity: 22.94%
 Query Match: 5.94% Mismatches: 115
 Indels: 111

RESULT 1373
 ID ABK84372 standard; cDNA; 37160 BP.
 DE Human cDNA differentially expressed in granulocytic cells #943.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Best Local Similarity: 26.70%
 Query Match: 5.94% Mismatches: 69
 Indels: 76
 RESULT 1374
 ID AAA29349 standard; DNA; 71989 BP.
 DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.
 Best Local Similarity: 21.71%
 Query Match: 5.94% Mismatches: 100
 Indels: 130
 RESULT 1375
 ID ADS73531 standard; cDNA; 73882 BP.
 DE tcp gene cluster.
 Best Local Similarity: 23.34%
 Query Match: 5.94% Mismatches: 92
 Indels: 100
 RESULT 1376
 ID ADQ74672 standard; DNA; 74787 BP.
 DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.
 Best Local Similarity: 26.59%
 Query Match: 5.94% Mismatches: 90
 Indels: 74
 RESULT 1377
 ID AAL61224 standard; DNA; 82746 BP.
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Best Local Similarity: 24.03%
 Query Match: 5.94% Mismatches: 89
 Indels: 82
 RESULT 1378
 Best Local Similarity: 26.78%
 Query Match: 5.94% Mismatches: 97
 Indels: 56
 RESULT 1379
 Best Local Similarity: 25.09%
 Query Match: 5.94% Mismatches: 98
 Indels: 78
 RESULT 1380
 Best Local Similarity: 26.78%
 Query Match: 5.94% Mismatches: 97
 Indels: 56
 RESULT 1381
 Best Local Similarity: 25.09%
 Query Match: 5.94% Mismatches: 98
 Indels: 78
 RESULT 1382
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1383
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1384
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1385
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1386
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1387
 Best Local Similarity: 24.42%
 Query Match: 5.94% Mismatches: 113
 Indels: 115
 RESULT 1388
 ID AAD25519 standard; DNA; 154746 BP.
 DE Human herpesvirus 2 complete DNA genome.
 PN WO200176643-A1.
 PD 18-OCT-2001.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 Best Local Similarity: 22.94%
 Query Match: 5.94% Mismatches: 115
 Indels: 111
 RESULT 1389
 ID ACH72734 standard; DNA; 593 BP.
 DE Human genome derived single exon probe #5929.
 PN US2003194704-A1.

PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Best Local Similarity: 27.84%
 Query Match: 5.90%
 Mismatches: 52
 Indels: 33
 RESULT 1390
 ID AAH68388 standard; DNA; 618 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 3423.
 PN EPI108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Best Local Similarity: 27.84%
 Query Match: 5.90%
 Mismatches: 72
 Indels: 35
 RESULT 1391
 ID AC01302 standard; DNA; 618 BP.
 DE C. glutamicum derived ORF SEQ ID 1293.
 PN DE10128510-A1.
 PD 19-DEC-2002.
 PA (DEGS) DEGUSSA AG.
 Best Local Similarity: 27.84%
 Query Match: 5.90%
 Mismatches: 72
 Indels: 35
 RESULT 1392
 ID AD054370 standard; DNA; 630 BP.
 DE Novel canine microarray-related DNA sequence SeqID5672.
 PN WO2004063324-A2.
 PD 29-JUL-2004.
 PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 Best Local Similarity: 28.99%
 Query Match: 5.90%
 Mismatches: 79
 Indels: 49
 RESULT 1393
 ID AAL50538 standard; DNA; 873 BP.
 DE Human B7-H1 protein open reading frame.
 PN US2002106730-A1.
 PD 08-AUG-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1394
 ID ADC78840 standard; DNA; 873 BP.
 DE Human PRO protein coding sequence #35.
 PN WO2003034984-A2.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1395
 ID ADH71945 standard; DNA; 873 BP.
 DE Human gene of the invention NOV35d SEQ ID NO:841.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1396
 ID AD076314 standard; cDNA; 873 BP.
 DE Human B7-H1 cDNA open reading frame.
 PN US2004137577-A1.
 PD 15-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1397
 ID ADH71939 standard; DNA; 874 BP.
 DE Human gene of the invention NOV35a SEQ ID NO:835.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1398
 ID ADH71943 standard; DNA; 900 BP.

DE Human gene of the invention NOV35c SEQ ID NO:839.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1399
 ID ADH71953 standard; DNA; 900 BP.
 DE Human gene of the invention NOV35h SEQ ID NO:849.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 24.49%
 Query Match: 5.90%
 Mismatches: 73
 Indels: 53
 RESULT 1400
 ID ABA03896 standard; cDNA; 967 BP.
 DE Human POLY17 nucleotide sequence SEQ ID NO:33.
 PN WO200179294-A2.
 PD 25-OCT-2001.
 PA (CURA-) CURAGEN CORP.
 Best Local Similarity: 27.66%
 Query Match: 5.90%
 Mismatches: 53
 Indels: 27
 RESULT 1401
 ID ABX56482 standard; cDNA; 967 BP.
 DE cDNA encoding novel human prohibitin-like protein.
 PN US2002123612-A1.
 PD 05-SEP-2002.
 PA (GERL) GERLACH V L.
 PA (ELLE) ELLERMAN K.
 PA (MACD) MACDOUGALL J R.
 PA (SMIT) SMITHSON G.
 Best Local Similarity: 27.66%
 Query Match: 5.90%
 Mismatches: 53
 Indels: 27
 RESULT 1402
 ID ADQ87187 standard; cDNA; 1140 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4064.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD) WU T D.
 PA (ZHOU) ZHOU Y.
 Best Local Similarity: 26.37%
 Query Match: 5.90%
 Mismatches: 93
 Indels: 82
 RESULT 1403
 ID ADQ84909 standard; cDNA; 1140 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1723.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD) WU T D.
 PA (ZHOU) ZHOU Y.
 Best Local Similarity: 26.37%
 Query Match: 5.90%
 Mismatches: 93
 Indels: 82
 RESULT 1404
 ID AAN80973 standard; DNA; 1152 BP.
 DE Sequence encoding adr type hepatitis B virus (HBV) surface antigen
 DE (HBSAG) L protein (M protein, S protein).
 PN EP288198-A.
 PD 26-OCT-1988.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Best Local Similarity: 26.57%
 Query Match: 5.90%
 Mismatches: 35
 Indels: 60
 RESULT 1405
 ID ACA26577 standard; DNA; 1179 BP.
 DE Prokaryotic essential gene #8234.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 25.56%
 Query Match: 5.90%
 Mismatches: 95
 Indels: 44
 RESULT 1406
 ID ABD17700 standard; DNA; 1251 BP.
 DE Pseudomonas aeruginosa polynucleotide #16304.

PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 31.22% Mismatches: 87
 Query Match: 5.90% Indels: 47
 RESULT 1407
 ID ADC30883 standard; cDNA; 1276 BP.
 DE Human novel cDNA sequence, SEQ ID NO:965.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 29.48% Mismatches: 72
 Query Match: 5.90% Indels: 89
 RESULT 1408
 ID ABV77054 standard; DNA; 1286 BP.
 DE Nucleotide sequence of a modified bacterial envelope (env) L protein.
 PN WO200286091-A2.
 PD 31-OCT-2002.
 PA (REGC) UNIV CALIFORNIA.
 Best Local Similarity: 25.84% Mismatches: 41
 Query Match: 5.90% Indels: 79
 RESULT 1409
 ID ABV76128 standard; cDNA; 1286 BP.
 DE Hepatitis B virus envelope L protein gene.
 PN WO200287594-A1.
 PD 07-NOV-2002.
 PA (REGC) UNIV CALIFORNIA.
 Best Local Similarity: 25.84% Mismatches: 41
 Query Match: 5.90% Indels: 79
 RESULT 1410
 ID AAH14847 standard; cDNA; 1301 BP.
 DE Human cDNA sequence SEQ ID NO:12675.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1411
 ID ADR92566 standard; DNA; 1311 BP.
 DE Novel S. pneumoniae DNA sequence, SEQ ID 1201.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.99% Mismatches: 70
 Query Match: 5.90% Indels: 51
 RESULT 1412
 ID ACA42334 standard; DNA; 1314 BP.
 DE Prokaryotic essential gene #23991.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 28.30% Mismatches: 90
 Query Match: 5.90% Indels: 73
 RESULT 1413
 ID ADT46053 standard; cDNA; 1323 BP.
 DE Bacterial polynucleotide #20804.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 22.65% Mismatches: 91
 Query Match: 5.90% Indels: 107
 RESULT 1414
 ID ACH87582 standard; DNA; 1324 BP.
 DE Human genome derived single exon probe #20777.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.

Best Local Similarity: 28.44% Mismatches: 78
 Query Match: 5.90% Indels: 58
 RESULT 1415
 ID ABX56047 standard; DNA; 1347 BP.
 DE M. echinopora calicheamicin biosynthesis gene calw.
 PN WO200279465-A2.
 PD 10-OCT-2002.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Best Local Similarity: 22.05% Mismatches: 83
 Query Match: 5.90% Indels: 85
 RESULT 1416
 ID AB17258 standard; DNA; 1380 BP.
 DE Pseudomonas aeruginosa polynucleotide #15862.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.61% Mismatches: 93
 Query Match: 5.90% Indels: 77
 RESULT 1417
 ID ADQ25304 standard; DNA; 1395 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8124.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity: 29.48% Mismatches: 72
 Query Match: 5.90% Indels: 89
 RESULT 1418
 ID ACC62520 standard; cDNA; 1406 BP.
 DE Human secreted protein #46 coding sequence SEQ ID 56.
 PN WO200299066-A2.
 PD 12-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 29.48% Mismatches: 72
 Query Match: 5.90% Indels: 89
 RESULT 1419
 ID ACC62491 standard; cDNA; 1406 BP.
 DE Human secreted protein #17 coding sequence SEQ ID 27.
 PN WO200299066-A2.
 PD 12-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 29.48% Mismatches: 72
 Query Match: 5.90% Indels: 89
 RESULT 1420
 ID ADT42234 standard; cDNA; 1413 BP.
 DE Bacterial polynucleotide #16985.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 21.95% Mismatches: 83
 Query Match: 5.90% Indels: 78
 RESULT 1421
 ID ADQ85209 standard; cDNA; 1528 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2023.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1422
 ID ADQ86369 standard; cDNA; 1528 BP.
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3241.
 PN WO2004060270-A2.
 PD 22-JUL-2004.
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139

Query Match: 5.90% Indels: 139
 RESULT 1423
 ID ABD02520 standard; DNA; 1533 BP.
 DE Pseudomonas aeruginosa polynucleotide #1124.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 23.92% Mismatches: 76
 Query Match: 5.90% Indels: 89
 RESULT 1424
 ID ACA26225 standard; DNA; 1545 BP.
 DE Prokaryotic essential gene #7882.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 25.68% Mismatches: 73
 Query Match: 5.90% Indels: 94
 RESULT 1425
 ID ABD16063 standard; DNA; 1545 BP.
 DE Pseudomonas aeruginosa polynucleotide #14667.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 21.86% Mismatches: 82
 Query Match: 5.90% Indels: 103
 RESULT 1426
 ID AAD02773 standard; cDNA; 1552 BP.
 DE Human B7-4 membrane (B7-4M) protein DNA.
 PN WO200114557-A1.
 PD 01-MAR-2001.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (GENY) GENETICS INST INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1427
 ID AAD02708 standard; cDNA; 1553 BP.
 DE Human B7-4 membrane (B7-4M) protein cDNA.
 PN WO200114556-A1.
 PD 01-MAR-2001.
 PA (DAND) DANA FARBER CANCER INST INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1428
 ID AAD51085 standard; DNA; 1553 BP.
 DE Human membrane B7-4 (B7-4M) DNA.
 PN WO200279499-A1.
 PD 10-OCT-2002.
 PA (AMHP) WYETH.
 PA (DAND) DANA FARBER CANCER INST INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1429
 ID ABT13989 standard; DNA; 1553 BP.
 DE Human PD-LiM coding sequence.
 PN WO200278731-A1.
 PD 10-OCT-2002.
 PA (AMHP) WYETH.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1430
 ID ADJ75002 standard; DNA; 1553 BP.
 DE Marker gene SEQ ID NO:254.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1431
 ID ABD05949 standard; DNA; 1572 BP.
 DE Pseudomonas aeruginosa polynucleotide #4553.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Best Local Similarity: 25.73% Mismatches: 67
 Query Match: 5.90% Indels: 68
 RESULT 1432
 ID ABD17809 standard; DNA; 1581 BP.
 DE Pseudomonas aeruginosa polynucleotide #16413.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 31.22% Mismatches: 87
 Query Match: 5.90% Indels: 47
 RESULT 1433
 ID ABX24010 standard; DNA; 1604 BP.
 DE DNA encoding B7-related protein, BSL1 #1.
 PN WO200194413-A2.
 PD 13-DEC-2001.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1434
 ID ADA24486 standard; cDNA; 1666 BP.
 DE Human cDNA differential expressed in adipose tissue, INCYTE209356CB1.
 PN US2003096272-A1.
 PD 22-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1435
 ID ABX75849 standard; cDNA; 1674 BP.
 DE Human NeuL cDNA #2.
 PN US2002132293-A1.
 PD 19-SEP-2002.
 PA (PALM/) PALM K.
 PA (TIMM/) TIMMUSK T.
 Best Local Similarity: 24.80% Mismatches: 119
 Query Match: 5.90% Indels: 52
 RESULT 1436
 ID AAL57526 standard; cDNA; 1674 BP.
 DE Human neuralised-like cDNA.
 PN WO2003061681-A2.
 PD 31-JUN-2003.
 PA (DEVE-) DEVELOPENTWICKLUNGSBIOLOGISCHE FORSCH.
 Best Local Similarity: 24.80% Mismatches: 119
 Query Match: 5.90% Indels: 52
 RESULT 1437
 ID ADS58584 standard; cDNA; 1677 BP.
 DE Bacterial polynucleotide #10571.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 22.02% Mismatches: 116
 Query Match: 5.90% Indels: 98
 RESULT 1438
 ID ABX63316 standard; cDNA; 1679 BP.
 DE Human cDNA #316 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1439
 ID ABD05695 standard; DNA; 1686 BP.
 DE Pseudomonas aeruginosa polynucleotide #4299.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 25.73% Mismatches: 67
 Query Match: 5.90% Indels: 68
 RESULT 1440
 ID ABX75848 standard; cDNA; 1725 BP.

DE Human Neu1 cDNA #1.
 PN US2002132293-A1.
 PD 19-SEP-2002.
 PA (PALM//) PALM K.
 PA (TIMM//) TIMMUSK T.
 Best Local Similarity: 24.80% Mismatches: 119
 Query Match: 5.90% Indels: 52
 RESULT 1441
 ID ABD16181 standard; DNA; 1767 BP.
 DE Pseudomonas aeruginosa polynucleotide #14785.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 21.86% Mismatches: 82
 Query Match: 5.90% Indels: 103
 RESULT 1442
 ID ADJ35133 standard; DNA; 1794 BP.
 DE DNA encoding xylanase from an environmental sample seq id 349.
 PN WO2003106654-A2.
 PD 24-DEC-2003.
 PA (DIVE-) DIVERSA CORP.
 Best Local Similarity: 25.22% Mismatches: 109
 Query Match: 5.90% Indels: 122
 RESULT 1443
 ID ADU62377 standard; DNA; 1798 BP.
 DE Human ovarian cancer DNA marker #20589.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1444
 ID AAS94795 standard; DNA; 1833 BP.
 DE Human DNA sequence #50 expressed during foam cell differentiation.
 PN WO200177389-A2.
 PD 18-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1445
 ID ADB47391 standard; cDNA; 1833 BP.
 DE Human cDNA upregulated in dendritic cells SEQ ID NO 91.
 PN US2003134283-A1.
 PD 17-JUL-2003.
 PA (PETE/) PETERSON D P.
 PA (PEAR/) PEARSON C I.
 PA (COCK/) COCKS B G.
 Best Local Similarity: 21.75% Mismatches: 107
 Query Match: 5.90% Indels: 139
 RESULT 1446
 ID ADS62794 standard; cDNA; 1860 BP.
 DE Bacterial polynucleotide #14781.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 22.65% Mismatches: 109
 Query Match: 5.90% Indels: 94
 RESULT 1447
 ID ADS62948 standard; cDNA; 1869 BP.
 DE Bacterial polynucleotide #14935.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 22.65% Mismatches: 109
 Query Match: 5.90% Indels: 94

RESULT 1448
 ID ADS59386 standard; cDNA; 1949 BP.
 DE Bacterial polynucleotide #11373.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Best Local Similarity: 22.65% Mismatches: 109
 Query Match: 5.90% Indels: 94
 RESULT 1449
 ID AAZ28095 standard; cDNA; 1976 BP.
 DE Human FREAC3 protein encoding cDNA.
 PN WO9954493-A2.
 PD 28-OCT-1999.
 PA (UYAL-) UNIV ALBERTA.
 Best Local Similarity: 25.91% Mismatches: 81
 Query Match: 5.90% Indels: 77
 RESULT 1450
 ID ABD09538 standard; DNA; 2031 BP.
 DE Pseudomonas aeruginosa polynucleotide #8142.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.38% Mismatches: 88
 Query Match: 5.90% Indels: 99
 RESULT 1451
 ID ABL17287 standard; DNA; 2106 BP.
 DE Pseudomonas aeruginosa polynucleotide #15891.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 24.61% Mismatches: 93
 Query Match: 5.90% Indels: 77
 RESULT 1452
 ID ACA26420 standard; DNA; 2184 BP.
 DE Prokaryotic essential gene #8077.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Best Local Similarity: 24.00% Mismatches: 105
 Query Match: 5.90% Indels: 49
 RESULT 1453
 ID AAX77135 standard; DNA; 2207 BP.
 DE Human nerve mutation factor protein encoding DNA.
 PN WO9925827-A1.
 PD 27-MAY-1999.
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 Best Local Similarity: 24.80% Mismatches: 119
 Query Match: 5.90% Indels: 52
 RESULT 1454
 ID AAH1621 standard; cDNA; 2314 BP.
 DE Human cDNA sequence SEQ ID NO:17145.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 21.05% Mismatches: 86
 Query Match: 5.90% Indels: 95
 RESULT 1455
 ID ABQ90266 standard; DNA; 2343 BP.
 DE M. capulatus gene #251 for DNA array.
 PN WO200255655-A2.
 PD 18-JUL-2002.
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
 PA (TIGR-) TIGR.
 Best Local Similarity: 25.09% Mismatches: 82
 Query Match: 5.90% Indels: 98
 RESULT 1456
 ID AAD07571 standard; cDNA; 2382 BP.
 DE Human secreted protein-encoding gene 1 cDNA clone HCE3T57, SEQ ID NO:11.
 PN WO200132676-A1.

PD 10-MAY-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1457
 ID AAQ63477 standard; DNA; 2386 BP.
 DE Micrococcal putrescine oxidase gene.
 PN JP06098778-A.
 PD 12-APR-1994.
 PA (BEPP/) BEPPU T.
 Best Local Similarity: 24.91% Mismatches: 116
 Query Match: 5.90% Indels: 62
 RESULT 1458
 ID AAK94224 standard; cDNA; 2472 BP.
 DE Human full-length cDNA, SEQ ID NO: 2806.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1459
 ID AD130773 standard; cDNA; 2472 BP.
 DE Full length human cDNA clone SeqID 2806.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1460
 ID AB033315 standard; cDNA; 2478 BP.
 DE Human cancer-associated (CA) cDNA HR07-056.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Best Local Similarity: 26.64% Mismatches: 82
 Query Match: 5.90% Indels: 76
 RESULT 1461
 ID ABX05463 standard; cDNA; 2484 BP.
 DE Human novel polynucleotide #478.
 PN WO200274961-A1.
 PD 26-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 26.64% Mismatches: 82
 Query Match: 5.90% Indels: 76
 RESULT 1462
 ID AAD33659 standard; cDNA; 2917 BP.
 DE Human TRICH-14 cDNA.
 PN WO200212340-A2.
 PD 14-FEB-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1463
 ID ACN42900 standard; cDNA; 2965 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1775.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 25.36% Mismatches: 112
 Query Match: 5.90% Indels: 72
 RESULT 1464
 ID ADD24552 standard; DNA; 3096 BP.
 DE DNA polymerase III subunit protein encoding DNA, dnaE #2, SEQ ID NO 71.
 PN WO200292769-A2.
 PD 21-NOV-2002.
 PA (REPL-) REPLIDYNE INC.
 Best Local Similarity: 25.00% Mismatches: 77
 Query Match: 5.90% Indels: 49
 RESULT 1465
 ID ADD24551 standard; DNA; 3096 BP.
 DE DNA polymerase III subunit protein encoding DNA, dnaE #2, SEQ ID NO 70.
 PN WO200292769-A2.
 PD 21-NOV-2002.
 PA (REPL-) REPLIDYNE INC.
 Best Local Similarity: 25.00% Mismatches: 77
 Query Match: 5.90% Indels: 49
 RESULT 1466
 ID ABD09490 standard; DNA; 3162 BP.
 DE Pseudomonas aeruginosa polynucleotide #8094.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Best Local Similarity: 22.38% Mismatches: 88
 Query Match: 5.90% Indels: 99
 RESULT 1467
 ID ACN43533 standard; cDNA; 3208 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2408.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1468
 ID ADQ18548 standard; DNA; 3291 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1367.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Best Local Similarity: 23.49% Mismatches: 129
 Query Match: 5.90% Indels: 93
 RESULT 1469
 ID ADI21763 standard; cDNA; 3323 BP.
 DE Novel human protein cDNA #22.
 PN WO2003025148-A2.
 PD 27-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1470
 ID ADQ97093 standard; DNA; 3331 BP.
 DE Human cancer associated sequence HR1-10-005, SEQ ID 69.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1471
 ID AAD21996 standard; cDNA; 3343 BP.
 DE Human transporters and ion channels (TRICH)-4 cDNA.
 PN WO200177174-A2.
 PD 18-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1472
 ID ADL12773 standard; cDNA; 3343 BP.
 DE Human steroid-induced C3A liver cell cDNA #502.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1473
 ID ACN43532 standard; cDNA; 3374 BP.
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2407.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Best Local Similarity: 22.64% Mismatches: 66
 Query Match: 5.90% Indels: 71
 RESULT 1474
 ID AAH75190 standard; cDNA; 3408 BP.
 DE Nucleotide sequence of a human 33894 transporter polypeptide.
 PN WO200164875-A2.
 PD 07-SEP-2001.
 PA (MILL-) MILLENNIUM PHARM INC.

Best Local Similarity: 22.64% Mismatches: 66
Query Match: 5.90% Indels: 71
ID AAX09012 standard; DNA; 3411 BP.
DE Human axin gene.
PN WO9902179-A1.
PD 21-JAN-1999.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1476
ID ABA82681 standard; DNA; 3411 BP.
DE Wnt signaling gene (AXIN) SEQ ID NO:67.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1477
ID ACC46001 standard; DNA; 3411 BP.
DE Human Wnt signalling gene AXIN.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1478
ID ADB98695 standard; DNA; 3411 BP.
DE Human axin (AXIN) DNA.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1479
ID ADD14620 standard; cDNA; 3411 BP.
DE Human src biomarker polynucleotide SEQ ID NO:14.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1480
ID ADE82491 standard; DNA; 3411 BP.
DE Human DNA sequence related to the invention #35.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Best Local Similarity: 22.22% Mismatches: 124
Query Match: 5.90% Indels: 113
RESULT 1481
ID ABT07557 standard; cDNA; 3414 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 36.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 19.54% Mismatches: 96
Query Match: 5.90% Indels: 65
RESULT 1482
ID ADD71208 standard; cDNA; 3489 BP.
DE Human intracellular signalling molecule INTS1G-45 cDNA SEQ ID NO:97.
PN WO2003039348-A2.
PD 15-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 26.56% Mismatches: 101
Query Match: 5.90% Indels: 60
RESULT 1483
ID ADQ97095 standard; DNA; 3503 BP.
DE Human cancer associated sequence HR2-10-005, SEQ ID 71.
PN WO2004060304-A2.

PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Best Local Similarity: 22.64% Mismatches: 66
Query Match: 5.90% Indels: 71
RESULT 1484
ID ACN43530 standard; cDNA; 3503 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2405.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 22.64% Mismatches: 66
Query Match: 5.90% Indels: 71
RESULT 1485
ID ABV74348 standard; DNA; 3512 BP.
DE Human ABC transporter ABCB9 encoding polynucleotide SEQ ID NO 1.
PN WO200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Best Local Similarity: 22.64% Mismatches: 66
Query Match: 5.90% Indels: 71
RESULT 1486
ID AAD06381 standard; cDNA; 3536 BP.
DE Human ATP binding cassette, ABCB9 transporter cDNA.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Best Local Similarity: 22.64% Mismatches: 66
Query Match: 5.90% Indels: 71
RESULT 1487
ID AAD05053 standard; cDNA; 3568 BP.
DE Human secreted protein-encoding gene 1 cDNA clone HDPAP35, SEQ ID NO:11.
PN WO200134768-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 24.49% Mismatches: 73
Query Match: 5.90% Indels: 53
RESULT 1488
ID AAS02121 standard; cDNA; 3575 BP.
DE Human TANGO 509, variant cDNA sequence #4.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.49% Mismatches: 73
Query Match: 5.90% Indels: 53
RESULT 1489
ID AAS02119 standard; cDNA; 3575 BP.
DE Human TANGO 509, alternative cDNA sequence #2.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.49% Mismatches: 73
Query Match: 5.90% Indels: 53
RESULT 1490
ID AAS02118 standard; cDNA; 3575 BP.
DE Human TANGO 509, alternative cDNA sequence #1.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.49% Mismatches: 73
Query Match: 5.90% Indels: 53
RESULT 1491
ID AAS02120 standard; cDNA; 3575 BP.
DE Human TANGO 509, alternative cDNA sequence #3.
PN WO200121631-A2.
PD 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.49% Mismatches: 73
Query Match: 5.90% Indels: 53
RESULT 1492
ID AAS02076 standard; cDNA; 3575 BP.
DE Human TANGO 509 cDNA sequence.
PN WO200121631-A2.
PD 29-MAR-2001.

PA (MILL-) MILLENNIUM PHARM INC.
 Query Match: 24.49% Mismatches: 73
 Indels: 53
 RESULT 1493
 ID AAD44205 standard; cDNA; 3575 BP.
 DE Human TANGO 509 cDNA.
 PN US2002055139-A1.
 PD 09-MAY-2002.
 PA (HOLT/) HOLTZMAN D A.
 PA (SHAR/) SHARP J D.
 PA (LEIB/) LEIBY K R.
 PA (BOSS/) BOSSONE S.
 PA (PANY/) PAN Y.
 PA (BARN/) BARNES T M.
 PA (FRAS/) FRASER C C.
 PA (WRIG/) WRIGHTON N.
 PA (MYER/) MYERS P S.
 PA (KING/) KINGSBURY G.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1494
 ID AAS06592 standard; cDNA; 3616 BP.
 DE Human immunoregulatory protein B7-H1 cDNA sequence.
 PN WO200139722-A2.
 PD 07-JUN-2001.
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1495
 ID ABK24011 standard; DNA; 3621 BP.
 DE DNA encoding B7-related protein, BSL1 #2.
 PN WO200194413-A2.
 PD 13-DEC-2001.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1496
 ID ADN05336 standard; cDNA; 3639 BP.
 DE Antipsoriatic cDNA sequence #890.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1497
 ID ADP55776 standard; cDNA; 3639 BP.
 DE Human PRO cDNA sequence SEQ ID NO:1752.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1498
 ID ADL45714 standard; DNA; 3660 BP.
 DE Human ovarian cancer DNA marker #19604.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Best Local Similarity: 24.49% Mismatches: 73
 Query Match: 5.90% Indels: 53
 RESULT 1499
 ID AAH42339 standard; DNA; 3726 BP.
 DE Nucleotide sequence of a human xylosyltransferase (XT) isoform XT-I.
 PN WO200149831-A2.
 PD 12-JUL-2001.
 PA (KLEE/) KLEESIEK K.
 Best Local Similarity: 26.64% Mismatches: 82
 Query Match: 5.90% Indels: 76
 RESULT 1500
 ID ADO31179 standard; DNA; 3728 BP.
 DE Human XT-I gene for glucosaminoglycan reduction in glial scars.
 PN WO2004041197-A2.
 PD 21-MAY-2004.

PA (UYCA-) UNIV CASE WESTERN RESERVE.
 Best Local Similarity: 26.64% Mismatches: 82
 Query Match: 5.90% Indels: 76

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2005, 08:04:14 ; Search time 182 Seconds

(without alignments)

2517.349 Million cell updates/sec

Title: US-10-015-388A-54

Perfect score: 1432

Sequence: 1 MCFNLKLLALLVGLWLFQIP.....LRAQPEPAERGRRGCSRA 280

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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-LIST=1500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	88.3	2240	4	US-09-799-451-571
C 2	111.5	7.8	4403765	3	US-09-103-840A-2
C 3	111.5	7.8	4411529	3	US-09-103-840A-1
C 4	109	7.6	1712	1	US-08-171-299B-1
C 5	106.5	7.4	12445	4	US-09-949-016-14632
C 6	106.5	7.4	21691	4	US-09-949-016-15748
C 7	104.5	7.3	1350	4	US-09-252-991A-690
C 8	104.5	7.3	3054	4	US-09-252-991A-720
C 9	104.5	7.3	6885	4	US-09-252-991A-660
C 10	104	7.3	6063	4	US-09-902-540-807
C 11	103.5	7.2	1131	4	US-09-252-991A-1675
C 12	103.5	7.2	2745	4	US-09-902-540-4835
C 13	103.5	7.2	26659	4	US-09-902-540-1237
C 14	103	7.2	1236	4	US-09-252-991A-8061
C 15	103	7.2	2556	4	US-09-252-991A-8202
C 16	101.5	7.1	1329	1	US-08-716-301-1
C 17	101.5	7.1	9301	3	US-09-449-218D-18
C 18	101.5	7.1	9301	4	US-09-668-529A-18
C 19	101.5	7.1	9301	4	US-09-668-037A-18
C 20	101.5	7.1	9301	4	US-09-668-021-18
C 21	99.5	6.9	1800	4	US-09-771-357-106
C 22	99.5	6.9	1800	4	US-10-059-579A-106
C 23	99.5	6.9	7057	4	US-09-799-451-112
C 24	99.5	6.9	29272	4	US-09-902-540-1217
C 25	99	6.9	1107	4	US-09-902-540-4129
C 26	99	6.9	1419	4	US-09-252-991A-6236
C 27	99	6.9	1476	4	US-09-252-991A-6067
C 28	99	6.9	9564	4	US-09-902-540-1026
C 29	98.5	6.9	1893	4	US-09-252-991A-9055
C 30	98.5	6.9	2555	4	US-09-949-016-2310
C 31	98	6.8	4403765	3	US-09-103-840A-2
C 32	98	6.8	4411529	3	US-09-103-840A-1
C 33	97.5	6.8	675	4	US-09-902-540-829
C 34	97.5	6.8	6159	4	US-09-902-540-829
C 35	97.5	6.8	11220	3	US-09-105-537-32
C 36	97.5	6.8	36778	3	US-09-105-537-5
C 37	97.5	6.8	38506	3	US-09-320-878-19
C 38	97.5	6.8	38506	4	US-09-141-908-1
C 39	97.5	6.8	38506	4	US-09-657-440-19
C 40	97	6.8	858	4	US-09-252-991A-3981
C 41	97	6.8	1482	4	US-09-252-991A-4050
C 42	97	6.8	1605	4	US-09-252-991A-3897
C 43	97	6.8	3223	2	US-08-620-694A-9
C 44	97	6.8	3223	3	US-09-022-255-9
C 45	97	6.8	3223	3	US-09-022-696-9
C 46	97	6.8	3223	3	US-08-978-773-3
C 47	97	6.8	3223	3	US-09-022-253-9
C 48	97	6.8	3223	3	US-09-022-259-9
C 49	97	6.8	3223	3	US-09-022-257-9
C 50	97	6.8	3223	3	US-09-549-679-9
C 51	97	6.8	3223	4	US-09-252-991A-5855
C 52	96.5	6.7	1311	4	US-09-902-540-8236
C 53	96.5	6.7	2145	4	US-09-902-540-8236
C 54	96.5	6.7	9472	4	US-09-902-540-851
C 55	96	6.7	1813	4	US-09-016-434-1229
C 56	96	6.7	2678	4	US-09-016-434-1229
C 57	96	6.7	10322	4	US-09-902-540-989
C 58	95.5	6.7	1965	4	US-09-252-991A-9230
C 59	95.5	6.7	2805	4	US-09-252-991A-9064
C 60	95.5	6.7	3453	4	US-09-252-991A-8100
C 61	95	6.6	8438	1	US-07-945-283-1
C 62	95	6.6	15271	4	US-09-902-540-1051
C 63	95	6.6	68750	3	US-09-335-409-1
C 64	95	6.6	68750	3	US-09-568-102-1
C 65	95	6.6	68750	3	US-09-567-969-1
C 66	95	6.6	68750	3	US-09-568-480-1
C 67	95	6.6	68750	3	US-09-568-486-1
C 68	95	6.6	68750	3	US-09-568-472-1
C 69	95	6.6	68750	3	US-09-567-899-1
C 70	94.5	6.6	1050	3	US-09-655-270A-16
C 71	94.5	6.6	1050	3	US-09-651-941-20
C 72	94.5	6.6	1050	3	US-09-955-597-20
C 73	94.5	6.6	10992	4	US-09-902-540-1081
C 74	94.5	6.6	12508	3	US-09-655-270A-1
C 75	94.5	6.6	12508	3	US-09-655-270A-1
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C 79	94.5	6.6	12523	3	US-09-955-597-1
C 80	94.5	6.6	22339	4	US-09-949-016-12411
C 81	94.5	6.6	22339	4	US-09-949-016-16154
C 82	94	6.6	891	4	US-09-252-991A-10527
C 83	94	6.6	1320	4	US-09-252-991A-10535
C 84	94	6.6	1473	4	US-09-252-991A-10639
C 85	94	6.6	1767	4	US-09-252-991A-14119

86	94	6.6	4287	4	US-09-252-991A-14160	Sequence 14160, A	159	90	6.3	18031	4	US-09-902-540-1180	Sequence 1180, Ap
87	93.5	6.5	1230	4	US-09-252-991A-12810	Sequence 12810, A	c 160	90	6.3	536165	4	US-09-214-808-1	Sequence 1, Appli
88	93.5	6.5	3542	4	US-09-620-312D-233	Sequence 233, App	c 161	89.5	6.2	1227	3	US-09-385-028-23	Sequence 23, Appl
89	93.5	6.5	5630	2	US-08-937-931-1	Sequence 1, Appli	c 162	89.5	6.2	1227	4	US-09-726-614-23	Sequence 23, Appl
90	93.5	6.5	5630	3	US-09-285-502-1	Sequence 1, Appli	c 163	89.5	6.2	1227	4	US-09-385-040-23	Sequence 23, Appl
91	93.5	6.5	5630	3	US-09-709-126-1	Sequence 1, Appli	c 164	89.5	6.2	1227	4	US-09-252-991A-8312	Sequence 8312, Ap
92	93.5	6.5	5630	3	US-09-871-385A-1	Sequence 1, Appli	c 165	89.5	6.2	1227	4	US-09-583-110-1147	Sequence 1147, Ap
93	93.5	6.5	1826	4	US-09-949-016-14118	Sequence 14118, A	c 166	89.5	6.2	1425	4	US-08-961-527-184	Sequence 184, App
94	93.5	6.5	1826	4	US-09-949-016-11838	Sequence 11838, A	c 167	89.5	6.2	1656	4	US-09-252-991A-3669	Sequence 3669, Ap
95	93.5	6.5	47981	4	US-09-679-275-1	Sequence 1, Appli	c 168	89.5	6.2	2469	4	US-09-252-991A-5349	Sequence 5349, Ap
96	93	6.5	990	4	US-09-252-991A-1499	Sequence 1499, Ap	c 169	89.5	6.2	2892	4	US-09-902-540-7217	Sequence 7217, Ap
97	93	6.5	1301	4	US-09-252-991A-6933	Sequence 6933, Ap	c 170	89.5	6.2	3003	3	US-09-423-340-1	Sequence 1, Appli
98	93	6.5	1320	4	US-09-252-991A-6860	Sequence 6860, Ap	c 171	89.5	6.2	3003	4	US-09-820-155-1	Sequence 1, Appli
99	93	6.5	1359	4	US-09-252-991A-6765	Sequence 6765, Ap	c 172	89.5	6.2	3612	4	US-09-902-540-674	Sequence 674, App
100	93	6.5	3089	4	US-09-902-540-6699	Sequence 6699, Ap	c 173	89.5	6.2	5103	4	US-09-252-991A-5192	Sequence 5192, App
101	93	6.5	4113	4	US-09-902-540-531	Sequence 531, App	c 174	89.5	6.2	6682	4	US-09-902-540-906	Sequence 906, App
102	93	6.5	6828	4	US-09-902-540-8354	Sequence 8354, Ap	c 175	89.5	6.2	6876	4	US-09-252-991A-5283	Sequence 5283, Ap
103	93	6.5	8056	4	US-09-902-540-874	Sequence 874, App	c 176	89.5	6.2	15079	3	US-09-385-028-1	Sequence 1, Appli
104	93	6.5	15923	4	US-09-902-540-1095	Sequence 1095, Ap	c 177	89.5	6.2	15079	4	US-09-726-614-1	Sequence 1, Appli
105	92.5	6.5	3030	3	US-09-484-970B-23	Sequence 23, Appl	c 178	89.5	6.2	15120	4	US-09-385-040-1	Sequence 1, Appli
106	92.5	6.5	35100	1	US-08-306-691B-19	Sequence 19, Appl	c 179	89.5	6.2	26173	3	US-09-453-702B-69	Sequence 69, Appl
107	92.5	6.5	35100	5	PCT-US93-06251-19	Sequence 19, Appl	c 180	89.5	6.2	36954	4	US-09-949-016-15304	Sequence 15304, A
108	92.5	6.5	455726	4	US-09-949-016-14157	Sequence 14157, A	c 181	89.5	6.2	60785	4	US-09-949-016-12774	Sequence 12774, A
109	92.5	6.5	481115	4	US-09-949-016-11940	Sequence 11940, A	c 182	89.5	6.2	60785	4	US-09-949-016-15665	Sequence 15665, A
110	92.5	6.5	786431	4	US-09-751-389-3	Sequence 3, Appli	c 183	89	6.2	732	4	US-09-252-991A-3282	Sequence 3282, Ap
111	92	6.4	1350	4	US-09-902-540-4545	Sequence 4545, Ap	c 184	89	6.2	771	4	US-09-252-991A-3257	Sequence 3257, Ap
112	92	6.4	1461	4	US-09-252-991A-7765	Sequence 7765, Ap	c 185	89	6.2	939	4	US-09-252-991A-3216	Sequence 3216, Ap
113	92	6.4	1881	4	US-09-774-528-52	Sequence 52, Appl	c 186	89	6.2	945	4	US-09-252-991A-3427	Sequence 3427, Ap
114	92	6.4	2490	4	US-09-902-540-3801	Sequence 3801, Ap	c 187	89	6.2	1182	4	US-09-252-991A-565	Sequence 565, App
115	92	6.4	10835	4	US-09-902-540-1031	Sequence 1031, Ap	c 188	89	6.2	1206	4	US-09-252-991A-519	Sequence 519, App
116	92	6.4	18551	4	US-09-902-540-1187	Sequence 1187, Ap	c 189	89	6.2	1338	4	US-09-902-540-5209	Sequence 5209, Ap
117	92	6.4	22773	4	US-09-990-613A-6	Sequence 6, Appli	c 190	89	6.2	1365	4	US-09-252-991A-3116	Sequence 3116, Ap
118	91.5	6.4	1254	4	US-09-902-540-7861	Sequence 7861, Ap	c 191	89	6.2	1746	4	US-09-252-991A-8948	Sequence 8948, Ap
119	91.5	6.4	6975	4	US-09-902-540-2386	Sequence 2386, Ap	c 192	89	6.2	2115	4	US-09-252-991A-5749	Sequence 5749, Ap
120	91.5	6.4	8614	4	US-09-902-540-7877	Sequence 7877, App	c 193	89	6.2	2160	4	US-09-252-991A-5707	Sequence 5707, Ap
121	91.5	6.4	13855	4	US-09-902-540-1117	Sequence 1117, Ap	c 194	89	6.2	2181	4	US-09-252-991A-493	Sequence 493, App
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123	91	6.4	678	4	US-09-252-991A-8932	Sequence 8932, Ap	c 196	89	6.2	2319	4	US-09-252-991A-15384	Sequence 15384, A
124	91	6.4	1257	4	US-09-902-540-8864	Sequence 8864, Ap	c 197	89	6.2	2427	4	US-09-252-991A-15396	Sequence 15396, A
125	91	6.4	1293	4	US-09-902-540-7230	Sequence 7230, Ap	c 198	89	6.2	2631	4	US-09-252-991A-16070	Sequence 16070, A
126	91	6.4	1590	3	US-09-434-288-1	Sequence 1, Appli	c 199	89	6.2	2694	4	US-09-902-540-4257	Sequence 4257, Ap
127	91	6.4	1908	3	US-08-993-774A-9	Sequence 9, Appli	c 200	89	6.2	3291	4	US-09-252-991A-2757	Sequence 2757, Ap
128	91	6.4	2540	1	US-08-027-986-4	Sequence 4, Appli	c 201	89	6.2	3916	4	US-09-902-540-463	Sequence 463, App
129	91	6.4	3784	4	US-09-902-540-580	Sequence 580, App	c 202	89	6.2	7571	4	US-09-949-016-12878	Sequence 12878, A
130	91	6.4	4486	4	US-09-902-540-677	Sequence 677, App	c 203	89	6.2	7571	4	US-09-949-016-17584	Sequence 17584, A
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132	91	6.4	18469	4	US-09-902-540-1205	Sequence 1205, Ap	c 205	89	6.2	13146	3	US-09-270-984A-3	Sequence 3, Appli
133	91	6.4	81384	4	US-09-902-540-12422	Sequence 12422, A	c 206	89	6.2	17622	4	US-09-902-540-1125	Sequence 1125, Ap
134	90.5	6.3	933	4	US-09-252-991A-14167	Sequence 14167, A	c 207	89	6.2	21010	4	US-09-902-540-1188	Sequence 1188, Ap
135	90.5	6.3	1158	4	US-09-252-991A-14214	Sequence 14214, A	c 208	89	6.2	24791	4	US-09-902-540-1211	Sequence 1211, Ap
136	90.5	6.3	12105	3	US-09-446-821A-1	Sequence 1, Appli	c 209	89	6.2	31826	4	US-09-252-991A-1163	Sequence 1163, Ap
137	90.5	6.3	2247	4	US-09-902-540-6649	Sequence 6649, Ap	c 210	88.5	6.2	1746	4	US-09-252-991A-1163	Sequence 1163, Ap
138	90.5	6.3	2262	4	US-09-902-540-9616	Sequence 9616, Ap	c 211	88.5	6.2	2190	4	US-09-252-991A-5685	Sequence 5685, Ap
139	90.5	6.3	2304	4	US-09-252-991A-8731	Sequence 8731, Ap	c 212	88.5	6.2	2579	3	US-08-444-818-29	Sequence 29, Appl
140	90.5	6.3	2598	4	US-09-902-540-507	Sequence 507, App	c 213	88.5	6.2	2850	4	US-09-252-991A-5730	Sequence 5730, Ap
141	90.5	6.3	2936	4	US-09-902-540-538	Sequence 538, App	c 214	88.5	6.2	4647	4	US-09-252-991A-5730	Sequence 5730, Ap
142	90.5	6.3	3231	4	US-09-902-540-6725	Sequence 6725, Ap	c 215	88.5	6.2	5360	3	US-08-444-818-53	Sequence 53, Appl
143	90.5	6.3	3343	4	US-09-902-540-515	Sequence 515, App	c 216	88.5	6.2	6785	3	US-08-444-818-65	Sequence 65, Appl
144	90.5	6.3	7229	4	US-09-902-540-919	Sequence 919, App	c 217	88.5	6.2	8316	3	US-08-444-818-98	Sequence 88, Appl
145	90.5	6.3	9472	4	US-09-902-540-851	Sequence 851, App	c 218	88.5	6.2	8987	3	US-08-444-818-137	Sequence 137, App
146	90.5	6.3	13631	4	US-09-902-540-1092	Sequence 1092, Ap	c 219	88.5	6.2	9185	3	US-08-444-818-122	Sequence 122, App
147	90.5	6.3	15312	4	US-09-902-540-1115	Sequence 1115, Ap	c 220	88.5	6.2	9185	3	US-08-444-818-123	Sequence 123, App
148	90.5	6.3	22512	4	US-09-902-540-1220	Sequence 1220, Ap	c 221	88.5	6.2	9379	3	US-08-444-818-176	Sequence 176, App
149	90.5	6.3	48908	3	US-09-453-702B-137	Sequence 137, App	c 222	88.5	6.2	9379	3	US-09-388-874-1	Sequence 1, Appli
150	90.5	6.3	197336	4	US-09-949-016-12881	Sequence 12881, A	c 223	88.5	6.2	9379	4	US-09-916-359-1	Sequence 1, Appli
151	90.5	6.3	197337	4	US-09-949-016-14376	Sequence 14376, A	c 224	88.5	6.2	9401	1	US-07-910-760-9	Sequence 9, Appli
152	90.5	6.3	234288	4	US-09-949-016-17272	Sequence 17272, A	c 225	88.5	6.2	9401	1	US-08-440-519-9	Sequence 9, Appli
153	90	6.3	1195	4	US-09-522-714-7	Sequence 7, Appli	c 226	88.5	6.2	9401	3	US-08-440-549-9	Sequence 9, Appli
154	90	6.3	1461	4	US-09-252-991A-180	Sequence 180, App	c 227	88.5	6.2	9401	3	US-08-823-895A-25	Sequence 25, Appl
155	90	6.3	4800	4	US-09-902-540-562	Sequence 562, App	c 228	88.5	6.2	12980	3	US-08-811-566-5	Sequence 5, Appli
156	90	6.3	6336	4	US-09-902-540-8124	Sequence 8124, Ap	c 229	88.5	6.2	12980	3	US-09-034-756-5	Sequence 5, Appli
157	90	6.3	6338	4	US-09-902-540-831	Sequence 831, App	c 230	88.5	6.2	20235	1	US-07-642-734C-3	Sequence 3, Appli
158	90	6.3	9497	4	US-09-902-540-1054	Sequence 1054, Ap	c 231	88.5	6.2	20235	3	US-08-439-009A-3	Sequence 3, Appli

c 232	88.5	6.2	29899	4	US-09-902-540-1265	Sequence 1265, Ap	305	86.5	6.0	1782	4	US-09-252-991A-15840	Sequence 15840, A
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c 234	88.5	6.2	41927	4	US-09-902-540-1268	Sequence 1268, A	c 307	86.5	6.0	1863	4	US-09-902-540-7315	Sequence 7315, Ap
c 235	88.5	6.2	50000	3	US-09-146-053-3	Sequence 3, Appli	c 308	86.5	6.0	2058	4	US-09-949-016-4862	Sequence 4862, Ap
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c 237	88	6.1	993	4	US-09-252-991A-10494	Sequence 10494, A	c 310	86.5	6.0	2169	4	US-09-949-016-280	Sequence 280, App
c 238	88	6.1	1782	4	US-09-902-540-4707	Sequence 4707, Ap	c 311	86.5	6.0	2294	3	US-09-643-597-123	Sequence 123, App
c 239	88	6.1	1821	3	US-09-486-382B-10	Sequence 10, Appl	c 312	86.5	6.0	2294	4	US-09-480-884A-123	Sequence 123, App
c 240	88	6.1	1866	4	US-09-252-991A-11804	Sequence 11804, A	c 313	86.5	6.0	2294	4	US-09-542-615A-123	Sequence 123, App
c 241	88	6.1	1941	4	US-09-252-991A-11635	Sequence 11635, A	c 314	86.5	6.0	2294	4	US-09-606-421B-123	Sequence 123, App
c 242	88	6.1	1941	4	US-09-949-016-5844	Sequence 5844, Ap	c 315	86.5	6.0	2294	4	US-09-023-655-1217	Sequence 1217, Ap
c 243	88	6.1	1836	3	US-09-147-236-1	Sequence 1, Appli	c 316	86.5	6.0	2294	4	US-09-221-107-123	Sequence 123, App
c 244	88	6.1	1836	3	US-09-147-236-10	Sequence 10, Appl	c 317	86.5	6.0	2294	4	US-09-486-396A-123	Sequence 123, App
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c 247	88	6.1	28558	4	US-09-902-540-1231	Sequence 1231, Ap	c 320	86.5	6.0	2294	4	US-09-285-479-123	Sequence 123, App
c 248	88	6.1	31467	4	US-09-949-016-13134	Sequence 13134, A	c 321	86.5	6.0	2301	6	5188829-2	Patent No. 5188829
c 249	88	6.1	31868	4	US-09-949-016-11907	Sequence 11907, A	c 322	86.5	6.0	2301	6	5188829-2	Patent No. 5188829
c 250	88	6.1	50725	4	US-09-902-540-1271	Sequence 1271, Ap	c 323	86.5	6.0	3006	4	US-09-252-991A-9720	Sequence 9720, Ap
c 251	87.5	6.1	1263	4	US-09-252-991A-9275	Sequence 9275, Ap	c 324	86.5	6.0	3144	4	US-09-252-991A-14688	Sequence 14688, A
c 252	87.5	6.1	1342	4	US-09-902-540-224	Sequence 224, App	c 325	86.5	6.0	3198	4	US-09-252-991A-15066	Sequence 15066, A
c 253	87.5	6.1	1347	4	US-09-902-540-7980	Sequence 7980, Ap	c 326	86.5	6.0	3471	4	US-09-902-540-8385	Sequence 8385, Ap
c 254	87.5	6.1	1617	4	US-09-252-991A-3842	Sequence 3842, Ap	c 327	86.5	6.0	4401	4	US-09-252-991A-13514	Sequence 13514, A
c 255	87.5	6.1	1631	4	US-09-949-016-3098	Sequence 3098, Ap	c 328	86.5	6.0	5764	4	US-09-902-540-693	Sequence 693, App
c 256	87.5	6.1	1808	4	US-09-949-016-3099	Sequence 3099, Ap	c 329	86.5	6.0	6380	4	US-09-902-540-891	Sequence 891, App
c 257	87.5	6.1	1864	4	US-09-016-434-1161	Sequence 1161, Ap	c 330	86.5	6.0	6458	4	US-09-949-016-16604	Sequence 16604, A
c 258	87.5	6.1	1891	4	US-09-949-016-5845	Sequence 5845, Ap	c 331	86.5	6.0	7186	4	US-09-902-540-879	Sequence 879, App
c 259	87.5	6.1	3744	4	US-09-252-991A-16389	Sequence 16389, A	c 332	86.5	6.0	10877	4	US-09-674-311-1	Sequence 1, Appli
c 260	87.5	6.1	6012	4	US-09-902-540-808	Sequence 808, App	c 333	86.5	6.0	13377	4	US-09-949-016-16358	Sequence 16358, A
c 261	87.5	6.1	7310	3	US-08-444-818-74	Sequence 74, Appl	c 334	86.5	6.0	13751	4	US-09-902-540-1099	Sequence 1099, Ap
c 262	87.5	6.1	9401	2	US-08-432-693-1	Sequence 1, Appli	c 335	86.5	6.0	23673	3	US-09-773-816-1	Sequence 1, Appli
c 263	87.5	6.1	9416	3	US-08-811-566-19	Sequence 19, Appl	c 336	86.5	6.0	48682	4	US-09-949-016-17236	Sequence 17236, A
c 264	87.5	6.1	9416	3	US-09-034-756-19	Sequence 19, Appl	c 337	86.5	6.0	48682	4	US-09-949-016-17237	Sequence 17237, A
c 265	87.5	6.1	9599	3	US-09-014-416-2	Sequence 2, Appli	c 338	86.5	6.0	48682	4	US-09-949-016-17238	Sequence 17238, A
c 266	87.5	6.1	9599	3	US-09-014-416-6	Sequence 6, Appli	c 339	86.5	6.0	48682	4	US-09-949-016-17239	Sequence 17239, A
c 267	87.5	6.1	9646	3	US-08-811-566-1	Sequence 1, Appli	c 340	86.5	6.0	51022	4	US-09-949-016-17135	Sequence 17135, A
c 268	87.5	6.1	9646	3	US-09-034-756-1	Sequence 1, Appli	c 341	86.5	6.0	51022	4	US-09-949-016-17137	Sequence 17137, A
c 269	87.5	6.1	11695	4	US-09-902-540-1045	Sequence 1045, Ap	c 342	86.5	6.0	51022	4	US-09-949-016-17138	Sequence 17138, A
c 270	87.5	6.1	12028	4	US-09-902-540-1071	Sequence 1071, Ap	c 343	86.5	6.0	51022	4	US-09-949-016-17138	Sequence 17138, A
c 271	87.5	6.1	12848	3	US-09-453-702B-252	Sequence 252, App	c 344	86.5	6.0	72704	4	US-09-902-540-1273	Sequence 1273, Ap
c 272	87.5	6.1	17226	4	US-09-902-540-1148	Sequence 1148, Ap	c 345	86.5	6.0	79858	4	US-09-949-016-16080	Sequence 16080, A
c 273	87.5	6.1	42800	2	US-08-804-227C-1	Sequence 1, Appli	c 346	86.5	6.0	86213	4	US-09-949-016-17240	Sequence 17240, A
c 274	87	6.1	1176	4	US-09-902-540-3067	Sequence 3067, Ap	c 347	86.5	6.0	86213	4	US-09-949-016-17241	Sequence 17241, A
c 275	87	6.1	1266	4	US-09-252-991A-15869	Sequence 15869, A	c 348	86.5	6.0	86213	4	US-09-949-016-17242	Sequence 17242, A
c 276	87	6.1	1362	4	US-09-252-991A-3258	Sequence 3258, Ap	c 349	86.5	6.0	86213	4	US-09-949-016-17243	Sequence 17243, A
c 277	87	6.1	1551	4	US-09-252-991A-3217	Sequence 3217, Ap	c 350	86.5	6.0	784019	4	US-09-949-016-14033	Sequence 14033, A
c 278	87	6.1	1941	4	US-09-902-540-4762	Sequence 4762, Ap	c 351	86.5	6.0	828152	4	US-09-949-016-12777	Sequence 12777, A
c 279	87	6.1	1995	4	US-09-252-991A-11521	Sequence 11521, A	c 352	86	6.0	636	4	US-09-252-991A-6400	Sequence 6400, Ap
c 280	87	6.1	5872	4	US-09-902-540-859	Sequence 859, App	c 353	86	6.0	981	4	US-09-252-991A-5003	Sequence 5003, Ap
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c 283	87	6.1	6492	4	US-09-902-540-1234	Sequence 1234, Ap	c 356	86	6.0	1083	4	US-09-252-991A-9481	Sequence 9481, Ap
c 284	87	6.1	28899	4	US-09-902-540-1265	Sequence 1265, Ap	c 357	86	6.0	1179	4	US-09-252-991A-2482	Sequence 2482, Ap
c 285	87	6.1	134008	4	US-09-949-016-13841	Sequence 13841, A	c 358	86	6.0	1233	1	US-08-254-922-1	Sequence 1, Appli
c 286	86.5	6.0	612	4	US-09-252-991A-3713	Sequence 3713, Ap	c 359	86	6.0	1233	1	US-08-286-748B-1	Sequence 1, Appli
c 287	86.5	6.0	963	4	US-09-252-991A-4485	Sequence 4485, Ap	c 360	86	6.0	1236	1	US-07-957-039A-7	Sequence 7, Appli
c 288	86.5	6.0	1098	4	US-09-252-991A-1304	Sequence 1304, Ap	c 361	86	6.0	1236	1	US-08-153-799-17	Sequence 17, Appl
c 289	86.5	6.0	1149	4	US-09-252-991A-8691	Sequence 8691, Ap	c 362	86	6.0	1236	1	US-09-880-503-12	Sequence 12, Appl
c 290	86.5	6.0	1323	4	US-09-252-991A-2253	Sequence 2253, Ap	c 363	86	6.0	1341	4	US-09-252-991A-2353	Sequence 2353, Ap
c 291	86.5	6.0	1372	6	5219569-1	Sequence 2253, Ap	c 364	86	6.0	1398	4	US-09-252-991A-2564	Sequence 2564, Ap
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c 294	86.5	6.0	1428	4	US-09-252-991A-4267	Sequence 4267, Ap	c 367	86	6.0	1500	4	US-09-881-165-1	Sequence 1, Appli
c 295	86.5	6.0	1475	3	US-09-643-597-122	Sequence 122, App	c 368	86	6.0	1500	4	US-09-786-960-1	Sequence 1, Appli
c 296	86.5	6.0	1475	4	US-09-480-884A-122	Sequence 122, App	c 369	86	6.0	1728	4	US-10-029-180-101	Sequence 101, App
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c 298	86.5	6.0	1475	4	US-09-606-421B-122	Sequence 122, App	c 371	86	6.0	1881	4	US-09-252-991A-7230	Sequence 7230, App
c 299	86.5	6.0	1475	4	US-09-221-107-122	Sequence 122, App	c 372	86	6.0	1932	4	US-09-252-991A-1654	Sequence 1654, Ap
c 300	86.5	6.0	1475	4	US-09-466-396A-122	Sequence 122, App	c 373	86	6.0	1986	4	US-09-252-991A-1654	Sequence 1, Appli
c 301	86.5	6.0	1475	4	US-09-476-496A-122	Sequence 122, App	c 374	86	6.0	2027	1	US-08-150-203A-1	Sequence 1, Appli
c 302	86.5	6.0	1475	4	US-09-630-940B-122	Sequence 122, App	c 375	86	6.0	2027	3	US-08-454-730-1	Sequence 1, Appli
c 303	86.5	6.0	1475	4	US-09-285-479-122	Sequence 122, App	c 376	86	6.0	2027	3	US-08-949-788-1	Sequence 1, Appli
c 304	86.5	6.0	1713	4	US-09-252-991A-14948	Sequence 14948, A	c 377	86	6.0	2040	1	US-08-247-475-36	Sequence 36, Appli

C 378	86	6.0	2040	1	US-08-479-650-36	Sequence 36, Appl	C 451	85	5.9	4145	4	US-09-912-161-5	Sequence 5, Appl
C 379	86	6.0	2040	1	US-08-191-866D-57	Sequence 57, Appl	C 452	85	5.9	4145	4	US-09-911-781-3	Sequence 3, Appl
C 380	86	6.0	2040	1	US-08-674-169-36	Sequence 36, Appl	C 453	85	5.9	4145	4	US-10-400-902-3	Sequence 3, Appl
C 381	86	6.0	2040	2	US-08-185-949B-57	Sequence 57, Appl	C 454	85	5.9	4212	3	US-08-221-017B-39	Sequence 39, Appl
C 382	86	6.0	2046	4	US-09-252-991A-7996	Sequence 7996, Ap	C 455	85	5.9	4237	4	US-09-949-016-2146	Sequence 2146, Ap
C 383	86	6.0	2046	4	US-09-252-991A-8058	Sequence 8058, Ap	C 456	85	5.9	4320	4	US-09-902-540-577	Sequence 577, Ap
C 384	86	6.0	2121	4	US-09-252-991A-8195	Sequence 8195, Ap	C 457	85	5.9	4320	4	US-09-902-540-6854	Sequence 6854, Ap
C 385	86	6.0	2715	4	US-09-252-991A-6631	Sequence 6631, Ap	C 458	85	5.9	4486	4	US-09-902-540-677	Sequence 677, Ap
C 386	86	6.0	2727	4	US-09-252-991A-8111	Sequence 8111, Ap	C 459	85	5.9	4509	4	US-09-647-140B-7	Sequence 7, Appl
C 387	86	6.0	2898	4	US-09-252-991A-7467	Sequence 7467, Ap	C 460	85	5.9	4512	4	US-09-792-616-2	Sequence 2, Appl
C 388	86	6.0	3109	4	US-09-902-540-413	Sequence 413, Ap	C 461	85	5.9	6083	4	US-09-902-540-763	Sequence 763, Ap
C 389	86	6.0	3699	4	US-09-902-540-3731	Sequence 3731, Ap	C 462	85	5.9	6196	4	US-09-902-540-788	Sequence 788, Ap
C 390	86	6.0	3702	4	US-09-252-991A-6666	Sequence 6666, Ap	C 463	85	5.9	8237	4	US-09-949-016-12067	Sequence 12067, A
C 391	86	6.0	4190	3	US-08-924-345-1	Sequence 1, Appl	C 464	85	5.9	8237	4	US-09-949-016-13888	Sequence 13888, A
C 392	86	6.0	17612	3	US-08-911-853-29	Sequence 29, Appl	C 465	85	5.9	9369	4	US-10-237-551-190	Sequence 190, Ap
C 393	86	6.0	17612	3	US-09-479-409-29	Sequence 29, Appl	C 466	85	5.9	9369	4	US-10-237-551-247	Sequence 247, Ap
C 394	86	6.0	17612	3	US-09-479-453-29	Sequence 29, Appl	C 467	85	5.9	23368	4	US-09-949-016-15418	Sequence 15418, A
C 395	86	6.0	17897	4	US-09-902-540-1182	Sequence 1182, Ap	C 468	85	5.9	33655	4	US-09-949-016-13947	Sequence 13947, A
C 396	86	6.0	19112	4	US-09-902-540-1181	Sequence 1181, Ap	C 469	85	5.9	34316	4	US-09-949-016-1257	Sequence 1257, Ap
C 397	86	6.0	20093	4	US-09-949-016-15207	Sequence 15207, A	C 470	85	5.9	71989	3	US-09-443-501A-2	Sequence 2, Appl
C 398	86	6.0	26640	4	US-09-949-016-17431	Sequence 17431, A	C 471	85	5.9	92334	4	US-09-949-016-13920	Sequence 13920, A
C 399	86	6.0	26420	4	US-09-949-016-12052	Sequence 12052, A	C 472	85	5.9	92363	4	US-09-949-016-12146	Sequence 12146, A
C 400	86	6.0	77772	4	US-09-949-016-17417	Sequence 17417, A	C 473	85	5.9	154746	4	US-09-827-688-8	Sequence 8, Appl
C 401	86	6.0	77997	4	US-09-949-016-12249	Sequence 12249, A	C 474	85	5.9	181429	4	US-09-949-016-12372	Sequence 12372, A
C 402	86	6.0	128470	4	US-09-949-016-13765	Sequence 13765, A	C 475	85	5.9	181430	4	US-09-949-016-15772	Sequence 15772, A
C 403	85.5	6.0	866	4	US-09-799-451-119	Sequence 119, Ap	C 476	84.5	5.9	870	4	US-09-451-291-2	Sequence 2, Appl
C 404	85.5	6.0	1254	4	US-09-252-991A-3594	Sequence 3594, Ap	C 477	84.5	5.9	873	4	US-09-910-174B-22	Sequence 22, Appl
C 405	85.5	6.0	1293	4	US-09-902-540-5995	Sequence 5995, Ap	C 478	84.5	5.9	873	4	US-09-620-461-22	Sequence 22, Appl
C 406	85.5	6.0	1470	4	US-09-252-991A-3169	Sequence 3169, Ap	C 479	84.5	5.9	1251	4	US-09-252-991A-16304	Sequence 16304, A
C 407	85.5	6.0	1521	4	US-09-902-540-6676	Sequence 6676, Ap	C 480	84.5	5.9	1286	4	US-10-133-907-3	Sequence 3, Appl
C 408	85.5	6.0	1545	4	US-09-902-540-5163	Sequence 5163, Ap	C 481	84.5	5.9	1311	4	US-09-107-433-1201	Sequence 1201, Ap
C 409	85.5	6.0	1764	4	US-09-252-991A-9797	Sequence 9797, Ap	C 482	84.5	5.9	1347	4	US-09-724-797-43	Sequence 43, Appl
C 410	85.5	6.0	1785	4	US-09-252-991A-3774	Sequence 3774, Ap	C 483	84.5	5.9	1380	4	US-09-252-991A-15862	Sequence 15862, A
C 411	85.5	6.0	2256	4	US-09-252-991A-8910	Sequence 8910, Ap	C 484	84.5	5.9	1443	4	US-09-902-540-4011	Sequence 4011, Ap
C 412	85.5	6.0	2637	4	US-09-902-540-3252	Sequence 3252, Ap	C 485	84.5	5.9	1533	4	US-09-252-991A-1124	Sequence 1124, Ap
C 413	85.5	6.0	5114	4	US-09-949-016-14195	Sequence 14195, A	C 486	84.5	5.9	1545	4	US-09-252-991A-14667	Sequence 14667, A
C 414	85.5	6.0	5421	4	US-09-949-016-11832	Sequence 11832, A	C 487	84.5	5.9	1553	4	US-09-645-069-3	Sequence 3, Appl
C 415	85.5	6.0	7301	4	US-09-949-016-14229	Sequence 14229, A	C 488	84.5	5.9	1572	4	US-09-252-991A-4553	Sequence 4553, Ap
C 416	85.5	6.0	8090	4	US-09-902-540-855	Sequence 855, Ap	C 489	84.5	5.9	1581	4	US-09-252-991A-16413	Sequence 16413, A
C 417	85.5	6.0	9165	4	US-09-902-540-1050	Sequence 1050, Ap	C 490	84.5	5.9	1614	4	US-09-949-016-2542	Sequence 2542, Ap
C 418	85.5	6.0	9401	5	PCT-US91-02225-9	Sequence 9, Appl	C 491	84.5	5.9	1686	4	US-09-252-991A-4299	Sequence 4299, Ap
C 419	85.5	6.0	10505	4	US-09-902-540-1044	Sequence 1044, Ap	C 492	84.5	5.9	1688	4	US-09-949-016-2187	Sequence 2187, Ap
C 420	85.5	6.0	11805	4	US-09-902-540-1016	Sequence 1016, Ap	C 493	84.5	5.9	1767	4	US-09-252-991A-14785	Sequence 14785, A
C 421	85.5	6.0	12225	4	US-09-949-016-17360	Sequence 17360, Ap	C 494	84.5	5.9	2031	4	US-09-252-991A-8142	Sequence 8142, Ap
C 422	85.5	6.0	12725	4	US-09-902-540-1139	Sequence 1139, Ap	C 495	84.5	5.9	2106	4	US-09-252-991A-15891	Sequence 15891, A
C 423	85.5	6.0	20441	4	US-09-949-016-13052	Sequence 13052, A	C 496	84.5	5.9	3162	4	US-09-252-991A-8094	Sequence 8094, Ap
C 424	85.5	6.0	28555	4	US-09-949-016-13106	Sequence 13106, A	C 497	84.5	5.9	3343	4	US-09-976-594-502	Sequence 502, Ap
C 425	85.5	6.0	29559	4	US-09-902-540-1254	Sequence 1254, Ap	C 498	84.5	5.9	3411	3	US-08-890-865A-3	Sequence 3, Appl
C 426	85.5	6.0	80161	3	US-09-036-987A-1	Sequence 1, Appl	C 499	84.5	5.9	3422	4	US-09-949-016-1919	Sequence 1919, Ap
C 427	85.5	6.0	80161	3	US-09-370-700-1	Sequence 1, Appl	C 500	84.5	5.9	3536	4	US-09-724-653-1	Sequence 1, Appl
C 428	85.5	6.0	80161	4	US-09-603-207-1	Sequence 1, Appl	C 501	84.5	5.9	3616	4	US-09-451-291-5	Sequence 5, Appl
C 429	85	5.9	606	3	US-08-998-416-119	Sequence 119, Ap	C 502	84.5	5.9	4236	4	US-09-252-991A-11837	Sequence 11837, A
C 430	85	5.9	850	4	US-09-270-767-6468	Sequence 6468, Ap	C 503	84.5	5.9	4432	4	US-09-774-528-148	Sequence 148, Ap
C 431	85	5.9	850	4	US-09-270-767-21750	Sequence 21750, A	C 504	84.5	5.9	4459	4	US-09-949-016-5641	Sequence 5641, Ap
C 432	85	5.9	996	4	US-09-252-991A-7732	Sequence 7732, Ap	C 505	84.5	5.9	6891	4	US-09-902-540-886	Sequence 886, Ap
C 433	85	5.9	1141	2	US-08-918-727-4	Sequence 4, Appl	C 506	84.5	5.9	10846	3	US-09-038-219B-5	Sequence 5, Appl
C 434	85	5.9	1141	3	US-09-205-680A-4	Sequence 4, Appl	C 507	84.5	5.9	10846	4	US-10-164-204-5	Sequence 5, Appl
C 435	85	5.9	1224	1	US-08-924-847A-1	Sequence 1, Appl	C 508	84.5	5.9	10846	4	US-09-923-109-5	Sequence 5, Appl
C 436	85	5.9	1224	1	US-08-924-847A-3	Sequence 3, Appl	C 509	84.5	5.9	10900	3	US-09-038-219B-6	Sequence 6, Appl
C 437	85	5.9	1224	3	US-09-120-052-1	Sequence 3, Appl	C 510	84.5	5.9	10900	4	US-10-164-204-6	Sequence 6, Appl
C 438	85	5.9	1224	3	US-09-120-052-3	Sequence 3, Appl	C 511	84.5	5.9	10900	4	US-09-923-109-6	Sequence 6, Appl
C 439	85	5.9	1224	4	US-09-252-991A-7567	Sequence 7567, Ap	C 512	84.5	5.9	11199	4	US-09-902-540-1017	Sequence 1017, Ap
C 440	85	5.9	1239	4	US-09-252-991A-6622	Sequence 6622, Ap	C 513	84.5	5.9	16350	4	US-09-902-540-1144	Sequence 1144, Ap
C 441	85	5.9	1415	4	US-09-902-540-3734	Sequence 3734, Ap	C 514	84.5	5.9	19954	4	US-09-902-540-1159	Sequence 1150, Ap
C 442	85	5.9	1449	4	US-09-252-991A-6642	Sequence 6642, Ap	C 515	84.5	5.9	26533	4	US-09-902-540-1199	Sequence 1199, Ap
C 443	85	5.9	1467	4	US-09-252-991A-13960	Sequence 13960, A	C 516	84.5	5.9	26831	4	US-09-949-016-16250	Sequence 16250, A
C 444	85	5.9	1643	4	US-09-799-451-167	Sequence 167, Ap	C 517	84.5	5.9	34266	4	US-09-949-016-13250	Sequence 13250, A
C 445	85	5.9	1647	4	US-09-252-991A-6576	Sequence 6576, Ap	C 518	84.5	5.9	36611	4	US-09-949-016-17287	Sequence 17287, A
C 446	85	5.9	2049	4	US-09-252-991A-13850	Sequence 13850, A	C 519	84.5	5.9	60917	4	US-09-949-016-12638	Sequence 12638, A
C 447	85	5.9	2387	4	US-09-647-492A-3	Sequence 3, Appl	C 520	84.5	5.9	60917	4	US-09-949-016-16057	Sequence 16057, A
C 448	85	5.9	3231	1	US-08-074-121-4	Sequence 4, Appl	C 521	84	5.9	780	4	US-09-252-991A-3741	Sequence 3741, Ap
C 449	85	5.9	3231	5	PCT-US94-06447-4	Sequence 4, Appl	C 522	84	5.9	960	4	US-09-252-991A-3730	Sequence 3730, Ap
C 450	85	5.9	4145	3	US-09-302-620B-82	Sequence 82, Appl	C 523	84	5.9	1089	4	US-09-252-991A-3785	Sequence 3785, Ap

524	84	5.9	1107	4	US-09-252-991A-456	Sequence 456, App	597	83	5.8	1038	4	US-09-902-540-5171	Sequence 5171, App
c 525	84	5.9	1226	4	US-09-489-039A-1526	Sequence 1526, App	c 598	83	5.8	1116	4	US-09-252-991A-2102	Sequence 2102, App
c 526	84	5.9	1237	4	US-09-252-991A-409	Sequence 409, App	c 599	83	5.8	1173	4	US-09-902-540-6402	Sequence 6402, App
527	84	5.9	1737	4	US-09-489-039A-1730	Sequence 1730, App	c 600	83	5.8	1194	4	US-09-902-540-7565	Sequence 7565, App
528	84	5.9	1761	4	US-09-252-991A-1730	Sequence 1730, App	c 601	83	5.8	1209	4	US-09-826-509-556	Sequence 556, App
c 529	84	5.9	1950	3	US-08-685-466C-1	Sequence 1, Appli	c 602	83	5.8	1224	4	US-08-252-991A-1793	Sequence 1793, App
c 530	84	5.9	2031	4	US-09-902-540-3637	Sequence 3637, App	c 603	83	5.8	1278	4	US-09-252-991A-11277	Sequence 11277, App
c 531	84	5.9	2125	4	US-09-949-016-3562	Sequence 3562, App	c 604	83	5.8	1335	4	US-09-252-991A-973	Sequence 973, App
c 532	84	5.9	2388	4	US-09-902-540-3283	Sequence 3283, App	c 605	83	5.8	1376	4	US-08-016-434-1361	Sequence 1361, App
c 533	84	5.9	2475	4	US-09-252-991A-15758	Sequence 15758, App	c 606	83	5.8	1394	2	US-08-068-729-3	Sequence 3, Appli
534	84	5.9	2781	4	US-09-344-624-20	Sequence 20, Appli	c 607	83	5.8	1394	3	US-09-255-671-3	Sequence 3, Appli
535	84	5.9	2785	4	US-09-949-016-1161	Sequence 1161, App	c 608	83	5.8	1394	3	US-09-395-366-3	Sequence 3, Appli
c 536	84	5.9	3489	4	US-09-252-991A-16193	Sequence 16193, App	c 609	83	5.8	1394	3	US-09-902-540-9658	Sequence 9658, App
c 537	84	5.9	4563	4	US-09-252-991A-930	Sequence 930, App	c 610	83	5.8	1614	4	US-08-616-289-45	Sequence 45, Appli
c 538	84	5.9	8230	4	US-09-949-016-15445	Sequence 15445, App	c 611	83	5.8	1650	4	US-09-252-991A-10150	Sequence 10150, App
539	84	5.9	10182	4	US-09-902-540-1049	Sequence 1049, App	c 612	83	5.8	1659	1	US-08-333-358-7	Sequence 7, Appli
c 540	84	5.9	12359	4	US-09-949-016-17004	Sequence 17004, App	c 613	83	5.8	1659	1	US-08-463-694-7	Sequence 7, Appli
c 541	84	5.9	19269	4	US-09-902-540-1175	Sequence 1175, App	c 614	83	5.8	1659	1	US-08-694-501-7	Sequence 7, Appli
c 542	84	5.9	27903	4	US-09-902-540-1235	Sequence 1235, App	c 615	83	5.8	1725	4	US-09-252-991A-9926	Sequence 9926, App
c 543	84	5.9	43550	4	US-09-949-016-12400	Sequence 12400, App	c 616	83	5.8	1806	4	US-09-252-991A-11213	Sequence 11213, App
c 544	84	5.9	43555	4	US-09-949-016-13993	Sequence 13993, App	c 617	83	5.8	2091	4	US-09-252-991A-12312	Sequence 12312, App
545	84	5.9	60990	4	US-09-949-016-14080	Sequence 14080, App	c 618	83	5.8	2529	4	US-09-902-540-7018	Sequence 7018, App
c 546	84	5.9	88758	4	US-09-949-016-113502	Sequence 113502, App	c 619	83	5.8	2802	4	US-09-417-157-134	Sequence 134, App
c 547	84	5.9	139936	4	US-09-949-016-11782	Sequence 11782, App	c 620	83	5.8	3650	4	US-09-949-016-5637	Sequence 5637, App
548	84	5.9	139952	4	US-09-949-016-13280	Sequence 13280, App	c 621	83	5.8	4003	4	US-09-902-540-618	Sequence 618, App
c 549	84	5.9	325034	4	US-09-949-016-14957	Sequence 14957, App	c 622	83	5.8	4761	4	US-09-902-540-739	Sequence 739, App
c 550	84	5.9	389504	4	US-09-949-016-11774	Sequence 11774, App	c 623	83	5.8	4826	4	US-09-772-304A-1	Sequence 1, Appli
c 551	83.5	5.8	601	4	US-09-949-016-24153	Sequence 24153, App	c 624	83	5.8	5455	1	US-08-342-930-1	Sequence 1, Appli
c 552	83.5	5.8	601	4	US-09-949-016-69020	Sequence 69020, App	c 625	83	5.8	6492	4	US-09-902-540-853	Sequence 853, App
c 553	83.5	5.8	831	4	US-09-252-991A-5118	Sequence 5118, App	c 626	83	5.8	9198	4	US-09-902-540-966	Sequence 966, App
c 554	83.5	5.8	863	4	US-09-902-540-144	Sequence 144, App	c 627	83	5.8	12865	4	US-09-902-540-1048	Sequence 1048, App
c 555	83.5	5.8	993	4	US-09-876-216-1	Sequence 1, Appli	c 628	83	5.8	14462	4	US-09-902-540-1090	Sequence 1090, App
c 556	83.5	5.8	1035	4	US-09-252-991A-15890	Sequence 15890, App	c 629	83	5.8	14462	4	US-09-902-540-1090	Sequence 1090, App
c 557	83.5	5.8	1086	4	US-09-902-540-6806	Sequence 6806, App	c 630	83	5.8	15125	4	US-09-949-016-14647	Sequence 14647, App
558	83.5	5.8	1265	4	US-09-252-991A-15921	Sequence 15921, App	c 631	83	5.8	18417	4	US-09-949-016-13389	Sequence 13389, App
c 559	83.5	5.8	1422	4	US-09-620-312D-892	Sequence 892, App	c 632	83	5.8	23091	4	US-09-902-540-1204	Sequence 1204, App
c 560	83.5	5.8	1422	4	US-09-252-991A-14835	Sequence 14835, App	c 633	83	5.8	23417	4	US-09-902-540-1207	Sequence 1207, App
c 561	83.5	5.8	1646	4	US-09-252-991A-15091	Sequence 15091, App	c 634	83	5.8	28058	4	US-09-902-540-1252	Sequence 1252, App
c 562	83.5	5.8	1649	2	US-08-466-120-1	Sequence 1, Appli	c 635	83	5.8	34199	4	US-09-902-540-1255	Sequence 1255, App
c 563	83.5	5.8	1649	5	PCT-US94-07266-1	Sequence 1, Appli	c 636	83	5.8	111509	4	US-09-949-016-17379	Sequence 17379, App
564	83.5	5.8	1782	4	US-09-252-991A-1412	Sequence 1412, App	c 637	83	5.8	139577	4	US-09-949-016-17398	Sequence 17398, App
c 565	83.5	5.8	1956	4	US-09-602-777A-53	Sequence 53, Appli	c 638	83	5.8	536165	4	US-09-949-016-12879	Sequence 12879, App
c 566	83.5	5.8	2194	4	US-09-949-016-2036	Sequence 2036, App	c 639	83	5.8	536165	4	US-09-214-808-1	Sequence 1, Appli
c 567	83.5	5.8	2376	4	US-09-252-991A-6630	Sequence 6630, App	c 640	83	5.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 568	83.5	5.8	2899	4	US-09-602-777A-49	Sequence 49, Appli	c 641	82.5	5.8	900	4	US-09-902-540-9504	Sequence 9504, App
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c 570	83.5	5.8	3144	4	US-09-855-323-8	Sequence 8, Appli	c 643	82.5	5.8	1161	4	US-09-252-991A-10489	Sequence 10489, App
571	83.5	5.8	3440	4	US-09-252-991A-1324	Sequence 1324, App	c 644	82.5	5.8	1305	4	US-09-252-991A-10664	Sequence 10664, App
572	83.5	5.8	4955	4	US-09-902-540-553	Sequence 553, App	c 645	82.5	5.8	1347	4	US-09-489-039A-5620	Sequence 5620, App
573	83.5	5.8	5153	5	PCT-US95-04910-8	Sequence 8, Appli	c 646	82.5	5.8	1386	4	US-09-016-434-1339	Sequence 1339, App
574	83.5	5.8	6351	4	US-09-902-540-757	Sequence 757, App	c 647	82.5	5.8	1476	4	US-09-585-174-99	Sequence 99, Appli
c 575	83.5	5.8	7515	4	US-09-902-540-888	Sequence 888, App	c 648	82.5	5.8	1509	4	US-09-252-991A-7072	Sequence 7072, App
c 576	83.5	5.8	8604	4	US-09-902-540-5331	Sequence 5331, App	c 649	82.5	5.8	1521	4	US-09-902-540-6676	Sequence 6676, App
c 577	83.5	5.8	9843	4	US-09-949-016-13133	Sequence 13133, App	c 650	82.5	5.8	1524	4	US-09-252-991A-7027	Sequence 7027, App
c 578	83.5	5.8	12425	4	US-09-616-289-50	Sequence 50, Appli	c 651	82.5	5.8	1554	1	US-08-469-486-1	Sequence 1, Appli
c 579	83.5	5.8	16047	4	US-09-902-540-1136	Sequence 1136, App	c 652	82.5	5.8	1554	2	US-08-469-658-1	Sequence 1, Appli
c 580	83.5	5.8	16047	4	US-09-902-540-1136	Sequence 1136, App	c 653	82.5	5.8	1575	4	US-09-252-991A-1139	Sequence 1139, App
c 581	83.5	5.8	20662	4	US-09-949-016-16717	Sequence 16717, App	c 654	82.5	5.8	1599	4	US-09-949-016-5029	Sequence 5029, App
c 582	83.5	5.8	2783	4	US-09-902-540-1242	Sequence 1242, App	c 655	82.5	5.8	1608	4	US-09-252-991A-9498	Sequence 9498, App
c 583	83.5	5.8	35100	2	US-08-770-379-19	Sequence 19, Appli	c 656	82.5	5.8	1616	4	US-09-949-016-330	Sequence 330, App
c 584	83.5	5.8	35100	3	US-08-757-669A-19	Sequence 19, Appli	c 657	82.5	5.8	1653	4	US-09-252-991A-1111	Sequence 1111, App
c 585	83.5	5.8	35100	3	US-09-230-371A-19	Sequence 19, Appli	c 658	82.5	5.8	1653	3	US-09-083-351-3	Sequence 3, Appli
c 586	83.5	5.8	35399	4	US-09-902-540-1260	Sequence 1260, App	c 659	82.5	5.8	1659	3	US-09-083-352-3	Sequence 3, Appli
c 587	83.5	5.8	38155	3	US-09-453-702B-79	Sequence 79, Appli	c 660	82.5	5.8	1662	4	US-09-612-809B-3	Sequence 3, Appli
588	83.5	5.8	4275	4	US-09-949-016-12533	Sequence 12533, App	c 661	82.5	5.8	1917	4	US-09-252-991A-10497	Sequence 10497, App
c 589	83.5	5.8	77626	4	US-09-949-016-12608	Sequence 12608, App	c 662	82.5	5.8	2013	4	US-09-252-991A-10296	Sequence 10296, App
c 590	83.5	5.8	160759	4	US-09-949-016-16514	Sequence 16514, App	c 663	82.5	5.8	2073	4	US-09-252-991A-10279	Sequence 10279, App
c 591	83.5	5.8	645	4	US-09-252-991A-2836	Sequence 2836, App	c 664	82.5	5.8	2112	4	US-09-270-767-13414	Sequence 13414, App
c 592	83	5.8	714	4	US-09-252-991A-11042	Sequence 11042, App	c 665	82.5	5.8	2266	4	US-09-799-451-917	Sequence 917, App
c 593	83	5.8	984	4	US-09-252-991A-3477	Sequence 3477, App	c 666	82.5	5.8	2290	4	US-09-799-451-864	Sequence 864, App
c 594	83	5.8	996	4	US-09-252-991A-4469	Sequence 4469, App	c 667	82.5	5.8	2379	4	US-09-252-991A-9252	Sequence 9252, App
c 595	83	5.8	1014	4	US-09-252-991A-3031	Sequence 3031, App	c 668	82.5	5.8				

670	82.5	5.8	2592	4	US-09-902-540-3407	Sequence 3407, Ap	C 743	82	5.7	2078	4	US-09-799-451-486	Sequence 486, App
671	82.5	5.8	2772	4	US-09-252-991A-10577	Sequence 10577, A	744	82	5.7	2265	4	US-09-252-991A-5738	Sequence 5738, Ap
672	82.5	5.8	2859	4	US-09-252-991A-944	Sequence 944, App	C 745	82	5.7	2625	4	US-09-902-540-8554	Sequence 8554, Ap
673	82.5	5.8	2865	4	US-09-252-991A-4675	Sequence 4675, Ap	746	82	5.7	3889	4	US-09-902-540-492	Sequence 492, App
674	82.5	5.8	3168	4	US-09-902-540-8270	Sequence 8270, Ap	747	82	5.7	4683	4	US-09-902-540-9346	Sequence 9346, Ap
675	82.5	5.8	3828	4	US-08-426-630-48	Sequence 48, App	C 748	82	5.7	4824	4	US-09-902-540-9627	Sequence 9627, Ap
676	82.5	5.8	3931	1	US-08-144-121-1	Sequence 1, Appl	C 749	82	5.7	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
677	82.5	5.8	3931	2	US-08-735-893-1	Sequence 1, Appl	750	82	5.7	7562	4	US-09-902-540-902	Sequence 902, App
678	82.5	5.8	3946	3	US-09-083-351-1	Sequence 1, Appl	751	82	5.7	7881	2	US-08-751-189-1	Sequence 1, Appl
679	82.5	5.8	3946	3	US-09-083-352-1	Sequence 1, Appl	752	82	5.7	7881	2	US-09-060-836-1	Sequence 1, Appl
680	82.5	5.8	4563	4	US-09-252-991A-4765	Sequence 4765, Ap	753	82	5.7	7881	3	US-09-184-445-1	Sequence 1, Appl
681	82.5	5.8	4825	4	US-09-949-016-15912	Sequence 15912, A	C 754	82	5.7	9399	4	US-09-949-016-13206	Sequence 13206, A
682	82.5	5.8	5661	4	US-09-555-166-3	Sequence 3, Appl	755	82	5.7	9905	4	US-09-902-540-998	Sequence 998, App
683	82.5	5.8	6114	4	US-09-914-272A-4	Sequence 4, Appl	C 756	82	5.7	11612	4	US-09-902-540-981	Sequence 981, App
684	82.5	5.8	6114	4	US-10-638-333-4	Sequence 4, Appl	C 757	82	5.7	16187	4	US-09-902-540-1093	Sequence 1093, Ap
685	82.5	5.8	6269	4	US-09-902-540-726	Sequence 726, App	C 758	82	5.7	19019	4	US-09-902-540-1171	Sequence 1171, Ap
686	82.5	5.8	6388	4	US-09-949-016-15137	Sequence 15137, A	C 759	82	5.7	19990	4	US-09-949-016-14967	Sequence 14967, A
687	82.5	5.8	6491	4	US-09-585-174-1	Sequence 1, Appl	C 760	82	5.7	21964	4	US-09-902-540-1190	Sequence 1190, Ap
688	82.5	5.8	6855	4	US-09-252-991A-6976	Sequence 6976, Ap	C 761	82	5.7	25048	4	US-09-902-540-1239	Sequence 1239, Ap
689	82.5	5.8	6930	4	US-09-902-540-856	Sequence 856, App	C 762	82	5.7	26289	4	US-09-902-540-1210	Sequence 1210, Ap
690	82.5	5.8	9036	4	US-09-949-016-16866	Sequence 16866, A	C 763	82	5.7	28493	4	US-09-902-540-1241	Sequence 1241, Ap
691	82.5	5.8	9165	4	US-09-902-540-1050	Sequence 1050, Ap	764	82	5.7	44377	2	US-08-804-227C-7	Sequence 7, Appl
692	82.5	5.8	13144	4	US-08-428-630-41	Sequence 41, Appl	765	82	5.7	44377	2	US-08-804-198-1	Sequence 1, Appl
693	82.5	5.8	14431	4	US-09-902-540-1149	Sequence 1149, Ap	766	82	5.7	51354	4	US-09-902-540-1270	Sequence 1270, Ap
694	82.5	5.8	16423	4	US-09-902-540-1120	Sequence 1120, Ap	767	82	5.7	51807	4	US-09-949-016-15333	Sequence 15333, A
695	82.5	5.8	17654	4	US-09-902-540-1161	Sequence 1161, Ap	C 768	82	5.7	68750	3	US-09-335-409-1	Sequence 1, Appl
696	82.5	5.8	21490	4	US-09-949-016-14168	Sequence 14168, A	C 769	82	5.7	68750	3	US-09-568-102-1	Sequence 1, Appl
697	82.5	5.8	25709	4	US-09-949-016-13338	Sequence 13338, A	C 770	82	5.7	68750	3	US-09-567-969-1	Sequence 1, Appl
698	82.5	5.8	25778	4	US-09-949-016-12167	Sequence 12167, A	C 771	82	5.7	68750	3	US-09-568-480-1	Sequence 1, Appl
699	82.5	5.8	27579	4	US-09-949-016-15005	Sequence 15005, A	C 772	82	5.7	68750	3	US-09-568-486-1	Sequence 1, Appl
700	82.5	5.8	3498	4	US-09-949-016-11982	Sequence 11982, A	C 773	82	5.7	68750	3	US-09-568-472-1	Sequence 1, Appl
701	82.5	5.8	33551	4	US-09-949-016-16666	Sequence 16666, A	C 774	82	5.7	68750	3	US-09-567-899-1	Sequence 1, Appl
702	82.5	5.8	36470	4	US-08-311-731A-123	Sequence 123, App	C 775	82	5.7	106450	4	US-09-949-016-13873	Sequence 13873, A
703	82.5	5.8	44377	2	US-08-804-227C-7	Sequence 7, Appl	776	82	5.7	455726	4	US-09-949-016-14157	Sequence 14157, A
704	82.5	5.8	44377	2	US-08-804-198-1	Sequence 1, Appl	777	82	5.7	481115	4	US-09-949-016-11940	Sequence 11940, A
705	82.5	5.8	50725	4	US-09-902-540-1271	Sequence 1271, Ap	C 778	81.5	5.7	601	4	US-09-949-016-92631	Sequence 92631, A
706	82.5	5.8	54484	4	US-09-902-540-1272	Sequence 1272, Ap	C 779	81.5	5.7	774	4	US-09-252-991A-9665	Sequence 9665, Ap
707	82.5	5.8	77536	4	US-09-410-551B-1	Sequence 1, Appl	C 780	81.5	5.7	966	4	US-09-902-540-4853	Sequence 4853, Ap
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709	82.5	5.8	131724	4	US-09-949-016-12893	Sequence 12893, A	C 782	81.5	5.7	1008	4	US-09-252-991A-15592	Sequence 15592, A
710	82	5.7	601	4	US-09-949-016-72838	Sequence 72838, A	783	81.5	5.7	1104	1	US-08-284-784-32	Sequence 32, Appl
711	82	5.7	836	3	US-09-077-675A-11	Sequence 11, Appl	784	81.5	5.7	1104	2	US-08-854-811-32	Sequence 32, Appl
712	82	5.7	836	4	US-09-077-674-11	Sequence 11, Appl	C 785	81.5	5.7	1131	4	US-09-252-991A-76	Sequence 76, Appl
713	82	5.7	885	4	US-09-252-991A-7021	Sequence 7021, Ap	C 786	81.5	5.7	1173	4	US-09-902-540-5559	Sequence 5559, Ap
714	82	5.7	900	4	US-09-902-540-6576	Sequence 6576, Ap	787	81.5	5.7	1213	4	US-09-902-540-3750	Sequence 3750, Ap
715	82	5.7	915	4	US-09-902-540-4912	Sequence 4912, Ap	C 788	81.5	5.7	1265	4	US-09-252-991A-15755	Sequence 15755, A
716	82	5.7	1068	4	US-09-252-991A-9933	Sequence 9933, Ap	C 789	81.5	5.7	1278	4	US-09-252-991A-8517	Sequence 8517, Ap
717	82	5.7	1088	3	US-09-077-675A-6	Sequence 6, Appl	790	81.5	5.7	1392	4	US-09-252-991A-3486	Sequence 3486, Ap
718	82	5.7	1095	4	US-09-077-674-6	Sequence 6, Appl	C 791	81.5	5.7	1467	4	US-09-252-991A-8763	Sequence 8763, Ap
719	82	5.7	1101	4	US-09-252-991A-3352	Sequence 3352, Ap	C 792	81.5	5.7	1528	4	US-09-016-434-1448	Sequence 1448, Ap
720	82	5.7	1101	4	US-09-016-434-1148	Sequence 1148, Ap	C 793	81.5	5.7	1528	4	US-10-329-668-1	Sequence 1, Appl
721	82	5.7	1101	4	US-09-170-496D-209	Sequence 87, Appl	C 794	81.5	5.7	1608	4	US-09-252-991A-11769	Sequence 11769, A
722	82	5.7	1101	4	US-09-364-425B-44	Sequence 209, App	C 795	81.5	5.7	1647	4	US-09-252-991A-6586	Sequence 6586, Ap
723	82	5.7	1101	4	US-09-434-288-9	Sequence 44, Appl	C 796	81.5	5.7	1758	4	US-09-252-991A-7085	Sequence 7085, Ap
724	82	5.7	1179	3	US-09-252-991A-1172	Sequence 9, Appl	C 797	81.5	5.7	1848	4	US-09-252-991A-6632	Sequence 6632, Ap
725	82	5.7	1185	4	US-09-252-991A-10495	Sequence 10495, A	798	81.5	5.7	1911	4	US-09-252-991A-6716	Sequence 6716, Ap
726	82	5.7	1212	4	US-09-880-503-15	Sequence 15, Appl	799	81.5	5.7	1951	3	US-08-910-973-16	Sequence 16, Appl
727	82	5.7	1221	4	US-09-252-991A-2160	Sequence 2160, Ap	800	81.5	5.7	1951	3	US-09-499-227-16	Sequence 16, Appl
728	82	5.7	1236	4	US-09-023-655-927	Sequence 927, App	801	81.5	5.7	2082	4	US-09-902-540-7754	Sequence 7754, Ap
729	82	5.7	1251	4	US-09-252-991A-10142	Sequence 10142, A	C 802	81.5	5.7	2136	4	US-09-252-991A-11628	Sequence 11628, A
730	82	5.7	1281	4	US-09-489-039A-2650	Sequence 2650, Ap	803	81.5	5.7	2478	3	US-08-485-355B-47	Sequence 47, Appl
731	82	5.7	1293	4	US-09-252-991A-12207	Sequence 12207, A	804	81.5	5.7	2478	3	US-08-485-355B-49	Sequence 49, Appl
732	82	5.7	1299	4	US-09-252-991A-14682	Sequence 14682, A	805	81.5	5.7	2478	3	US-09-194-613-1	Sequence 1, Appl
733	82	5.7	1338	4	US-09-252-991A-12135	Sequence 12135, A	806	81.5	5.7	2478	3	US-08-485-355B-51	Sequence 51, Appl
734	82	5.7	1482	4	US-09-252-991A-1723	Sequence 1723, Ap	807	81.5	5.7	2484	4	US-09-252-991A-1388	Sequence 1388, Ap
735	82	5.7	1494	3	US-08-724-466B-5	Sequence 5, Appl	808	81.5	5.7	2499	4	US-09-252-991A-2681	Sequence 2681, Ap
736	82	5.7	1494	3	US-08-882-164D-5	Sequence 5, Appl	809	81.5	5.7	2544	4	US-09-252-991A-2775	Sequence 2775, Ap
737	82	5.7	1542	4	US-09-252-991A-16087	Sequence 16087, A	810	81.5	5.7	2544	4	US-09-949-016-1140	Sequence 1140, Ap
738	82	5.7	1659	4	US-09-252-991A-5713	Sequence 5713, Ap	811	81.5	5.7	2671	6	5168051-9	Patent No. 5168051
739	82	5.7	1659	4	US-09-252-991A-12388	Sequence 12388, A	812	81.5	5.7	2671	6	5168051-9	Patent No. 5168051
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741	82	5.7	1692	4	US-09-902-540-4219	Sequence 4219, Ap	814	81.5	5.7	2691	4	US-09-252-991A-3187	Sequence 3187, Ap
742	82	5.7	1869	4	US-09-252-991A-11876	Sequence 11876, A	C 815	81.5	5.7	2730	2	US-08-811-897A-39	Sequence 39, Appl

962	80.5	5.6	1725	4	US-09-252-991A-14297	Sequence 14297, A	c1035	80	5.6	1122	4	US-09-252-991A-2855	Sequence 2855, Ap
c 963	80.5	5.6	1746	4	US-09-252-991A-8948	Sequence 8948, Ap	1036	80	5.6	1134	4	US-09-949-016-90	Sequence 90, Appl
c 964	80.5	5.6	1746	4	US-09-485-529-57	Sequence 57, Appl	c1037	80	5.6	1194	4	US-08-724-737-25	Sequence 25, Appl
c 965	80.5	5.6	1776	4	US-09-902-540-7046	Sequence 7046, Ap	c1038	80	5.6	1221	4	US-09-252-991A-7990	Sequence 7990, Ap
c 966	80.5	5.6	1833	4	US-09-252-991A-3525	Sequence 3525, Ap	1039	80	5.6	1233	4	US-09-252-991A-8268	Sequence 8268, Ap
c 967	80.5	5.6	1845	4	US-09-902-540-7042	Sequence 7042, Ap	1040	80	5.6	1260	4	US-09-252-991A-928	Sequence 928, App
c 968	80.5	5.6	1893	4	US-09-252-991A-9055	Sequence 9055, Ap	c1041	80	5.6	1320	4	US-09-902-540-8133	Sequence 8133, Ap
c 969	80.5	5.6	2052	4	US-09-252-991A-12103	Sequence 12103, A	1042	80	5.6	1341	3	US-09-199-637A-133	Sequence 133, App
c 970	80.5	5.6	2184	4	US-09-902-540-5116	Sequence 5116, Ap	1043	80	5.6	1368	4	US-09-252-991A-971	Sequence 971, App
c 971	80.5	5.6	2256	4	US-09-252-991A-6199	Sequence 6199, Ap	1044	80	5.6	1440	4	US-09-252-991A-10395	Sequence 10395, A
c 972	80.5	5.6	2271	4	US-09-902-540-6006	Sequence 6006, Ap	c1045	80	5.6	1555	4	US-09-902-540-267	Sequence 267, App
c 973	80.5	5.6	2304	4	US-09-252-991A-8731	Sequence 8731, Ap	c1046	80	5.6	1557	4	US-09-252-991A-7033	Sequence 7033, Ap
c 974	80.5	5.6	2389	4	US-09-902-540-4764	Sequence 4764, Ap	c1047	80	5.6	1758	4	US-09-252-991A-1644	Sequence 1644, Ap
c 975	80.5	5.6	2407	4	US-09-949-016-2650	Sequence 2650, Ap	c1048	80	5.6	1785	4	US-09-252-991A-10764	Sequence 10764, A
c 976	80.5	5.6	2445	4	US-09-252-991A-6352	Sequence 6352, Ap	c1049	80	5.6	1795	4	US-09-620-312D-864	Sequence 864, App
c 977	80.5	5.6	2495	3	US-09-141-027-1	Sequence 1, Appl	c1050	80	5.6	2049	4	US-09-252-991A-15326	Sequence 15326, A
c 978	80.5	5.6	2495	4	US-09-617-804-1	Sequence 1, Appl	c1051	80	5.6	2098	1	US-08-153-848-41	Sequence 41, Appl
c 979	80.5	5.6	2500	4	US-09-949-016-791	Sequence 791, App	c1052	80	5.6	2098	3	US-09-299-843A-41	Sequence 41, Appl
c 980	80.5	5.6	2525	2	US-08-973-008-1	Sequence 1, Appl	c1053	80	5.6	2098	3	US-09-088-337B-41	Sequence 41, Appl
c 981	80.5	5.6	2525	3	US-09-267-409-1	Sequence 1, Appl	c1054	80	5.6	2098	5	PCT-US93-11153-41	Sequence 41, Appl
c 982	80.5	5.6	2709	4	US-09-485-529-3	Sequence 3, Appl	c1055	80	5.6	2127	4	US-09-252-991A-15511	Sequence 15511, A
c 983	80.5	5.6	2796	4	US-09-252-991A-9979	Sequence 9979, Ap	c1056	80	5.6	2132	4	US-09-270-767-12419	Sequence 12419, A
c 984	80.5	5.6	2988	4	US-09-949-016-2460	Sequence 2460, Ap	c1057	80	5.6	2200	1	US-08-592-126-102	Sequence 102, App
c 985	80.5	5.6	3162	4	US-09-252-991A-4429	Sequence 4429, Ap	c1058	80	5.6	2200	4	US-09-168-595-102	Sequence 102, App
c 986	80.5	5.6	3346	4	US-09-684-405-5	Sequence 5, Appl	c1059	80	5.6	2232	4	US-09-489-039A-4139	Sequence 4139, Ap
c 987	80.5	5.6	3739	4	US-09-902-540-477	Sequence 477, App	c1060	80	5.6	2325	4	US-09-252-991A-8052	Sequence 8052, Ap
c 988	80.5	5.6	3924	4	US-09-902-540-680	Sequence 680, App	c1061	80	5.6	2448	4	US-09-252-991A-10680	Sequence 10680, Ap
c 989	80.5	5.6	4087	4	US-09-902-540-625	Sequence 625, App	c1062	80	5.6	2751	4	US-09-252-991A-7066	Sequence 7066, Ap
c 990	80.5	5.6	4167	4	US-09-169-768-12	Sequence 12, Appl	c1063	80	5.6	3024	4	US-09-902-540-1868	Sequence 1868, Ap
c 991	80.5	5.6	4176	4	US-09-902-540-872	Sequence 872, App	c1064	80	5.6	3186	4	US-09-489-039A-5569	Sequence 5569, Ap
c 992	80.5	5.6	4237	1	US-07-844-298B-1	Sequence 1, Appl	c1065	80	5.6	3618	4	US-09-902-540-9652	Sequence 9652, Ap
c 993	80.5	5.6	4329	4	US-09-902-540-2431	Sequence 2431, Ap	c1066	80	5.6	3968	4	US-09-949-016-1601	Sequence 1601, Ap
c 994	80.5	5.6	4465	4	US-09-949-016-2042	Sequence 2042, Ap	c1067	80	5.6	4895	3	US-09-053-866-1	Sequence 1, Appl
c 995	80.5	5.6	4532	4	US-09-902-540-626	Sequence 626, App	c1068	80	5.6	4895	3	US-09-479-130-1	Sequence 1, Appl
c 996	80.5	5.6	4604	4	US-09-902-540-602	Sequence 602, App	c1069	80	5.6	4895	4	US-09-472-130A-1	Sequence 1, Appl
c 997	80.5	5.6	5535	1	US-08-089-755A-1	Sequence 1, Appl	c1070	80	5.6	5656	4	US-09-902-540-694	Sequence 694, App
c 998	80.5	5.6	5535	1	US-08-089-755A-4	Sequence 4, Appl	c1071	80	5.6	6404	4	US-09-902-540-760	Sequence 760, App
c 999	80.5	5.6	5535	1	US-08-421-754-1	Sequence 1, Appl	c1072	80	5.6	6436	4	US-09-600-099-1	Sequence 1, Appl
1000	80.5	5.6	5535	2	US-08-421-754-1	Sequence 1, Appl	c1073	80	5.6	7152	4	US-09-492-709A-142	Sequence 142, App
1001	80.5	5.6	5535	2	US-08-421-791-1	Sequence 1, Appl	c1074	80	5.6	8773	4	US-09-902-540-965	Sequence 965, App
1002	80.5	5.6	5535	2	US-08-421-791-1	Sequence 1, Appl	c1075	80	5.6	8983	4	US-09-949-016-15437	Sequence 15437, A
1003	80.5	5.6	7490	4	US-09-949-016-17606	Sequence 17606, A	c1076	80	5.6	9164	4	US-09-814-915A-80	Sequence 80, Appl
c1004	80.5	5.6	9365	4	US-09-827-688-7	Sequence 7, Appl	c1077	80	5.6	18632	4	US-09-949-016-16574	Sequence 16574, A
c1005	80.5	5.6	10276	4	US-09-902-540-975	Sequence 975, App	c1078	80	5.6	21330	4	US-09-902-540-1209	Sequence 1209, Ap
c1006	80.5	5.6	10317	4	US-09-902-540-1027	Sequence 1027, Ap	c1079	80	5.6	21511	4	US-09-902-540-1201	Sequence 1201, Ap
c1007	80.5	5.6	10505	4	US-09-902-540-1044	Sequence 1044, Ap	c1080	80	5.6	23417	4	US-09-902-540-1207	Sequence 1207, Ap
c1008	80.5	5.6	10644	4	US-09-902-540-1028	Sequence 1028, Ap	c1081	80	5.6	30780	4	US-09-902-540-1243	Sequence 1243, Ap
c1009	80.5	5.6	11662	4	US-09-949-016-16978	Sequence 16978, A	c1082	80	5.6	31035	4	US-09-949-016-12272	Sequence 12272, A
c1010	80.5	5.6	12317	4	US-09-949-016-14782	Sequence 14782, A	c1083	80	5.6	31035	4	US-09-949-016-17266	Sequence 17266, A
c1011	80.5	5.6	13332	4	US-09-902-540-1047	Sequence 1047, Ap	c1084	80	5.6	34662	4	US-09-902-540-1261	Sequence 1261, Ap
c1012	80.5	5.6	13871	4	US-09-949-016-12037	Sequence 12037, A	c1085	80	5.6	57280	4	US-09-949-016-11796	Sequence 11796, A
c1013	80.5	5.6	13871	4	US-09-949-016-15363	Sequence 15363, A	c1086	80	5.6	57280	4	US-09-949-016-12843	Sequence 12843, A
c1014	80.5	5.6	14809	4	US-09-902-540-1032	Sequence 1032, Ap	c1087	80	5.6	57280	4	US-09-949-016-12844	Sequence 12844, A
c1015	80.5	5.6	14899	4	US-09-902-540-1107	Sequence 1107, Ap	c1088	80	5.6	57280	4	US-09-949-016-12846	Sequence 12846, A
c1016	80.5	5.6	17415	3	US-08-486-343A-1	Sequence 1, Appl	c1089	80	5.6	57280	4	US-09-949-016-13542	Sequence 13542, A
c1017	80.5	5.6	17415	4	US-09-423-821B-1	Sequence 1, Appl	c1090	80	5.6	57280	4	US-09-949-016-13543	Sequence 13543, A
c1018	80.5	5.6	17415	5	PCT-US95-07349-1	Sequence 1, Appl	c1091	80	5.6	57280	4	US-09-949-016-13544	Sequence 13544, A
c1019	80.5	5.6	28509	4	US-09-902-540-1240	Sequence 1240, Ap	c1092	80	5.6	57280	4	US-09-949-016-13545	Sequence 13545, A
c1020	80.5	5.6	34094	4	US-09-292-034-1	Sequence 1, Appl	c1093	80	5.6	57280	4	US-09-949-016-14633	Sequence 14633, A
c1021	80.5	5.6	41768	4	US-09-902-540-1266	Sequence 1266, Ap	c1094	80	5.6	57280	4	US-09-949-016-14634	Sequence 14634, A
c1022	80.5	5.6	55216	4	US-09-716-865-23	Sequence 23, Appl	c1095	80	5.6	57280	4	US-09-949-016-14635	Sequence 14635, A
c1023	80.5	5.6	70000	3	US-09-851-896-3	Sequence 3, Appl	c1096	80	5.6	57280	4	US-09-949-016-14636	Sequence 14636, A
c1024	80.5	5.6	76399	4	US-09-949-016-16819	Sequence 16819, A	c1097	80	5.6	57280	4	US-09-949-016-14637	Sequence 14637, A
c1025	80.5	5.6	251769	4	US-09-949-016-13185	Sequence 13185, A	c1098	80	5.6	57280	4	US-09-949-016-14638	Sequence 14638, A
c1026	80.5	5.6	251769	4	US-09-949-016-13186	Sequence 13186, A	c1099	80	5.6	57280	4	US-09-949-016-14639	Sequence 14639, A
c1027	80.5	5.6	266748	4	US-09-949-016-13187	Sequence 13187, A	c1100	80	5.6	57280	4	US-09-949-016-14640	Sequence 14640, A
c1028	80.5	5.6	266748	4	US-09-949-016-13188	Sequence 13188, A	c1101	80	5.6	60990	4	US-09-949-016-14080	Sequence 14080, A
c1029	80	5.6	601	4	US-09-949-016-46365	Sequence 46365, A	c1102	80	5.6	77536	4	US-09-410-551B-1	Sequence 1, Appl
c1030	80	5.6	601	4	US-09-949-016-53376	Sequence 53376, A	c1103	80	5.6	77536	4	US-09-940-316B-1	Sequence 1, Appl
c1031	80	5.6	601	4	US-09-949-016-132487	Sequence 132487, A	c1104	80	5.6	450395	4	US-09-949-016-15473	Sequence 15473, A
c1032	80	5.6	828	4	US-09-252-991A-2146	Sequence 2146, Ap	c1105	79.5	5.6	484	3	US-09-643-597-198	Sequence 198, App
c1033	80	5.6	954	4	US-09-252-991A-13130	Sequence 13130, A	c1106	79.5	5.6	484	4	US-09-480-884A-198	Sequence 198, App
c1034	80	5.6	1035	4	US-09-902-540-5365	Sequence 5365, Ap	c1107	79.5	5.6	484	4	US-09-542-615A-198	Sequence 198, App

c1108	79.5	5.6	484	4	US-09-606-421B-198	Sequence 199, App	1181	79.5	5.6	14158	4	US-09-902-540-1069	Sequence 1069, Ap
c1109	79.5	5.6	484	4	US-09-466-396A-198	Sequence 199, App	c1182	79.5	5.6	17247	4	US-09-902-540-1185	Sequence 1185, Ap
c1110	79.5	5.6	484	4	US-09-476-496A-198	Sequence 199, App	c1183	79.5	5.6	18324	4	US-09-902-540-1196	Sequence 1196, Ap
c1111	79.5	5.6	484	4	US-09-630-940B-198	Sequence 198, App	c1184	79.5	5.6	18848	4	US-09-902-540-1174	Sequence 1174, Ap
c1112	79.5	5.6	507	4	US-09-270-767-5332	Sequence 5332, App	c1185	79.5	5.6	21964	4	US-09-902-540-1190	Sequence 1190, Ap
c1113	79.5	5.6	507	4	US-09-270-767-20614	Sequence 20614, A	c1186	79.5	5.6	26103	4	US-09-949-016-15685	Sequence 15685, A
c1114	79.5	5.6	601	4	US-09-949-016-71124	Sequence 71124, A	c1187	79.5	5.6	26105	4	US-09-949-016-11879	Sequence 11879, A
c1115	79.5	5.6	714	4	US-09-328-352-4055	Sequence 4055, App	c1188	79.5	5.6	29433	4	US-09-949-016-15740	Sequence 15740, A
c1116	79.5	5.6	738	4	US-09-252-991A-9456	Sequence 9456, App	c1189	79.5	5.6	33529	3	US-09-144-085-3	Sequence 3, Appli
c1117	79.5	5.6	750	4	US-09-902-540-7791	Sequence 7791, App	1190	79.5	5.6	36519	3	US-08-923-137-2	Sequence 2, Appli
c1118	79.5	5.6	816	4	US-09-252-991A-9480	Sequence 9480, App	1191	79.5	5.6	38078	4	US-09-949-016-12429	Sequence 12429, A
c1119	79.5	5.6	843	4	US-09-252-991A-2829	Sequence 2829, App	1192	79.5	5.6	38084	4	US-09-949-016-16459	Sequence 16459, A
c1120	79.5	5.6	846	4	US-09-252-991A-3196	Sequence 3196, App	c1193	79.5	5.6	41927	4	US-09-902-540-1268	Sequence 1268, Ap
c1121	79.5	5.6	995	3	US-09-540-014-10	Sequence 10, Appl	c1194	79.5	5.6	58821	4	US-09-949-016-15897	Sequence 15897, A
c1122	79.5	5.6	995	3	US-09-540-014-23	Sequence 23, Appl	1195	79.5	5.6	58824	4	US-09-949-016-12615	Sequence 12615, A
c1123	79.5	5.6	995	4	US-10-091-841A-10	Sequence 10, Appl	c1196	79.5	5.6	76264	4	US-09-949-016-15773	Sequence 15773, A
c1124	79.5	5.6	995	4	US-10-091-841A-23	Sequence 23, Appl	c1197	79.5	5.6	83617	4	US-09-949-016-12254	Sequence 12254, A
c1125	79.5	5.6	1014	4	US-09-252-991A-12024	Sequence 12024, A	1198	79.5	5.6	86380	4	US-09-949-016-14837	Sequence 14837, A
c1126	79.5	5.6	1071	4	US-09-252-991A-15521	Sequence 15521, A	c1199	79.5	5.6	86956	4	US-09-949-016-12994	Sequence 12994, A
c1127	79.5	5.6	1107	4	US-09-252-991A-3087	Sequence 3087, App	c1200	79.5	5.6	90150	4	US-09-949-016-17383	Sequence 17383, A
c1128	79.5	5.6	1107	4	US-09-902-540-6053	Sequence 6053, App	c1201	79.5	5.6	99748	4	US-09-949-016-11990	Sequence 11990, A
c1129	79.5	5.6	1108	4	US-09-949-016-355	Sequence 355, App	c1202	79.5	5.6	99749	4	US-09-949-016-16518	Sequence 16518, A
c1130	79.5	5.6	1108	4	US-09-902-540-249	Sequence 249, App	1203	79.5	5.6	325034	4	US-09-949-016-14957	Sequence 14957, A
c1131	79.5	5.6	1119	4	US-09-252-991A-11990	Sequence 11990, A	1204	79.5	5.6	389504	4	US-09-949-016-11774	Sequence 11774, A
c1132	79.5	5.6	1122	4	US-09-252-991A-3335	Sequence 3335, App	c1205	79.5	5.6	525	4	US-09-902-540-8594	Sequence 8594, Ap
c1133	79.5	5.6	1122	4	US-09-949-016-3915	Sequence 3915, App	c1206	79.5	5.6	601	4	US-09-949-016-46366	Sequence 46366, A
c1134	79.5	5.6	1134	4	US-09-622-439-21	Sequence 21, Appl	c1207	79.5	5.6	651	4	US-09-252-991A-7997	Sequence 7997, Ap
c1135	79.5	5.6	1134	4	US-10-318-142-21	Sequence 21, Appl	c1208	79.5	5.6	741	4	US-09-252-991A-16102	Sequence 16102, A
c1136	79.5	5.6	1140	4	US-09-252-991A-11857	Sequence 11857, A	c1209	79.5	5.6	906	4	US-09-252-991A-2239	Sequence 2239, Ap
c1137	79.5	5.6	1173	4	US-09-252-991A-3233	Sequence 3233, App	c1210	79.5	5.6	963	4	US-09-252-991A-16178	Sequence 16178, A
c1138	79.5	5.6	1177	4	US-09-270-767-11017	Sequence 11017, A	c1211	79.5	5.6	972	4	US-09-949-016-4316	Sequence 4316, Ap
c1139	79.5	5.6	1215	4	US-09-252-991A-1312	Sequence 1312, App	c1212	79.5	5.6	1002	4	US-09-902-540-8031	Sequence 8031, Ap
c1140	79.5	5.6	1248	4	US-09-252-991A-4042	Sequence 4042, App	c1213	79.5	5.6	1014	4	US-09-252-991A-9420	Sequence 9420, Ap
c1141	79.5	5.6	1290	4	US-09-252-991A-6985	Sequence 6985, App	1214	79.5	5.6	1014	4	US-09-252-991A-15280	Sequence 15280, A
c1142	79.5	5.6	1371	4	US-09-252-991A-15313	Sequence 15313, A	1215	79.5	5.6	1014	4	US-09-902-540-1879	Sequence 1879, Ap
c1143	79.5	5.6	1398	4	US-09-252-991A-91	Sequence 91, Appl	c1216	79.5	5.6	1032	4	US-09-252-991A-6591	Sequence 6591, Ap
c1144	79.5	5.6	1432	4	US-09-902-540-264	Sequence 264, App	c1217	79.5	5.6	1047	4	US-09-902-540-7125	Sequence 7125, Ap
c1145	79.5	5.6	1432	4	US-09-902-540-6080	Sequence 6080, App	c1218	79.5	5.6	1058	4	US-09-634-137-39	Sequence 29, Appl
c1146	79.5	5.6	1452	4	US-09-252-991A-3933	Sequence 3933, App	1219	79.5	5.6	1089	4	US-09-252-991A-3785	Sequence 3785, Ap
c1147	79.5	5.6	1506	4	US-09-902-540-9624	Sequence 9624, App	c1220	79.5	5.6	1125	4	US-09-252-991A-6994	Sequence 6994, Ap
c1148	79.5	5.6	1554	4	US-09-252-991A-9350	Sequence 9350, App	c1221	79.5	5.6	1179	4	US-09-252-991A-3430	Sequence 3430, Ap
c1149	79.5	5.6	1590	4	US-09-489-039A-1653	Sequence 1653, App	c1222	79.5	5.6	1197	4	US-09-902-540-3968	Sequence 3968, Ap
c1150	79.5	5.6	1617	4	US-09-902-540-4903	Sequence 4903, App	c1223	79.5	5.6	1218	4	US-09-252-991A-7912	Sequence 7912, Ap
c1151	79.5	5.6	1752	4	US-09-252-991A-4682	Sequence 4682, App	1224	79.5	5.6	1257	4	US-09-252-991A-1027	Sequence 1027, Ap
c1152	79.5	5.6	1878	4	US-09-252-991A-3300	Sequence 3309, App	c1225	79.5	5.6	1290	4	US-09-902-540-6370	Sequence 6370, Ap
c1153	79.5	5.6	1917	4	US-09-252-991A-3039	Sequence 3039, App	c1226	79.5	5.6	1302	3	US-09-199-637A-348	Sequence 348, App
c1154	79.5	5.6	2013	4	US-09-902-540-5920	Sequence 5920, App	1227	79.5	5.6	1329	4	US-09-252-991A-6714	Sequence 6714, Ap
c1155	79.5	5.6	2039	4	US-09-902-540-179	Sequence 179, App	c1228	79.5	5.6	1332	4	US-09-252-991A-4685	Sequence 4685, Ap
c1156	79.5	5.6	2404	4	US-09-902-540-3817	Sequence 3817, App	c1229	79.5	5.6	1334	3	US-09-199-637A-350	Sequence 350, App
c1157	79.5	5.6	2412	4	US-09-252-991A-2921	Sequence 2921, App	c1230	79.5	5.6	1344	4	US-09-252-991A-16526	Sequence 16526, A
c1158	79.5	5.6	2449	4	US-09-949-016-4067	Sequence 4067, App	c1231	79.5	5.6	1413	4	US-09-252-991A-9741	Sequence 9741, Ap
c1159	79.5	5.6	2754	4	US-09-902-540-5587	Sequence 5587, App	1232	79.5	5.6	1428	4	US-09-252-991A-9266	Sequence 9266, Ap
c1160	79.5	5.6	2823	4	US-09-252-991A-2840	Sequence 2840, App	1233	79.5	5.6	1439	3	US-09-056-556-167	Sequence 167, App
c1161	79.5	5.6	2934	4	US-09-252-991A-84	Sequence 84, Appl	1234	79.5	5.6	1439	3	US-09-072-596-162	Sequence 162, App
c1162	79.5	5.6	3204	4	US-09-252-991A-3126	Sequence 3126, App	1235	79.5	5.6	1439	4	US-09-072-967-167	Sequence 167, App
c1163	79.5	5.6	3225	4	US-09-252-991A-4622	Sequence 4622, App	c1236	79.5	5.6	1440	4	US-09-902-540-9640	Sequence 9640, App
c1164	79.5	5.6	3435	1	PCT-US96-00005-1	Sequence 1, Appli	c1237	79.5	5.6	1476	4	US-09-252-991A-4812	Sequence 4812, Ap
c1165	79.5	5.6	3435	1	US-08-035-558-1	Sequence 1, Appli	1238	79.5	5.6	1476	4	US-09-252-991A-2443	Sequence 2443, Ap
c1166	79.5	5.6	3519	1	US-08-035-558-1	Sequence 1, Appli	c1239	79.5	5.6	1509	4	US-09-252-991A-6819	Sequence 6819, Ap
c1167	79.5	5.6	3981	4	US-09-252-991A-1361	Sequence 1361, App	1240	79.5	5.6	1545	4	US-09-252-991A-9274	Sequence 9274, Ap
c1168	79.5	5.6	4179	4	US-09-252-991A-1244	Sequence 1244, App	c1241	79.5	5.6	1551	4	US-09-252-991A-4758	Sequence 4758, Ap
c1169	79.5	5.6	4261	4	US-09-949-016-3867	Sequence 3867, App	1242	79.5	5.6	1560	4	US-09-252-991A-8114	Sequence 8114, Ap
c1170	79.5	5.6	4284	4	US-09-252-991A-4006	Sequence 4006, App	1243	79.5	5.6	1566	4	US-09-252-991A-14361	Sequence 14361, A
c1171	79.5	5.6	5001	4	US-09-902-540-8618	Sequence 8618, App	1244	79.5	5.6	1642	4	US-09-799-451-873	Sequence 873, App
c1172	79.5	5.6	5561	2	US-08-400-159-1	Sequence 1, Appli	1245	79.5	5.6	1674	4	US-09-252-991A-12046	Sequence 12046, A
c1173	79.5	5.6	5561	3	US-08-611-729A-1	Sequence 1, Appli	1246	79.5	5.6	1692	4	US-09-252-991A-978	Sequence 978, App
c1174	79.5	5.6	5561	4	US-09-195-524-1	Sequence 1, Appli	c1247	79.5	5.6	1695	4	US-09-252-991A-9380	Sequence 9380, App
c1175	79.5	5.6	8154	4	US-09-949-016-15657	Sequence 15657, A	c1248	79.5	5.6	1770	4	US-09-902-540-7790	Sequence 7790, Ap
c1176	79.5	5.6	1032	4	US-09-949-016-13070	Sequence 13070, A	c1249	79.5	5.6	1835	3	US-08-923-454A-7	Sequence 7, Appli
c1177	79.5	5.6	1092	4	US-09-902-540-960	Sequence 960, App	c1250	79.5	5.6	1842	4	US-09-252-991A-15508	Sequence 15508, A
c1178	79.5	5.6	12194	4	US-09-902-540-1091	Sequence 1091, App	1251	79.5	5.6	1869	4	US-09-252-991A-3231	Sequence 3231, Ap
c1179	79.5	5.6	12253	4	US-09-902-540-1060	Sequence 1060, App	c1252	79.5	5.6	1878	4	US-09-252-991A-11966	Sequence 11966, A
c1180	79.5	5.6	13631	4	US-09-902-540-1092	Sequence 1092, App	c1253	79.5	5.6	1929	4	US-09-252-991A-7017	Sequence 7017, Ap

1254	79	5.5	1932	4	US-09-252-991A-1911	Sequence 1911, Ap	c1327	79	5.5	30360	4	US-09-949-016-15716	Sequence 15716, A
c1255	79	5.5	1939	4	US-09-949-016-715	Sequence 715, App	c1328	79	5.5	33218	4	US-09-949-016-12495	Sequence 12495, A
1256	79	5.5	1947	4	US-09-252-991A-7111	Sequence 711, Ap	c1329	79	5.5	33319	4	US-09-949-016-15963	Sequence 15963, A
c1257	79	5.5	1950	3	US-08-911-853-14	Sequence 14, Appl	c1330	79	5.5	36851	4	US-09-949-016-14674	Sequence 14674, A
c1258	79	5.5	1950	3	US-09-479-409-14	Sequence 14, Appl	c1331	79	5.5	42235	3	US-09-199-637A-1	Sequence 1, Appl
c1259	79	5.5	1950	3	US-09-479-453-14	Sequence 14, Appl	1332	79	5.5	44952	4	US-09-949-016-12197	Sequence 12197, A
1260	79	5.5	2082	4	US-09-252-991A-9500	Sequence 9500, Ap	1333	79	5.5	44960	4	US-09-949-016-17583	Sequence 17583, A
c1261	79	5.5	2166	3	US-09-232-200-101	Sequence 101, App	1334	79	5.5	51552	4	US-08-733-294A-30	Sequence 30, Appl
c1262	79	5.5	2166	3	US-09-232-197-101	Sequence 101, App	c1335	79	5.5	57559	4	US-09-949-016-13077	Sequence 13077, A
c1263	79	5.5	2166	3	US-09-232-201-101	Sequence 101, App	c1336	79	5.5	57560	4	US-09-949-016-12536	Sequence 12536, A
c1264	79	5.5	2166	3	US-09-232-195-101	Sequence 101, App	c1337	79	5.5	58014	4	US-09-949-016-17448	Sequence 17448, A
c1265	79	5.5	2187	3	US-08-923-454A-23	Sequence 23, Appl	1338	79	5.5	67345	4	US-09-949-016-12270	Sequence 12270, A
c1266	79	5.5	2220	4	US-09-252-991A-16207	Sequence 16207, A	c1339	79	5.5	67745	4	US-09-949-016-17251	Sequence 17251, A
1267	79	5.5	2256	4	US-09-252-991A-10853	Sequence 10853, A	1340	79	5.5	89916	4	US-09-816-095-3	Sequence 3, Appl
c1268	79	5.5	2415	4	US-09-252-991A-5105	Sequence 5105, Ap	1341	79	5.5	109690	4	US-09-949-016-13525	Sequence 13525, A
1269	79	5.5	2469	4	US-09-252-991A-6679	Sequence 6679, Ap	c1342	79	5.5	125188	4	US-09-949-016-11980	Sequence 11980, A
1270	79	5.5	2505	4	US-09-252-991A-1830	Sequence 1830, Ap	c1343	79	5.5	132438	4	US-09-949-016-14349	Sequence 14349, A
c1271	79	5.5	2571	4	US-09-252-991A-8190	Sequence 8190, Ap	c1344	79	5.5	132438	4	US-09-949-016-14350	Sequence 14350, A
1272	79	5.5	2766	4	US-09-252-991A-3756	Sequence 3756, Ap	c1345	79	5.5	194889	4	US-09-949-016-15654	Sequence 15654, A
1273	79	5.5	2874	4	US-09-252-991A-3837	Sequence 3837, Ap	1346	79	5.5	194889	4	US-09-949-016-12675	Sequence 12675, A
1274	79	5.5	2910	4	US-09-252-991A-9547	Sequence 9547, Ap	1347	79	5.5	197132	4	US-09-949-016-17170	Sequence 17170, A
c1275	79	5.5	3033	4	US-09-724-797-81	Sequence 81, Appl	c1348	79	5.5	529885	4	US-09-949-016-14340	Sequence 14340, A
c1276	79	5.5	3225	4	US-09-902-540-3099	Sequence 3099, Ap	c1349	79	5.5	529885	4	US-09-949-016-14341	Sequence 14341, A
1277	79	5.5	3783	4	US-09-902-540-4846	Sequence 4846, Ap	c1350	79	5.5	529885	4	US-09-949-016-14342	Sequence 14342, A
1278	79	5.5	3813	2	US-08-650-000-3	Sequence 3, Appl	c1351	79	5.5	529885	4	US-09-949-016-14343	Sequence 14343, A
1279	79	5.5	3813	4	US-09-758-124-3	Sequence 3, Appl	c1352	79	5.5	529885	4	US-09-949-016-14344	Sequence 14344, A
c1280	79	5.5	3813	4	US-09-902-540-7085	Sequence 7085, Ap	c1353	79	5.5	529885	4	US-09-949-016-14345	Sequence 14345, A
1281	79	5.5	3813	6	5395760-3	Patent No. 5395760	c1354	79	5.5	529885	4	US-09-949-016-14346	Sequence 14346, A
1282	79	5.5	3813	6	5395760-3	Patent No. 5395760	c1355	79	5.5	529885	4	US-09-949-016-14347	Sequence 14347, A
1283	79	5.5	3815	4	US-09-902-540-634	Sequence 634, App	1356	79	5.5	5230230	4	US-09-438-185A-1	Sequence 1, Appl
1284	79	5.5	3861	4	US-09-252-991A-8018	Sequence 8018, Ap	1357	78.5	5.5	582	4	US-09-874-923-114	Sequence 114, App
c1285	79	5.5	3946	4	US-09-949-016-2607	Sequence 2607, Ap	c1358	78.5	5.5	600	4	US-09-252-991A-3659	Sequence 3659, Ap
c1286	79	5.5	3946	4	US-09-949-016-2608	Sequence 2608, Ap	c1359	78.5	5.5	601	4	US-09-949-016-49806	Sequence 49806, A
1287	79	5.5	4200	4	US-08-912-951-6	Sequence 6, Appl	c1360	78.5	5.5	601	4	US-09-949-016-145812	Sequence 145812, A
c1288	79	5.5	4284	4	US-09-252-991A-4006	Sequence 4006, Ap	c1361	78.5	5.5	601	4	US-09-949-016-146080	Sequence 146080, A
1289	79	5.5	4321	3	US-08-402-181B-6	Sequence 6, Appl	c1362	78.5	5.5	611	3	US-09-949-016-146348	Sequence 146348, A
1290	79	5.5	4335	3	US-08-974-549A-6	Sequence 6, Appl	c1363	78.5	5.5	711	3	US-09-655-270A-18	Sequence 18, Appl
1291	79	5.5	4430	4	US-09-721-456-6	Sequence 6, Appl	c1364	78.5	5.5	711	3	US-09-651-941-22	Sequence 22, Appl
c1292	79	5.5	4704	4	US-09-902-540-491	Sequence 491, App	c1365	78.5	5.5	711	3	US-09-955-597-22	Sequence 22, Appl
1293	79	5.5	4928	4	US-09-252-991A-3906	Sequence 3906, Ap	c1366	78.5	5.5	882	4	US-09-252-991A-5870	Sequence 5870, Ap
c1294	79	5.5	4928	4	US-09-578-063-67	Sequence 67, Appl	c1367	78.5	5.5	894	4	US-09-902-540-6139	Sequence 6139, Ap
c1295	79	5.5	4978	4	US-09-902-540-775	Sequence 775, App	c1368	78.5	5.5	1032	4	US-09-252-991A-14504	Sequence 14504, A
c1296	79	5.5	5117	4	US-09-949-016-2598	Sequence 2598, Ap	c1369	78.5	5.5	1137	4	US-09-252-991A-5529	Sequence 5529, Ap
c1297	79	5.5	5117	4	US-09-949-016-2599	Sequence 2599, Ap	c1370	78.5	5.5	1155	4	US-09-252-991A-412	Sequence 412, App
c1298	79	5.5	5117	4	US-09-949-016-2600	Sequence 2600, Ap	c1371	78.5	5.5	1173	4	US-09-894-844-60	Sequence 60, Appl
c1299	79	5.5	5117	4	US-09-949-016-2601	Sequence 2601, Ap	1372	78.5	5.5	1200	3	US-08-854-531-5	Sequence 5, Appl
c1300	79	5.5	5303	4	US-09-943-016-2602	Sequence 2602, Ap	1373	78.5	5.5	1200	5	PCT-US95-13552-5	Sequence 5, Appl
c1301	79	5.5	5303	4	US-09-949-016-2603	Sequence 2603, Ap	1374	78.5	5.5	1212	4	US-09-489-039A-4706	Sequence 4706, Ap
c1302	79	5.5	5303	4	US-09-949-016-2604	Sequence 2604, Ap	c1375	78.5	5.5	1212	4	US-09-902-540-3501	Sequence 3501, Ap
c1303	79	5.5	5303	4	US-09-949-016-2605	Sequence 2605, Ap	c1376	78.5	5.5	1233	4	US-09-489-039A-4691	Sequence 4691, Ap
c1304	79	5.5	5497	4	US-09-902-540-652	Sequence 652, App	c1377	78.5	5.5	1233	4	US-09-252-991A-14606	Sequence 14606, A
c1305	79	5.5	6655	4	US-09-902-540-777	Sequence 777, App	c1378	78.5	5.5	1396	4	US-09-902-540-2306	Sequence 2306, Ap
c1306	79	5.5	6715	4	US-09-902-540-818	Sequence 818, App	1379	78.5	5.5	1404	4	US-09-252-991A-14856	Sequence 14856, A
1307	79	5.5	7225	4	US-09-902-540-876	Sequence 876, App	1380	78.5	5.5	1476	4	US-09-902-540-6774	Sequence 6774, Ap
1308	79	5.5	7261	4	US-09-902-540-845	Sequence 845, App	c1381	78.5	5.5	1503	4	US-09-687-360-1	Sequence 1, Appl
c1309	79	5.5	8241	4	US-09-902-540-798	Sequence 798, App	c1382	78.5	5.5	1509	4	US-09-252-991A-3614	Sequence 3614, Ap
c1310	79	5.5	9996	4	US-09-902-540-999	Sequence 999, App	c1383	78.5	5.5	1545	4	US-09-252-991A-5553	Sequence 5553, Ap
1311	79	5.5	12739	4	US-09-902-540-1011	Sequence 1011, Ap	c1384	78.5	5.5	1560	4	US-09-252-991A-15609	Sequence 15609, A
c1312	79	5.5	14467	4	US-09-902-540-1058	Sequence 1058, Ap	c1385	78.5	5.5	1584	4	US-09-252-991A-15886	Sequence 15886, A
1313	79	5.5	15418	4	US-09-783-203-1	Sequence 1, Appl	c1386	78.5	5.5	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
1314	79	5.5	15418	4	US-09-994-427A-1	Sequence 1, Appl	1387	78.5	5.5	1671	4	US-09-252-991A-9711	Sequence 9711, Ap
1315	79	5.5	15418	4	US-09-244-438-1	Sequence 1, Appl	c1388	78.5	5.5	1680	4	US-09-252-991A-15645	Sequence 15645, A
c1316	79	5.5	15499	4	US-09-902-540-1140	Sequence 1140, Ap	1389	78.5	5.5	1690	4	US-09-620-312D-69	Sequence 69, Appl
c1317	79	5.5	15742	4	US-09-949-016-13762	Sequence 13762, A	1390	78.5	5.5	1702	4	US-09-902-540-292	Sequence 292, App
1318	79	5.5	15782	4	US-09-902-540-1094	Sequence 1094, Ap	c1391	78.5	5.5	1716	4	US-09-252-991A-9577	Sequence 9577, Ap
1319	79	5.5	16162	3	US-08-911-853-29	Sequence 29, Appl	c1392	78.5	5.5	1734	4	US-09-711-164-179	Sequence 179, App
1320	79	5.5	16162	3	US-09-479-409-29	Sequence 29, Appl	1393	78.5	5.5	1758	4	US-09-252-991A-15835	Sequence 15835, A
1321	79	5.5	17612	3	US-09-479-453-29	Sequence 29, Appl	c1394	78.5	5.5	1824	4	US-09-252-991A-16072	Sequence 16072, A
1322	79	5.5	18324	4	US-09-902-540-1196	Sequence 1196, Ap	1395	78.5	5.5	1842	4	US-09-543-681A-1840	Sequence 1840, Ap
1323	79	5.5	19455	4	US-09-902-540-1147	Sequence 1147, Ap	1396	78.5	5.5	1899	4	US-09-252-991A-15709	Sequence 15709, A
c1324	79	5.5	21758	4	US-09-902-540-1238	Sequence 1238, Ap	1397	78.5	5.5	1914	4	US-09-252-991A-5670	Sequence 5670, Ap
c1325	79	5.5	21602	4	US-09-902-540-1208	Sequence 1202, Ap	1398	78.5	5.5	1964	4	US-09-774-528-308	Sequence 308, App
1326	79	5.5	23384	4	US-09-902-540-1229	Sequence 1229, Ap	c1399	78.5	5.5	2034	4	US-09-252-991A-9000	Sequence 9000, Ap

c1400	78.5	5.5	2070	4	US-09-252-991A-14761	Sequence 14761, A	1473	78.5	5.5	41310	4	US-09-902-540-1264	Sequence 1264, Ap
c1401	78.5	5.5	2112	4	US-09-902-540-3277	Sequence 3277, Ap	1474	78.5	5.5	41522	4	US-09-949-016-11932	Sequence 11932, A
c1402	78.5	5.5	2157	4	US-09-252-991A-10969	Sequence 10969, Ap	1475	78.5	5.5	41523	4	US-09-949-016-15764	Sequence 15764, A
c1403	78.5	5.5	2265	4	US-09-252-991A-2367	Sequence 2367, Ap	1476	78.5	5.5	41768	4	US-09-902-540-1266	Sequence 1266, Ap
c1404	78.5	5.5	2287	4	US-09-223-040-1	Sequence 1, Appli	c1477	78.5	5.5	49225	4	US-09-902-540-1269	Sequence 1269, Ap
c1405	78.5	5.5	2287	4	US-09-287-849-1	Sequence 1, Appli	c1478	78.5	5.5	57299	4	US-09-949-016-12141	Sequence 12141, A
c1406	78.5	5.5	2343	4	US-09-252-991A-2549	Sequence 2549, Ap	1479	78.5	5.5	57978	4	US-09-949-016-16667	Sequence 16667, A
c1407	78.5	5.5	2397	4	US-09-252-991A-8738	Sequence 8738, Ap	c1480	78.5	5.5	71278	4	US-09-949-016-11851	Sequence 11851, A
c1408	78.5	5.5	2403	4	US-09-902-540-4394	Sequence 4394, Ap	c1481	78.5	5.5	71278	4	US-09-949-016-17563	Sequence 17563, A
c1409	78.5	5.5	2477	4	US-09-902-540-1971	Sequence 1971, Ap	c1482	78.5	5.5	86414	4	US-09-949-016-12345	Sequence 12345, A
c1410	78.5	5.5	2526	4	US-09-758-282B-213	Sequence 213, App	1483	78.5	5.5	86414	4	US-09-949-016-15758	Sequence 15758, A
c1411	78.5	5.5	2526	4	US-09-577-304A-213	Sequence 213, App	1484	78.5	5.5	128470	4	US-09-949-016-13765	Sequence 13765, A
c1412	78.5	5.5	2610	4	US-09-252-991A-1107	Sequence 1107, Ap	c1485	78.5	5.5	152524	4	US-09-949-016-12683	Sequence 12683, A
c1413	78.5	5.5	2754	4	US-09-252-991A-1147	Sequence 1147, Ap	c1486	78.5	5.5	152524	4	US-09-949-016-13194	Sequence 13194, A
c1414	78.5	5.5	2976	4	US-09-902-540-554	Sequence 554, App	c1487	78.5	5.5	168174	4	US-10-071-411A-63	Sequence 63, Appli
c1415	78.5	5.5	3024	4	US-09-252-991A-2043	Sequence 2043, Ap	c1488	78.5	5.5	168273	4	US-10-071-411A-2	Sequence 2, Appli
c1416	78.5	5.5	3046	1	US-08-276-099A-1	Sequence 1, Appli	1489	78.5	5.5	229354	4	US-09-705-400-64	Sequence 64, Appli
c1417	78.5	5.5	3046	1	US-08-781-890-1	Sequence 1, Appli	1490	78.5	5.5	321022	4	US-09-949-016-11852	Sequence 11852, A
c1418	78.5	5.5	3046	3	US-09-087-805A-1	Sequence 11, Appli	1491	78.5	5.5	321022	4	US-09-949-016-14166	Sequence 14166, A
c1419	78.5	5.5	3046	4	US-09-972-800A-9	Sequence 9, Appli	c1492	78.5	5.4	444	4	US-09-252-991A-5849	Sequence 5849, Ap
c1420	78.5	5.5	3046	4	US-09-023-655-1444	Sequence 1444, Ap	1493	78.5	5.4	456	4	US-09-252-991A-634	Sequence 634, App
c1421	78.5	5.5	3114	4	US-09-252-991A-977	Sequence 977, App	1494	78.5	5.4	591	4	US-09-252-991A-4707	Sequence 4707, Ap
c1422	78.5	5.5	3195	4	US-09-252-991A-937	Sequence 937, App	c1496	78.5	5.4	601	4	US-09-949-016-45122	Sequence 45122, A
c1423	78.5	5.5	3371	3	US-09-116-473-1	Sequence 1, Appli	c1496	78.5	5.4	834	4	US-09-252-991A-16311	Sequence 16311, A
c1424	78.5	5.5	3375	3	US-09-511-625B-67	Sequence 67, Appli	c1497	78.5	5.4	837	4	US-09-252-991A-15832	Sequence 15832, A
c1425	78.5	5.5	3540	4	US-09-252-991A-1324	Sequence 1324, Ap	1498	78.5	5.4	855	4	US-09-252-991A-773	Sequence 773, App
c1426	78.5	5.5	3667	3	US-09-511-625B-1	Sequence 1, Appli	1499	78.5	5.4	864	4	US-09-252-991A-773	Sequence 773, App
c1427	78.5	5.5	3759	4	US-09-560-385A-15	Sequence 15, Appli	1500	78.5	5.4	873	4	US-09-252-991A-6226	Sequence 6226, Ap
c1428	78.5	5.5	3894	3	US-09-511-625B-3	Sequence 3, Appli							
c1429	78.5	5.5	3930	4	US-09-560-385A-13	Sequence 13, Appli							
c1430	78.5	5.5	3941	3	US-09-408-865-2	Sequence 2, Appli							
c1431	78.5	5.5	3971	4	US-09-876-176-1	Sequence 1, Appli							
c1432	78.5	5.5	4089	4	US-09-902-540-7372	Sequence 7372, Ap							
c1433	78.5	5.5	4090	4	US-09-902-540-706	Sequence 706, App							
c1434	78.5	5.5	4108	4	US-09-919-172-15	Sequence 15, Appli							
c1435	78.5	5.5	4617	4	US-09-902-540-547	Sequence 547, App							
c1436	78.5	5.5	4695	4	US-09-902-540-8855	Sequence 8855, Ap							
c1437	78.5	5.5	4884	4	US-09-252-991A-3824	Sequence 3824, Ap							
c1438	78.5	5.5	5120	4	US-09-949-016-4772	Sequence 4772, Ap							
c1439	78.5	5.5	5275	4	US-09-902-540-771	Sequence 771, App							
c1440	78.5	5.5	5463	4	US-09-902-540-9150	Sequence 9150, Ap							
c1441	78.5	5.5	5515	3	US-09-125-642C-8	Sequence 8, Appli							
c1442	78.5	5.5	5781	4	US-09-902-540-711	Sequence 711, App							
c1443	78.5	5.5	5868	3	US-08-516-859A-3	Sequence 3, Appli							
c1444	78.5	5.5	5868	3	US-09-586-472-3	Sequence 3, Appli							
c1445	78.5	5.5	5868	3	US-09-528-706-3	Sequence 3, Appli							
c1446	78.5	5.5	6360	3	US-09-171-699-9	Sequence 9, Appli							
c1447	78.5	5.5	6445	4	US-09-620-312D-324	Sequence 324, App							
c1448	78.5	5.5	6487	4	US-09-620-312D-323	Sequence 323, App							
c1449	78.5	5.5	6821	4	US-09-902-540-907	Sequence 907, App							
c1450	78.5	5.5	7404	4	US-09-902-540-3115	Sequence 3115, Ap							
c1451	78.5	5.5	7812	3	US-09-368-590-1	Sequence 1, Appli							
c1452	78.5	5.5	7881	2	US-08-751-189-1	Sequence 1, Appli							
c1453	78.5	5.5	7881	2	US-09-060-836-1	Sequence 1, Appli							
c1454	78.5	5.5	8297	3	US-09-184-445-1	Sequence 1, Appli							
c1455	78.5	5.5	8891	4	US-09-949-016-14843	Sequence 14843, A							
c1456	78.5	5.5	8658	4	US-09-902-540-943	Sequence 943, App							
c1457	78.5	5.5	8756	4	US-09-949-016-1438	Sequence 1438, Ap							
c1458	78.5	5.5	9710	4	US-09-902-540-978	Sequence 978, App							
c1459	78.5	5.5	1256	4	US-09-902-540-1006	Sequence 1006, Ap							
c1460	78.5	5.5	16423	4	US-09-902-540-1120	Sequence 1120, Ap							
c1461	78.5	5.5	16541	4	US-09-902-540-1165	Sequence 1165, Ap							
c1462	78.5	5.5	16833	4	US-09-902-540-1112	Sequence 1112, Ap							
c1463	78.5	5.5	17245	4	US-09-902-540-1073	Sequence 1073, Ap							
c1464	78.5	5.5	17480	4	US-09-902-540-1151	Sequence 1151, Ap							
c1465	78.5	5.5	18471	4	US-09-902-540-1167	Sequence 1167, Ap							
c1466	78.5	5.5	18809	4	US-09-902-540-1141	Sequence 1141, Ap							
c1467	78.5	5.5	21330	4	US-09-902-540-1209	Sequence 1209, Ap							
c1468	78.5	5.5	23704	4	US-09-949-016-12104	Sequence 12104, A							
c1469	78.5	5.5	23704	4	US-09-949-016-15312	Sequence 15312, A							
c1470	78.5	5.5	24984	4	US-09-949-016-14950	Sequence 14950, A							
c1471	78.5	5.5	34185	3	US-09-545-481-3	Sequence 3, Appli							
c1472	78.5	5.5	37004	4	US-09-949-016-15317	Sequence 15317, A							

ALIGNMENTS

RESULT 1

US-09-799-451-571
; Sequence 571, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qian-Rui
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radjoe T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799, 451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 571
; LENGTH: 2240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1779)
US-09-799-451-571

Alignment Scores:
Pred. No.: 2,33e-132 Length: 2240

Score: 1265.00 Matches: 246
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.34% Indels: 0
DB: 4 Gaps: 0

US-10-015-388A-54 (1-280) x US-09-799-451-571 (1-2240)

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QY 1 MetCysPheLeuAsnLysLeuLeuLeuAlaValLeuGlyThrPheGlnIlePro 20
DB 352 AIGTGTTCCTGAACAGCTGCTACTTGTCTGCTGGCTGCTTTTCAGATTCC 411
QY 21 ThrValProGluAspLeuPheLeuGluGluGlyProSerTyrAlaPheGluValAsp 40
DB 412 ACAGTCCCTGAGGACTGTGCTTTCTGGAAGAGGTCCCTCATATGCTTTGAGGTGAC 471
QY 41 ThrValAlaProGluHisGlyLeuAspAlaProValValAspGlnLeuLeuTyr 60
DB 472 ACAGTAGCCCAAGAGCATGGCTTGACCAATGCGCTGTGGTGGACAGCAGCTGCTCTAC 531
QY 61 ThrCysCysProTyrIleGlyGluLeuArgLysLeuAlaSerTrpValSerGlySer 80
DB 532 ACTGCTGCCCTACATCGAGAGCTCCGAAACTGCTGCTTCGTGGGTGTCAGGCAGT 591
QY 81 SerGlyArgSerGlyPheMetArgLysIleThrProThrThrThrSerLeuGly 100
DB 592 AGTGACGAGTGGGGCTTCATGAGGAAATCACCCACCATACCCAGCCTGGGA 651
QY 101 AlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
DB 652 GCCCAGCCTTCCACAGCAGCAGCGGCTGCAGGCACAGCTGCCCGAGCCTTTTTCAC 711
QY 121 AsnGlnProProSerLeuArgThrValGluPheValAlaGluArgIleGlySerAsn 140
DB 712 AACAGCGCCCTCTTCGCGCGACCGTAGAGTTCTGGCGCAAGAAATTGGATCAAC 771
QY 141 CysValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeu 160
DB 772 TGTGTCAACATATCAAGCTACACTGTGGTGGCAGATCTGGTGGCCAGGACAGTCACTT 831
QY 161 LeuGlnGluGlnLeuValThrGlnGlyGluGluGlyAspProAlaGlnLeuLeuGlu 180
DB 832 CTCCAAGAGCAGCTGGTGACAGGAGGAGGAAGGGGAGAGCCCAAGCCAGCTGTGTGAG 891
QY 181 IleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPhe 200
DB 892 ATCTGTGTCCACCTGTGCTCCTACCGGGCCAGGCAATTGGCCCTGGGGGGAGTTC 951
QY 201 CysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluThrProAlaAla 220
DB 952 TGTCAAGGAAGAGCCCTGGGCTGTGGCGCTGTCTTCCAGAGGAGACCCCGGACGCC 1011
QY 221 ValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrp 240
DB 1012 GTTCTGAGCAGTGCAGAGAACTGCTGTGGGCTGTGCAAGAGAAAGCCTGTGCTTGG 1071
QY 241 LeuSerAlaAsnIleThr 246
DB 1072 CTGTGAGCCACATCACA 1089
```

RESULT 2

US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 5.55e+03 Length: 4403765
Score: 111.50 Matches: 61
Percent Similarity: 37.92% Conservatives: 30
Best Local Similarity: 25.42% Mismatches: 89
Query Match: 7.79% Indels: 60
DB: 3 Gaps: 11

US-10-015-388A-54 (1-280) x US-09-103-840A-2 (1-4403765)

```
QY 65 TyrIleGlyGluLeuArgLysLeuAla-----SerTrpValSerGlySerSer 81
DB 2472859 TTCAATCGAATCCCTGGCCAGCTAATCGCTGTCGACAAAGCTTGGTGCCCGGTCCGCGC 2472800
QY 82 GlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGlyAla 101
DB 2472799 GGTGAGGAGGCGCTGTATCTGCGCCGCTTATCTTCCGACCCGCGGACTGGGCGTG 2472740
QY 102 GlnPro---SerGlnThrSerGlnGluGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
DB 2472739 CGGCTGCGCCACCAATACCGTTACTGTTGATCGCTCGCGCGCGGTGCGTACTTCAAG 2472680
QY 121 Asn-----GlnProProSerLeuArgThrValGluPheValAlaGluArgIleGly 138
DB 2472679 GGCGCATCGCCCTGTGAGGCTGCGAGGTTCGAGGAGTAGTGTACGGGCGCTGTCGCGGC 2472620
QY 139 SerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGlu 158
DB 2472619 GGCAACGGTGGCGCAAGTTCGCGCGCAACTACGCCGCGCTCGTGTGCTGCGCGCAGCCGAA 2472560
QY 159 SerLeuLeuGlnGlnLeuValThrGlnGlyGluGluGlyAspProAlaGlnLeu 178
DB 2472559 GCC-----GCCGAGAACGATGCGACCCAGTGGTGTGGTGG 2472527
QY 179 LeuGluIleLeuCysSerGlnLeuLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArg 198
DB 2472526 CTGGAC-----GCTGTGGAAGCC 2472509
QY 199 GluPheCysGlnArgLys-----SerProGlyAla 208
DB 2472508 CGCTATATCGAAGAGATGGTGGCATCATCTTCTTCTGTCGCGCGCGGATCG 2472449
QY 209 ValArgAlaLeuLeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIle 228
DB 2472448 GCGCGGTGGTTCACCCCGGAG-----CTGTGCGGT-----TCCCTG 2472413
QY 229 AlaValGlyLeuAlaThrGlu-LysAlaCysAlaTrpLeu-----Se 242
DB 2472412 CTGCCCCGGGATCACACGGGATTCGTTGTGAGTTGGCTATGATGCGGATTCGCGGTC 2472353
QY 242 rAlaAsnIle-----ThrAlaIleArgArgGluValLysAlaAlaValSe 258
DB 2472352 GAGGAACGAGGATTGATATCGACAGTGGCAGAAAGAGCCCGCGCGGAGATCAACC 2472293
QY 258 rArgThrLeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyCys 277
DB 2472292 GAGGTGTTTGGTGGCAGCCGCGCTGTATCATCACCCCGGTGCG-----CGCGGGTGC 2472241
RESULT 3
US-09-103-840A-1/c
```



```
Qy 53 -----ValValAspGlnGlnLeuLeuLeuThrCys----- 62
Db 1315 GGAGTGTGAGATAGCGTGTGTGCGCCACCTTGCCTTCCACTGCTGTTGAAGGC 1256
Qy 63 CysProTyrIleGlyGluLeuArgLysLeu-----LeuAlaSerTrpValSerGlySer 80
Db 1255 ATCCCGCGCAGCGGTGCCACGAAAGTCTTCACTACCTGTTTTCAGCGCTCCGCTCTTC 1196
Qy 81 SerGlyArgSerGlyGlyPheMetArg-----LysIleThrProThr 94
Db 1195 GAAGCCCGCGGACATACCTTGTGTGATCAGCTTTTGTCCCGCATCCAGCTCTGCCCTG 1136
Qy 95 ThrThrThrSerLeu-----GlyAlaGlnProSerGlnThrSer 107
Db 1135 ACCGAGCGGATTCAGTCCGGTAGTGAATGCCGGTGTAGAGCAACAGCGCATCAC 1076
Qy 108 GlnGlyLeuGlnAlaGlnLeu-----AlaGlnAlaPhePheHisAsnGlnPro 123
Db 1075 TTCGGCGTCACTGTGGATGCCACAGGCTGTGTGCCAGGTACTTTTCCGCATCCGCCCC 1016
Qy 124 ProSerLeu-----ArgArgThrValGluPheVal 133
Db 1015 GAACCGCTTACACAGGCCCATCCGACGCGCTTGTCCGCCGATACTCTGCTGACCTGCT 956
Qy 134 AlaGluArgIleGlySerAsnCys---ValLysHisIleLysAlaThrLeuValAlaAsp 152
Db 955 CTCTACCGCTGGCGCAACAGTGCAGCTCGTCACTTACCTGATGCAACTGGTGGTGAT 896
Qy 153 LeuValArgGlnAlaGluSerLeuLeuGlnGlnGlnValThrGlnGlyGluGly 172
Db 895 TTCGGCGCGAGTTCGGGCTTGTGTGAGCACCAGTTG---ACTCGCGGACCGCGCTG 839
Qy 173 Gly-----AspProLagln----- 177
Db 838 GGTGCCCACTGTCTGACGCGGATCCCGCGATGCTCCGTTTCGACAGCGCGCGACGCTG 779
Qy 178 -----LeuLeuGluIleLeuCysSerGlnLeuCys-----Pro 188
Db 778 GATACGGGACTCTCTGACTGGC-TGCCGGCACGATCCCGCCNAGCGGTGCTCAGCG 720
Qy 189 HisGlyAlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGlyAla 208
Db 719 AACGACGCGCCCATCTCCG-CTGCCAGCGGGAGTGTCTCCGCGCCAGTCTCTCCGCT 661
Qy 209 ValArg-----AlaLeuLeuProGluThrProAlaAlaValLeu----- 222
Db 660 GTCAGGTCGCCAGCTCGCTTGTGAGTCTCCCTTCAAGGTCAATGGCAATGCTCTGCG 601
Qy 223 -----SerSerAlaGluAsnIleAlaValGlyLeuAlaThrGlu 235
Db 600 TGCAGCACCATCTGTGTAACACGAGCGCGGAGACATGACCGGAGGTGCGGCTCTGTA 541
Qy 236 LysAlaCys-----AlaTrpLeuSerAlaAsnIleThrAlaLeuIleArgArg 251
Db 540 CTGGCTCGCGGCGCGTGGCGGCTGG-----GAGCCCAACAGTGTGCCCGCCAG 490
Qy 252 GluValLysAlaAlaValSerArgThr-----LeuArgAlaGlnGlyProGlu 267
Db 489 TCCATGATGTCACGACGAGCGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 430
Qy 268 Pro 268
Db 429 CCC 427
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RESULT 5

```
US-09-949-016-14632/c
; Sequence 14632, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14632
; LENGTH: 12445
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(12445)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14632

Alignment Scores:
Pred. No.: 1.84 Length: 12445
Score: 106.50 Matches: 79
Percent Similarity: 34.29% Conservative: 17
Best Local Similarity: 28.21% Mismatches: 102
Query Match: 7.44% Indels: 83
DB: 4 Gaps: 14

US-10-015-388A-54 (1-280) x US-09-949-016-14632 (1-12445)
Qy 56 GlnGlnLeuLeuTyrThrCysCysProTyrIleGlyGluLeuArgLysLeuAlaSer 75
Db 10612 CAGCACCACTTACTCAGCTGTCTCTGCATT-----CAACTCTGC 10571
Qy 76 TrpValSerGlySerSergly-----ArgSerGlyGlyPheMetArgLysIle----- 91
Db 10570 TGGGCCACAGGCTCTCGGGAGACCCACCCAGCTGGGAGGAGGAGGAGGAGGAGGAG 10511
Qy 92 -----ThrProThrThrThrSerLeuGlyAlaGlnProSerGln 105
Db 10510 CCCAGCGCTGGATGGTGTCTCCCTGTCACAGCCAGCGTGGTGGCCACCCAGCAGCAG 10451
Qy 106 ---ThrSerGlnGlyLeuGlnAlaGlnAlaGlnAlaPhePheHisAsnGlnPro 124
Db 10450 TTCTCTCTACTTGGTCTCAGCTGGACGACGACGACGACGACGACGACGACGACGACG 10397
Qy 125 SerLeuArgArgThrValGluPheValAla-----GluArgIleGlySerAsn 140
Db 10396 TCGGTGACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 10340
Qy 141 CysValLysHisIleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSer--- 159
Db 10339 -----GTGGTGGCGGCACTCGGCGCTGTCTGTAGGAGGCTTGTGTAGCAGGG 10292
Qy 160 -----LeuLeuGlnGlnGlnLeuValThrGlnGlyGluGluGly----- 172
Db 10291 GGCCTCTGCATCTTCTGCAGAAAGTAACAGTAGGCAAGGAGGAGGAGGAGGAGGAGGAGG 10232
Qy 173 -----GlyAspProAlaGlnLeuLeuGluIleLeuCys----- 183
Db 10231 GGCCCGTCGACGCGCGCGCTTGTGTTC-CTAAGATGTTGCGGCGCGCGCGCGCTGTGCG 10173
Qy 184 -----SerGlnLeuCysProHisGlyAlaGlnAlaLeuAla 195
Db 10172 GGCCCGCGCGGCGACCTTCGCGCGAGCGCGCTGCTTGTGAGGCGCGACCTTCTCTGGGG 10113
Qy 196 LeuGlyArgGluPheCysGlnArgLysSerPro-----GlyAlaVal 209
Db 10112 GATGCGCGTCAACACAGGCGCTCGTAGAGCCCTCTCGGCTGCATCATACCGGGCTTCT 10053
Qy 210 ArgAlaLeuLeuProGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAla 229
Db 10052 CCAGCCACACCTCCCGAACCAAGTGCCTGTGAGGCTGCCCGAGCGGGGCTGTGACCG 9993
```


US-10-015-388A-54 (1-280) x US-09-902-540-807 (1-6063)

```
QY 69 LeuArgLysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGly----- 85
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5140 GTGGCGAGGCGATGCATACCTGG-----GGTAGCTCTCGGTGAGGGAGCGGAGC 5193
QY 86 -----GlyPhe 87
Db ATGTCCCGGACCGCGGTTTCATCGGAACGGATCCACGCCCGGAGCAGGTCTCCGCGGAG 5253
QY 88 MetArgLysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGly----- 99
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5254 GAAGCCCGGACCGTCCCGGCGGATCCACCTCGCTGATGGACGCCAGCCATCGGGGAGC 5313
QY 99 ----- 99
Db 5314 CTGAGCGCGGTTGTGAAGCCCTCTTCGCTCCACGGAGACAGCGTCCAGTGGGCGTGG 5373
QY 100 -----GlyAlaGlnProSerGlnThrSerGlnGly 109
Db 5374 CGGGTGCTGAAGTGGCGGAAGCGGGTCCGGCGCGCGGCCCTCGGCCAGCTCC----- 5427
QY 110 LeuGlnAlaGlnLeuAlaGlnAlaPhePheHisAsnGlnProProSerLeuArgThr 129
Db 5428 -----GCCCGTCAGTGGCGGCTCGAGTTCCTGGATCGCTCGGCCCGCCATGTGCGCGCGC 5484
QY 130 ValGluPheValAlaGluArgIleGlySerAsnCysValLysHisIleLysAlaThrLeu 149
Db 5485 -----GTGGCGGAGCTCTGGGTACAGACCTGTGGCAGCGGTGTGACGGCG 5535
QY 150 ValAlaAppLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeuValThrGlnGly 169
Db 5536 CTGGGCGCGCGCGTCCCGGCTCCACCGAGGAGTGCAGCATGAGCTG-----GGC 5586
QY 170 GluGluGlyGlyAspProAlaGlnLeuLeuLysLeuCysSerGlnLeuCysProHis 189
Db 5587 GAGGAC-----CTCCAGGTCTCTGCTC-----CAC 5610
QY 190 GlyAlaGlnAla-----LeuAlaLeu 196
Db 5611 GCGCGCCAGCGCGCTGGGACCGCGCGCTGGAGCAGGGGCTCTGTCTCACCTG 5670
QY 197 GlyArg-----GluPheCysGlnArgLysSerProGlyAla-----ValArgAlaLeu 212
Db 5671 GCGCGGCTCGCGGATTCGCGCGGGGAGCGCGCGCGCTGAGCTGCGCGCGCC 5730
QY 213 LeuProGluGluThr----- 217
Db 5731 CTGGAGCGCTTCACCCACTCCCTGTCCGAGCTGATGACCGCGCGCGCTACCGCGC 5790
QY 218 -----ProAlaAlaValLeuSerSerAlaGluAsnIleAla-----ValGlyLeuAlaThr 234
Db 5791 GCGTGGGAAGCGCGGAGACGAGCTGCCAGTCCGCGCGGTGCTGGCGCGCGGAGAC 5850
QY 235 GluLysAlaCysAlaTrpLeuSerAlaAsnIle-----ThrAlaLeuIleArgArgGlu 252
Db 5851 CCGGCTCTCTGCTGTGATGGCGGACCATCTGTCCAGACAGCTTCTCGCTGGCGGCAAC 5910
QY 253 ValLysAlaAlaValSerArgThrLeuArgAlaGlnGly----- 265
Db 5911 GCCCAGGCTCGTC-----CGACGCTCGCGAGCTGGGAGAGCTGTCCACGAGTAGTTCG 5967
QY 266 ProGluProAlaAlaArgGlyGluArgArgGlyCys 277
Db 5968 CCGGAC-----GCCTGCTCACTCGGCCACGAGGATGC 6000
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RESULT 11

US-09-252-991A-1675
; Sequence 1675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1675
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1675

Alignment Scores:

Pred. No.:	0.0894	Length:	1131
Score:	103.50	Matches:	77
Percent Similarity:	32.94%	Conservative:	36
Best Local Similarity:	22.45%	Mismatches:	110
Query Match:	7.23%	Indels:	121
Db:	4	Gaps:	14

US-10-015-388A-54 (1-280) x US-09-252-991A-1675 (1-1131)

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QY 33 ProSerTrpAlaPheGluValAsp-----ThrValAlaProGluHisGlyLeu 48
Db 109 CCAGCCAGGCGCGGATGATATAGGGCGGATATAGGGCGGCGGCGGCGGCGC 168
QY 49 AsphenAlaProValValAspGlnGlnLeuLeuTrpThrCysCysProTrpIleGlyGlu 68
Db 169 GAGAATGCGCGCCAGGTT-----GTAGGCGCGC 195
QY 69 LeuArgLysLeuLeuAlaSerTrpValSerGlySerSerGlyArgSerGlyGlyPheMe 88
Db 196 CGACGCGCGCGGTGAGCGCACGCTGGTGGGGAATATTTCCGGCAGCAGCGCCCATCGG 255
QY 88 tArgLysIleThrProThrThrThrSerLeu----- 99
Db 256 GGCGAAGGTGACCCCATCAGGAACAGCTCATGTCAGAGNAACAGGGGCGGCGTGAACGT 315
QY 99 ----- 99
Db 316 CGAGCCCTGGGTGAGCAGCGGCTCCATGGCGAAGCGGAGCGGATCGCGCGCAGGCTGCC 375
QY 100 -----GlyAlaGlnPro-----SerGlnThrSerGlnGlyLeuGlu 111
Db 376 GAGCAGCAGTACCGGCTTGGTCCGAAAGCGGCTCGCTGAGCCAGGCGCGCGGCTGGC 435
QY 111 nAlaGlnLeuAlaGlnAlaPhePheHisAsnGlnProProSerLeuArgArg----- 128
Db 436 GGCGGCCATGAGAGCACCGCGAGGCGACAGCAGACCAAGNACTCTCTCGCGGCTGAAGCC 495
QY 128 ----- 128
Db 496 GAGGCTGGCCACCCCGTAGCTCAGCGAGAAACACCGTGGAGATATAGAACGCGCATAAAC 555
QY 129 -----ThrValGluPheValAlaGluArgIleGlySerAsnCysValLysHisIleLysAl 147
Db 556 CACCACCATCCGACGGCGCGGAGCGGTGCGGCCCGCCAGTGTGTGGCGGAACAGCTCGGC 615
QY 147 aThrLeuValAlaAsp-----LeuVal-----Ar 155
Db 616 GATCGG-CAGCGGCGCCCTCTCGTGTCTGGCCATGGCTTGGCGAACCACCGGGGTTTCCG 674
QY 155 gGlnAlaGluSerLeuLeuGln-----GluGlnLeuValThrGlnGlyGluGlyGlyAs 174
Db 675 CCAGCTTCAGCGGTACGTAGAGCGCGCACCAACACAGCGCGCGCTGAGCAGGAACCGGA 734
QY 174 p-----ProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuLeuCysProHisGlyAlaGlnAl 193
Db 735 TCGGCCAGCCCACTACGGAACACTCTCTCTGCTGAGCAGCATCGCCAGGCG-----CAGGA 791
```

```
Qy 193 aleuAlaLeuGlyArgGluPheCysGlnArgLysSer-----Pr 206
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
792 ACAGCCCTGGCGCGGAGGCGATCGACGGCGGAGTGGGGAAACATGCGGAACC 851
Qy 206 oGlyAlaValArgAlaLeuProGluGluThrProAlaAlaValLeuSerSerAlaG1 226
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
852 AGGCGCGTTCGCGG-----CGGCGGTTCCTCCGTGGCCAGCA 890
Qy 226 uAsnIleAlaValGlyLeuAlaThrGluLysAlaCysAlaTrpLeuSerAlaAsnIleTh 246
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
891 GCGGGCGCGCCCGCCACTCGCGCGGAGCGCGAGCCCTCGCGGAAGCGCA----- 942
Qy 246 rAlaLeuIleArgGluValLysAlaAlaValSerArgThrLeuArgAlaGlnGly-- 265
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
943 -----GCAGCGAGCAGCAACGCGCGCCAGTAGCCGATGCTGTCTGAACCGCGGAGG 995
Qy 266 -----ProGluProAlaAlaArgGlyGluArgGlyCy 277
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
996 ACGCGATCAGGGTGGTGCACACCCCATCGACGAGCGAGCGGACGAGGGTTGACTTG 1055
Qy 277 sSerArg 279
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1056 CGCCCGA 1062

RESULT 12
US-09-902-540-4835
; Sequence 4835, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4835
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4835

Alignment Scores:
Pred. No.: 0.365 Length: 2745
Score: 103.50 Matches: 68
Percent Similarity: 40.16% Conservative: 34
Best Local Similarity: 26.77% Mismatches: 102
Query Match: 7.23% Indels: 52
DB: 4 Gaps: 13

US-10-015-388A-54 (1-280) x US-09-902-540-4835 (1-2745)

Qy 75 SerTrpValSerGlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThr 94
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1445 ACCTGGACACCGCATGACGACGCGCGCGAGGTGGACGCGA-----ACGCGCGCT 1498
Qy 95 ThrThrThrSerLeuGlyAla-----GlnProSerGlnThr----- 106
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1499 GCAAGACGACGCGGTGAGCCCTGCTGTTGCGCGTCAACCTCGCGAGGCTGCGCGCACCC 1558
Qy 107 -----SerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhePhe-----HisAsn 121
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1559 GGCGGACCGCAGGGGAC-GAGGCGTGTCTGCGGAGGCGCCCTCACGTGGCGGCAACACAGC 1617
Qy 122 GlnPro-----ProSer-----LeuArgArgThrValGlu-----PheValAlaGlu 135
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1618 AACCCCATGCCAGGACGCGGTGTATGCCGTGTACGTGAGGGCGGCTTCTGCTGGAT 1677
Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAla----- 151
```

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Db 1678 TCCGACAGAGCCCGGGGCTGGCGCTGCTGGCGGAGACCATCACCGAGCGGAGGCATTG 1737
Qy |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
152 -----AspLeuValArgGlnAlaGluSerLeuGlnGluGlnLeuValThr 167
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1738 CCTCGGGAGATTCACTGGCGCGGAGCGCTGGGGGCTGAGCTATTCTGCTGCTGACG 1797
Qy 168 GlnGlyGluGlyGlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuCys 187
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1798 GACGCGGCAAGGCGGCGAGTACACCCAGCGCTTGGAGTTGATGGCGCGCAGCTTGCC 1857
Qy 188 ProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu-----PheCysGlnArgLysSerPro 206
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1858 ACGCCCGTGGCCCGAGCGCTGCGCCTTTCGCGCGGCTGATGCGAGCGAC-GGTGCT 1916
Qy 207 GlyAlaValArgAlaLeuLeuPro-----GluGluThrProAlaAlaVal 221
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1917 GGTGCGCGCGGAGCGCAAGCCAGGTGCTGGGCCACTACGAGACGGACCGCAGGGGCC 1976
Qy 222 LeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLys---AlaCysAlaTrp 240
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
1977 ATTCATCGCGCGACACCTCGCGCTGGTCCGATCGGCTGCTGAGGTGTTGCGTGG 2036
Qy 241 LeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLys----- 254
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
2037 CTGCGAGCGGTGAGCGTGTGCTGCGCGCCCGCTCTTCGCGCACACGACGACCTGTGCC 2096
Qy 255 -----AlaAlaValSerArgThrLeuArgAlaGlnGlyProGlu----- 267
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
2097 GCGGAGGTGCTGGAGCTTCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAC 2156
Qy 268 ---ProAlaAlaArgGlyGluArgArgGlyCysSerArgAla 280
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
2157 GGCGCGCGGCTGCTGCTCCAGCGTGGATGCGCGCGCT 2198

RESULT 13
US-09-902-540-1237/c
; Sequence 1237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1237
; LENGTH: 26659
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Alignment Scores:
Pred. No.: 13.4 Length: 26659
Score: 103.50 Matches: 68
Percent Similarity: 40.16% Conservative: 34
Best Local Similarity: 26.77% Mismatches: 102
Query Match: 7.23% Indels: 52
DB: 4 Gaps: 13

US-10-015-388A-54 (1-280) x US-09-902-540-1237 (1-26659)

Qy 75 SerTrpValSerGlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThr 94
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
20267 ACCTGGACACCGCATGACGACGCGCGCGAGGTGGACGCGA-----ACGCGCGCT 20214
Qy 95 ThrThrThrSerLeuGlyAla-----GlnProSerGlnThr----- 106
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
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Db 20213 GCAAGAACGACGCGTGTCTGTCGCGCTCAACCTCGCGAGTGTGTCGCGCACCC 20154
 QY 107 -----SerGluGlyLeuGlnAlaGlnLeuAlaGlnAlaPhe-----HisAla 121
 Db 20153 GCGCGAAGCCAGGGGAC-GAGCGGTGTGTCGCGCAGCGCCCTCACGTGGGCCCAACACACAGC 20095
 QY 122 GlnPro---ProSer-----LeuArgArgThrValGlu-----PheValAlaGlu 135
 Db 20094 AACCCCATGCCAGCAGCGCGGTGTATGCCGTTCAGTGTGAGGGCGCTTCTGTGTGAT 20035
 QY 136 ArgIleGlySerAsnCysValIysHisIleLysAlaThrLeuValAla----- 151
 Db 20034 TCCGACAGACCGCGGGGTGCGTGTCTGCGCGACACCATCATCAGCGCGGAGGATG 19975
 QY 152 -----AspLeuValArgGlnAlaGlnAlaGlnLeuGlnGlnLeuValThr 167
 Db 19974 CTCTGGGGAGATTCTCTGCGCGGAGGCGCTGGCGCTGAGTATTCGTCGCTGTCACG 19915
 QY 168 GlnGlyGluGlyGlyAspProAlaGlnLeuGluLeuLeuCysSerGlnLeuCys 187
 Db 19914 GACGCGGGCAAGCGCGGAGTACACCCAGGCGTTGGAGTTGATGGCGCGGAGCTTGGC 19855
 QY 188 ProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu-----PheCysGlnArgIysSerPro 206
 Db 19854 ACGCCGCTGCCCCACGCGCTGCGCCCTTGGCGGCGGCGTGCATGGCGAGCGAC-GGTGCT 19796
 QY 207 GlyAlaValArgAlaLeuLeuPro-----GluGluThrProAlaAlaVal 221
 Db 19795 GTTGGCGCGCGGAGCGACGAGCCAGGTGTGGGCCACTACGAGACGGACCGGAGGGGCC 19736
 QY 222 LeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGluLys---AlaCysAlaTrp 240
 Db 19735 ATTCTATCGCGCGGACACCTCGCGCTGTGTCGCGATCGGCTGCGTGGAGTGTTCGTTG 19676
 QY 241 LeuSerAlaAsnIleThrAlaLeuIleArgGluValLys----- 254
 Db 19675 CTGCGAGCGCGGAGCGTGTCTGTCGCGCGCGCTCTTTCGCGCACACGAGACCTGTTGCC 19616
 QY 255 -----AlaAlaValSerArgThrLeuArgAlaGlnGlyProGlu----- 267
 Db 19615 GCGGAGGTGCTCGAGCTTCGCGCTCGCGCGCACGCGCCGCGCGCACCGCCAC 19556
 QY 268 ---ProAlaAlaArgGlyGluArgGlyCysSerArgAla 280
 Db 19555 GCGCGCGCGGTGCTGCTCTCCAGCGTGTGATGCGCGCGCT 19514

RESULT 14

US-09-252-991A-8061/c
 ; Sequence 8061, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8061
 ; LENGTH: 1236
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8061

Alignment Scores:

Pred. No.:	0.117	Length:	1236
Score:	103.00	Matches:	74
Percent Similarity:	32.81%	Conservative:	31
Best Local Similarity:	23.12%	Mismatches:	114

Query Match: 7.19% Indels: 101
 Db: 4 Gaps: 15
 US-10-015-388A-54 (1-280) x US-09-252-991A-8061 (1-1236)

QY 29 LeuGluGluGlyProSerTyAlaPheGluValAlaAspThrValAlaProGluHisGlyLeu 48
 Db 1123 CTTGACGAGGCGCGGGGTTTCTTGGCGG-----CCTTGGCCCGACCGCGGGTCT 1073
 QY 49 AspAsnAlaProValAlaAspGlnLeuLeuTyThrCysCysProTyIleGlyGlu 68
 Db 1072 TCTTCGTGCGG-----CCGCGCGGCTTCG 1046
 QY 69 LeuArgIysLeuLeuAlaSerTrpValSerGly---SerSerGlyArgSerGlyGly--- 86
 Db 1045 CTTGCGCAGTTGCGCGGCGCATGCGCCAGTGGCGTTCGCGTGGCGGTCGCGGCGACGCCT 986
 QY 87 -----PheMetArgLysIleThrPro 93
 Db 985 CGGATTCACAGATCTGGTAGCGGAACTCTCGTATGCGTTCGTCGCGGCG----- 935
 QY 94 ThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGln 113
 Db 934 -----TCATGGGTGTCTCTCTGGCGGCGGCGGTAAGACAGGTTCACGGGAAA 887
 QY 114 LeuAlaGlnAlaPhePheHisAsnGlnProPro----- 124
 Db 886 GTGCGCGAGCACTTCGGACAGGCTCAGGTGCTGCTGGCGAGCGGATGTTGGAAAA 827
 QY 125 -----SerLeuArgArgThrValGluPheValAlaGlu 135
 Db 826 CAGCGCGGTGTGATTCGGAGAGACTCGGCGGCGAGCAGCAGCAGGTGTGCGCCCA 767
 QY 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeu---Val 154
 Db 766 GGCCTCGCG-----CGGCACCTGCGGTGCGTGGCGTGGCGAGCAGCGGCGCA 719
 QY 155 ArgGlnAlaGluSerLeuGlnGluGlnLeuValThrGlnGlyGlu---GluGlyGly 173
 Db 718 GCGCAGCGCGGAGCACACACAGCAGCAACCGTGACACTGCGCGCGGCGAGAGCGCAG 659
 QY 174 AspProAlaGlnLeuGluIle-LeuCysSerGlnLeuCysProHisGlyAlaGlnAl 193
 Db 658 GACCG-----CTCGGATGTCTGCGCGCTGACCTCCAGGGGCGAGGTATGTC 614
 QY 193 aLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGly-----AlaValArgAl 211
 Db 613 GCGCTCGCGGAACAGGCGCGCTGCTCCGCGCGAGCCCGCAGCACGCGCGGCGATCAGG 554
 QY 211 aLeuLeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValG 231
 Db 553 CTGCTTCATGCGA-----CGTTCGCGCCAGTGTCTCCAGCAGTTCGCGGAGGCGGTGCG 500
 QY 231 YLeuAlaThrGluLysAlaCys----- 238
 Db 499 GCGCGCAGCGCGCGCGCTGCGCGGCGAAAGTCCACCGCGCTCGCGTTCGCGGTTCGAC 440
 QY 239 -----AlaTrpLeuSerAlaAsnIleThrAlaLeuIleAr 250
 Db 439 CAGGCTGAAGTCCAGTCTCTGCGCGCCCTGATAGATCGGGGATACCCGCGGAGGTGAG 380
 QY 250 gArg-----GluValLysAlaAlaValSerArgThr----- 260
 Db 379 GCGCAGCAGGCATTTGGCGGAGGCATTCAGGGCGCGCGCGCGCATCATGTCGACCGCG 320
 QY 261 -LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgGlyCysSerArg 279
 Db 319 GTTGCCACGCACTGGCGGCGAGGCGCTGGGCGAGTGGCGCGGAGGAGTGTTCACGA 262

RESULT 15

US-09-252-991A-8202
 ; Sequence 8202, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8202
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8202

Alignment Scores:
Pred. No.: 0.371 Length: 2556
Score: 103.00 Matches: 74
Percent Similarity: 32.81% Conservative: 31
Best Local Similarity: 23.12% Mismatches: 114
Query Match: 7.19% Indels: 101
DB: 4 Gaps: 15

US-10-015-388a-54 (1-280) x US-09-252-991A-8202 (1-2556)

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Qy 29 LeuGluGluGlyProSerTyAlaPheGluValAspThrValAlaProGluHisGlyLeu 48
Db 160 CTTCGAGCAGCGCGGGGTTCTCTGCGG-----CCTTGGCCCGACCGGGGTCT 210
Qy 49 AspAenAlaProValValAspGlnGlnLeuLeuTyThrCysCysProTyrIleGlyGlu 68
Db 211 TCTTCGGTCCG-----CCCGCGGGCTCCG 237
Qy 69 LeuArgLysLeuLeuAlaSerTrpValSerGly---SerSerGlyArgSerGlyGly--- 86
Db 238 CTTCGGCCAGTTGCGCGGCCATGGCCAGTGGCGGTTCGGCTGGCGGTCGGCGGAGCCCT 297
Qy 87 -----PheMetArgLysIleThrPro 93
Db 298 CGGATTCACAGACTGGTAGGCGAACTCTGTAATCGTTTTCGTGCGGCG----- 348
Qy 94 ThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGln 113
Db 349 -----TCATGGGGTCTCTCTGGCGAGGCGGTAAAGCAGGTTGACGGGAAA 396
Qy 114 LeuAlaGlnAlaPhePheHisGlnProPro----- 124
Db 397 GTCGGCGAGCACTTCGGACAGGCTCAGGTGCCCGTGGCGAGCGGCGATGGTGGA AAA 456
Qy 125 -----SerLeuArgArgThrValGluPheValAlaGlu 135
Db 457 CAGCGCGCTGAGTGTCATTCCGAGAGACTCGCGCGGACGACGACGAGGTTGCGCCCA 516
Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeu---Val 154
Db 517 GCCTTCGGC-----CGGCACCTGGCGTGGCGTGGCGGCGGCGAGCGGCGCA 564
Qy 155 ArgGlnAlaGluSerLeuLeuGlnGlnGlnLeuValThrGlnGlyGlu---GluGlyGly 173
Db 565 GGCCAGGCGCGGACCAACCAGCAGCAACCGTGACGACTGGCGCGGGCGAAGGCCAG 624
Qy 174 AspProAlaGlnLeuLeuGluIle-LeuCysSerGlnLeuCysProHisGlyAlaGlnAl 193
Db 625 GACCG-----CTCGGCATGCTCGCGCTGACCTCCAGGGGCGAGGTAGTC 669
Qy 193 aLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGly-----AlaValArgAl 211
Db 670 GCCGTGGCGAACAGCCCGGCTGATCCCGCGAGCCCGACGACGCGGGCGGATCAGGGT 729
Qy 211 aLeuLeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValGl 231
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Db 730 CTGCTTGATGCGA-----CGTCCGCCAGTCTCCAGCAGTTCCGGGAGGGCGTCGG 783
Qy 231 yLeuAlaThrGluLysAlaCys----- 238
Db 784 CGCGCCAGGCGGGCGGTGCGGGGGAAGTCCACCGGCTCCGGTTGTCCGGGTGAC 843
Qy 239 -----AlaTrpLeuSerAlaAsnIleThrAlaLeuIleAr 250
Db 844 CAGGCTGAAGTCCCACTCTCGCGCCCTGTGTAGAGATCGGGGATACCGGGCAGGTCA 903
Qy 250 gArg-----GluValLysAlaAlaValSerArgThr----- 260
Db 904 GCGCAGCAGGCAATTGGGCGAGGCCATTCCAGGGCCCCCGGCGCATCAGTCGCACCGCC 963
Qy 261 -LeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgArgGlyCysSerArg 279
Db 964 GTTGGCCAGCACTGGCGCAGGGCTGGGCCAGTGGCGCGCGCAGGAGCTGTTCCAGA 1021
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Search completed: March 29, 2005, 12:39:38
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GenCore version 5.1.6
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3202.712 Million cell updates/sec

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Maximum Match 100%

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SUMMARIES

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c 68	112	7.8	17761	9	US-09-764-847-1596	Sequence 1596, Ap
c 69	112	7.8	17761	14	US-10-092-154-1596	Sequence 1596, Ap
70	111.5	7.8	1104	17	US-10-282-122A-28537	Sequence 28537, A
71	111.5	7.8	1104	18	US-10-481-265-42	Sequence 42, Appl
72	111.5	7.8	1107	17	US-10-282-122A-28487	Sequence 28487, A
73	109	7.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 74	108.5	7.6	1457	9	US-09-954-531-982	Sequence 982, App
c 75	107.5	7.5	1678	16	US-10-240-365-119	Sequence 119, App
76	105.5	7.4	1664	18	US-10-723-860-5164	Sequence 5164, Ap
77	104.5	7.3	1122	15	US-10-156-761-5336	Sequence 5336, Ap
c 78	104.5	7.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
79	103.5	7.2	2054	18	US-10-425-115-163963	Sequence 163963,
80	103	7.2	1594	17	US-10-425-114-32954	Sequence 32954, A
c 81	102.5	7.2	1467	17	US-10-062-674-1950	Sequence 1950, Ap
c 82	102	7.1	1101	17	US-10-369-493-39041	Sequence 39041, A
c 83	102	7.1	1104	17	US-10-369-493-39408	Sequence 39408, A
c 84	102	7.1	1374	17	US-10-369-493-39794	Sequence 39794, A
85	102	7.1	1649	17	US-10-425-114-26399	Sequence 26399, A
c 86	102	7.1	2031	15	US-10-156-761-2451	Sequence 2451, Ap
c 87	101.5	7.1	1182	15	US-10-156-761-6347	Sequence 6347, Ap
88	101.5	7.1	3400	17	US-10-464-368-11	Sequence 11, Appl
c 89	101.5	7.1	7099	18	US-10-311-490A-3	Sequence 3, Appli
c 90	101.5	7.1	9301	16	US-10-384-893-18	Sequence 18, Appl
91	101.5	7.1	9301	17	US-10-463-190-18	Sequence 18, Appl
92	101.5	7.1	9301	17	US-10-095-248A-18	Sequence 18, Appl
93	101.5	7.1	9301	18	US-10-788-606-18	Sequence 18, Appl
94	101.5	7.1	21501	17	US-10-377-315-1	Sequence 1, Appli
c 95	101.5	7.1	94752	17	US-10-408-168-34	Sequence 34, Appl
c 96	101.5	7.1	130320	17	US-10-408-168-1	Sequence 1, Appli
c 97	101	7.1	1810	19	US-09-814-353-19133	Sequence 19133, A
c 98	101	7.1	2064	19	US-10-741-600-440	Sequence 440, App
99	101	7.1	2064	19	US-10-741-600-439	Sequence 439, App
c 100	100.5	7.0	5408	16	US-10-252-157-491	Sequence 491, App
c 101	100	7.0	1664	18	US-10-739-930-58	Sequence 58, Appl
c 102	100	7.0	2285	17	US-10-715-872-38	Sequence 38, Appl
c 103	100	7.0	6825	18	US-10-367-502-156	Sequence 156, App
104	100	7.0	10692	15	US-10-156-761-414	Sequence 414, App
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c 107	99.5	6.9	1706	17	US-10-425-114-17275	Sequence 17275, A
c 108	99.5	6.9	1756	18	US-10-425-115-138078	Sequence 138078,
c 109	99.5	6.9	1800	10	US-09-771-357-106	Sequence 106, App
c 110	99.5	6.9	1800	15	US-10-059-579-106	Sequence 106, App
c 111	99.5	6.9	2870	18	US-10-723-860-501	Sequence 501, App
c 112	99.5	6.9	7057	17	US-10-302-172-112	Sequence 112, App
c 113	99.5	6.9	27189	13	US-10-087-192-1828	Sequence 1828, Ap
c 114	98.5	6.9	2922	15	US-10-156-761-1749	Sequence 1749, Ap
c 115	98.5	6.9	2256646	18	US-10-470-565-1	Sequence 1, Appli
c 116	98	6.8	888	15	US-10-156-761-2771	Sequence 2771, Ap
c 117	98	6.8	1204	9	US-09-822-849A-22	Sequence 22, Appl
c 118	98	6.8	1493	17	US-10-172-118-757	Sequence 757, App
c 119	98	6.8	1493	17	US-10-340-425-1328	Sequence 1328, Ap
c 120	98	6.8	1493	17	US-10-342-887-757	Sequence 757, App
c 121	98	6.8	1493	18	US-10-472-516-3	Sequence 3, Appli
c 122	98	6.8	3222	18	US-10-437-963-8258	Sequence 8258, Ap
c 123	97.5	6.8	609	16	US-10-029-386-22740	Sequence 22740, A
c 124	97.5	6.8	1308	17	US-10-425-114-24302	Sequence 24302, A
c 125	97.5	6.8	1636	18	US-10-425-115-54996	Sequence 54996, A
c 126	97.5	6.8	11220	9	US-09-861-289-32	Sequence 32, Appl
c 127	97.5	6.8	11220	9	US-09-860-846-32	Sequence 32, Appl
c 128	97.5	6.8	11220	10	US-09-988-384B-32	Sequence 32, Appl
c 129	97.5	6.8	11220	10	US-09-836-821-32	Sequence 32, Appl
c 130	97.5	6.8	11220	16	US-10-271-889-32	Sequence 32, Appl
c 131	97.5	6.8	36778	9	US-09-861-289-5	Sequence 5, Appli
c 132	97.5	6.8	36778	9	US-09-860-846-5	Sequence 5, Appli
c 133	97.5	6.8	36778	10	US-09-836-821-5	Sequence 5, Appli
c 134	97.5	6.8	36778	16	US-10-271-889-48	Sequence 48, Appl
c 135	97.5	6.8	37948	10	US-09-988-384B-5	Sequence 5, Appli

C 136	97.5	6.8	38506	10	US-09-793-708-19	Sequence 19, Appl	209	94	6.6	1460	17	US-10-425-114-5256	Sequence 5256, Ap
C 137	97.5	6.8	38506	15	US-10-201-365-1	Sequence 1, Appl	210	94	6.6	1832	17	US-10-425-114-2852	Sequence 2852, Ap
C 138	97.5	6.8	38506	16	US-10-160-539-19	Sequence 19, Appl	211	94	6.6	1832	17	US-10-425-114-2852	Sequence 2852, Ap
C 139	97.5	6.8	38506	19	US-10-468-828-19	Sequence 19, Appl	212	94	6.6	2170	18	US-10-425-115-161538	Sequence 161538, A
C 140	97	6.8	1347	17	US-10-282-122A-14155	Sequence 14155, A	C 213	94	6.6	2215	17	US-10-282-122A-33208	Sequence 33208, A
C 141	97	6.8	1499	17	US-10-131-410-4	Sequence 4, Appl	214	94	6.6	3118	18	US-10-425-115-104412	Sequence 104412, A
C 142	97	6.8	1938	15	US-10-156-761-4392	Sequence 4392, Ap	215	94	6.6	4248	17	US-10-282-122A-30505	Sequence 30505, A
C 143	97	6.8	3120	15	US-10-207-655-1036	Sequence 106, App	216	94	6.6	5159	17	US-10-334-143-111	Sequence 111, App
C 144	97	6.8	3120	18	US-10-717-597-84	Sequence 84, Appl	C 217	94	6.6	20311	18	US-10-719-993-7068	Sequence 7068, Ap
C 145	97	6.8	3223	18	US-10-742-661-9	Sequence 9, Appl	C 218	93.5	6.5	1078	18	US-10-767-701-658	Sequence 658, App
C 146	97	6.8	3223	18	US-10-742-372-9	Sequence 9, Appl	C 219	93.5	6.5	1224	18	US-10-437-963-21764	Sequence 21764, A
C 147	97	6.8	3223	18	US-10-646-308-3	Sequence 3, Appl	C 220	93.5	6.5	1284	15	US-10-156-761-3832	Sequence 3832, Ap
C 148	97	6.8	7438	16	US-10-359-050-11	Sequence 11, Appl	C 221	93.5	6.5	1495	17	US-10-425-114-20830	Sequence 20830, A
C 149	97	6.8	7438	17	US-10-014-099F-5	Sequence 5, Appl	C 222	93.5	6.5	1553	18	US-10-425-115-52255	Sequence 52255, A
C 150	97	6.8	7523	17	US-10-014-099F-79	Sequence 79, Appl	C 223	93.5	6.5	3542	15	US-10-037-270-233	Sequence 233, App
C 151	97	6.8	7608	17	US-10-014-099F-78	Sequence 78, Appl	C 224	93.5	6.5	3542	17	US-10-117-722-233	Sequence 233, App
C 152	97	6.8	7803	17	US-10-014-099F-82	Sequence 82, Appl	C 225	93.5	6.5	3768	15	US-10-156-761-2190	Sequence 2190, Ap
C 153	97	6.8	8167	17	US-10-014-099F-83	Sequence 83, Appl	C 226	93.5	6.5	5630	9	US-09-871-388-1	Sequence 1, Appl
C 154	97	6.8	20574	18	US-10-719-993-7067	Sequence 7067, Ap	C 227	93.5	6.5	17596	18	US-10-611-442-2	Sequence 2, Appl
C 155	97	6.8	30624	18	US-10-719-993-6888	Sequence 6888, Ap	C 228	93	6.5	1119	15	US-10-156-761-4303	Sequence 4303, Ap
C 156	96.5	6.7	969	17	US-10-260-238-5454	Sequence 5454, Ap	C 229	93	6.5	1909	17	US-10-112-944-172	Sequence 172, App
C 157	96.5	6.7	1263	15	US-10-156-761-2071	Sequence 2071, Ap	C 230	93	6.5	2211	18	US-10-437-963-63253	Sequence 63253, A
C 158	96.5	6.7	3278	17	US-10-094-749-1011	Sequence 1011, Ap	C 231	93	6.5	46338	18	US-10-322-281-595	Sequence 595, App
C 159	96.5	6.7	3291	17	US-10-418-861B-60	Sequence 60, Appl	C 232	93	6.5	88421	9	US-09-997-722-64	Sequence 64, Appl
C 160	96	6.7	1433	16	US-10-029-386-20893	Sequence 20893, A	C 233	93	6.5	88421	9	US-09-976-059-1	Sequence 1, Appl
C 161	96	6.7	1458	16	US-10-029-386-20288	Sequence 20288, A	C 234	93	6.5	137560	18	US-10-481-112-1	Sequence 1, Appl
C 162	96	6.7	1813	10	US-09-993-731-11	Sequence 11, Appl	C 235	92.5	6.5	1224	18	US-10-767-701-12453	Sequence 12453, A
C 163	96	6.7	1813	17	US-10-641-643-1471	Sequence 1471, Ap	C 236	92.5	6.5	1284	18	US-10-425-115-30454	Sequence 30454, A
C 164	96	6.7	1831	17	US-10-282-122A-19371	Sequence 19371, A	C 237	92.5	6.5	2766	17	US-10-369-493-37700	Sequence 37700, A
C 165	96	6.7	2661	16	US-10-252-157-472	Sequence 472, App	C 238	92.5	6.5	2787	18	US-10-437-963-41070	Sequence 41070, A
C 166	96	6.7	2678	9	US-09-964-824A-252	Sequence 252, App	C 239	92.5	6.5	2858	13	US-10-087-192-1307	Sequence 1307, Ap
C 167	96	6.7	2678	17	US-10-305-720-1229	Sequence 1229, Ap	C 240	92.5	6.5	2880	18	US-10-425-115-113929	Sequence 113929, A
C 168	96	6.7	77294	19	US-10-729-802-1	Sequence 1, Appl	C 241	92.5	6.5	3111	18	US-10-425-115-114937	Sequence 114937, A
C 169	95.5	6.7	945	18	US-10-437-963-92374	Sequence 92374, A	C 242	92.5	6.5	3227	13	US-10-027-632-115536	Sequence 115536, A
C 170	95.5	6.7	1011	15	US-10-146-772-345	Sequence 345, App	C 243	92.5	6.5	3227	13	US-10-027-632-115536	Sequence 115536, A
C 171	95.5	6.7	1011	17	US-10-241-742-345	Sequence 345, App	C 244	92.5	6.5	3389	15	US-10-224-356-12	Sequence 12, Appl
C 172	95.5	6.7	1011	17	US-10-440-523-345	Sequence 345, App	C 245	92.5	6.5	3493	17	US-10-112-944-77	Sequence 77, Appl
C 173	95.5	6.7	1011	17	US-10-440-523-345	Sequence 345, App	C 246	92.5	6.5	3750	17	US-10-389-647-147	Sequence 147, App
C 174	95.5	6.7	1011	17	US-10-461-925-345	Sequence 345, App	C 247	92.5	6.5	4551	15	US-10-156-761-7163	Sequence 7163, Ap
C 175	95.5	6.7	1372	18	US-10-437-963-97239	Sequence 97239, A	C 248	92.5	6.5	5166	18	US-10-425-115-114965	Sequence 114965, A
C 176	95.5	6.7	1687	18	US-10-767-701-13851	Sequence 13851, A	C 249	92.5	6.5	20478	13	US-10-087-192-1306	Sequence 1306, Ap
C 177	95.5	6.7	2493	17	US-10-282-122A-25747	Sequence 25747, A	C 250	92.5	6.5	21185	18	US-10-159-257A-2	Sequence 2, Appl
C 178	95.5	6.7	2940	15	US-10-156-761-3172	Sequence 3172, Ap	C 251	92.5	6.5	50552	16	US-10-719-993-6905	Sequence 6905, Ap
C 179	95.5	6.7	64492	17	US-10-378-083-1	Sequence 1, Appl	C 252	92.5	6.5	63158	18	US-10-392-198-1	Sequence 1, Appl
C 180	95	6.6	875	16	US-10-029-386-20568	Sequence 20568, A	C 253	92.5	6.5	86941	17	US-10-461-194-2	Sequence 2, Appl
C 181	95	6.6	957	11	US-09-758-759-88	Sequence 88, Appl	C 254	92.5	6.5	493999	18	US-10-719-993-6787	Sequence 6787, Ap
C 182	95	6.6	1534	18	US-10-425-115-67410	Sequence 67410, A	C 255	92.5	6.5	786431	16	US-10-412-277-3	Sequence 3, Appl
C 183	95	6.6	1950	18	US-10-767-701-15092	Sequence 15092, A	C 256	92	6.4	1321	17	US-10-428-275-77	Sequence 77, Appl
C 184	95	6.6	2612	18	US-10-425-115-116024	Sequence 116024, A	C 257	92	6.4	1469	17	US-10-425-114-31292	Sequence 31292, A
C 185	95	6.6	5960	17	US-10-172-118-16	Sequence 16, Appl	C 258	92	6.4	1608	17	US-10-282-122A-30209	Sequence 30209, A
C 186	95	6.6	5960	17	US-10-342-887-16	Sequence 16, Appl	C 259	92	6.4	1608	17	US-10-389-647-178	Sequence 178, App
C 187	95	6.6	6075	17	US-10-161-927-7	Sequence 7, Appl	C 260	92	6.4	1644	18	US-10-425-115-14950	Sequence 14950, A
C 188	95	6.6	13766	16	US-10-105-616-1	Sequence 1, Appl	C 261	92	6.4	1881	17	US-10-420-988-52	Sequence 52, Appl
C 189	95	6.6	17493	19	US-10-211-028-10	Sequence 10, Appl	C 262	92	6.4	2094	17	US-10-369-493-43107	Sequence 43107, A
C 190	95	6.6	30000	11	US-09-980-217-3	Sequence 3, Appl	C 263	92	6.4	2224	17	US-10-104-047-1325	Sequence 1325, App
C 191	95	6.6	68750	13	US-10-014-717-1	Sequence 1, Appl	C 264	92	6.4	2646	15	US-10-156-761-139	Sequence 139, App
C 192	95	6.6	90597	19	US-10-211-028-1	Sequence 1, Appl	C 265	92	6.4	2973	15	US-10-156-761-2660	Sequence 2660, Ap
C 193	95	6.6	90597	19	US-10-211-028-1	Sequence 1, Appl	C 266	92	6.4	3029	17	US-10-108-260A-1476	Sequence 1476, Ap
C 194	95	6.6	109519	11	US-09-758-759-1	Sequence 1, Appl	C 267	92	6.4	2452	9	US-09-764-868-1487	Sequence 1487, Ap
C 195	94.5	6.6	640	17	US-10-424-599-52734	Sequence 52734, A	C 268	92	6.4	22452	9	US-09-764-868-1489	Sequence 1489, Ap
C 196	94.5	6.6	1050	9	US-09-955-597-20	Sequence 20, Appl	C 269	92	6.4	22783	10	US-09-990-613-6	Sequence 6, Appl
C 197	94.5	6.6	1607	18	US-10-425-115-58267	Sequence 58267, A	C 270	91.5	6.4	820	13	US-10-425-115-170178	Sequence 179178, A
C 198	94.5	6.6	1629	17	US-10-282-122A-14086	Sequence 14086, A	C 271	91.5	6.4	956	13	US-10-087-192-506	Sequence 506, App
C 199	94.5	6.6	2286	17	US-10-282-122A-33104	Sequence 33104, A	C 272	91.5	6.4	1113	18	US-10-437-963-84153	Sequence 84153, A
C 200	94.5	6.6	7033	18	US-10-678-816-5	Sequence 5, Appl	C 273	91.5	6.4	1174	18	US-10-437-963-38585	Sequence 38585, A
C 201	94.5	6.6	12523	9	US-09-955-597-1	Sequence 1, Appl	C 274	91.5	6.4	1182	18	US-10-425-115-153333	Sequence 153333, A
C 202	94.5	6.6	12523	9	US-09-955-597-1	Sequence 1, Appl	C 275	91.5	6.4	1187	18	US-10-739-930-2475	Sequence 2475, Ap
C 203	94.5	6.6	88624	16	US-10-292-081A-1	Sequence 1, Appl	C 276	91.5	6.4	1285	18	US-10-425-115-171088	Sequence 171088, A
C 204	94.5	6.6	88624	17	US-10-608-397-1	Sequence 1, Appl	C 277	91.5	6.4	1425	17	US-10-282-122A-37790	Sequence 37790, A
C 205	94.5	6.6	1900090	18	US-10-719-993-6815	Sequence 6815, Ap	C 278	91.5	6.4	1623	17	US-10-437-963-2083	Sequence 2083, Ap
C 206	94.5	6.6	1980090	19	US-10-741-600-17676	Sequence 17676, A	C 279	91.5	6.4	2792	17	US-10-104-047-458	Sequence 458, App
C 207	94	6.6	1026	15	US-10-156-761-4890	Sequence 4890, Ap	C 280	91.5	6.4	3044	17	US-10-108-260A-938	Sequence 938, App
C 208	94	6.6	1339	17	US-10-425-114-35313	Sequence 35313, A	C 281	91.5	6.4	3073	18	US-10-479-435-39	Sequence 39, Appl

282	91.5	6.4	3393	15	US-10-224-356-14	Sequence 14, Appl	C 355	90	6.3	2055	17	US-10-389-647-125	Sequence 125, App
283	91.5	6.4	3393	15	US-10-224-356-15	Sequence 15, Appl	C 356	90	6.3	2442	17	US-10-369-493-40548	Sequence 40548, A
C 284	91.5	6.4	7140	19	US-10-211-028-3	Sequence 3, Appl	C 357	90	6.3	2694	14	US-10-050-704-40	Sequence 40, Appl
C 285	91.5	6.4	8321	16	US-10-329-079-17	Sequence 17, Appl	C 358	90	6.3	2694	17	US-10-798-512-40	Sequence 40, Appl
C 286	91.5	6.4	20956	13	US-10-087-192-505	Sequence 505, App	C 359	90	6.3	2878	17	US-10-453-420-7	Sequence 7, Appl
C 287	91.5	6.4	23580	9	US-09-764-860-990	Sequence 990, App	C 360	90	6.3	2878	17	US-10-295-027-259	Sequence 259, App
C 288	91.5	6.4	23580	14	US-10-074-095-990	Sequence 990, App	C 361	90	6.3	3090	15	US-10-156-761-7457	Sequence 7457, App
C 289	91.5	6.4	23580	17	US-10-212-872-990	Sequence 990, App	C 362	90	6.3	7282	15	US-10-213-948-11	Sequence 11, Appl
C 290	91.5	6.4	72069	19	US-10-741-600-17775	Sequence 17775, A	C 363	90	6.3	59816	17	US-10-084-846A-1	Sequence 1, Appl
C 291	91.5	6.4	86080	18	US-10-450-826-71	Sequence 71, Appl	C 364	90	6.3	59816	17	US-10-084-846A-2	Sequence 2, Appl
C 292	91.5	6.4	86080	18	US-10-723-860-1697	Sequence 1697, App	C 365	90	6.3	59855	13	US-10-087-192-664	Sequence 664, App
C 293	91	6.4	748	18	US-10-425-115-2506	Sequence 2506, App	C 366	90	6.3	94001	17	US-10-210-838-20	Sequence 20, Appl
C 294	91	6.4	866	18	US-10-437-963-92621	Sequence 92621, App	C 367	90	6.3	536165	10	US-09-339-964-1	Sequence 1, Appl
C 295	91	6.4	1113	17	US-10-282-122A-25330	Sequence 25330, A	C 368	90	6.3	618	17	US-10-425-114-15293	Sequence 1, Appl
C 296	91	6.4	1171	18	US-10-739-930-4421	Sequence 4421, App	C 369	89.5	6.2	688	18	US-10-437-963-71008	Sequence 71008, A
C 297	91	6.4	1315	17	US-10-425-114-19238	Sequence 19238, A	C 370	89.5	6.2	843	15	US-10-156-761-5578	Sequence 5578, App
C 298	91	6.4	1538	18	US-10-425-115-20700	Sequence 20700, A	C 371	89.5	6.2	854	18	US-10-425-115-25512	Sequence 25512, A
C 299	91	6.4	1555	18	US-10-767-701-11840	Sequence 11840, A	C 372	89.5	6.2	1145	18	US-10-425-115-136719	Sequence 136719, A
C 300	91	6.4	1590	16	US-10-271-889-1	Sequence 1, Appl	C 373	89.5	6.2	1227	17	US-10-458-201-23	Sequence 23, Appl
C 301	91	6.4	1713	18	US-10-425-115-58909	Sequence 58909, A	C 374	89.5	6.2	1374	17	US-10-236-417-7	Sequence 7, Appl
C 302	91	6.4	1727	18	US-10-437-963-10917	Sequence 10917, A	C 375	89.5	6.2	1422	19	US-10-472-928-2227	Sequence 2227, App
C 303	91	6.4	1807	17	US-10-425-114-28103	Sequence 28103, A	C 376	89.5	6.2	1468	9	US-09-822-830A-34	Sequence 34, Appl
C 304	91	6.4	1943	18	US-10-425-115-122168	Sequence 122168, A	C 377	89.5	6.2	1470	18	US-10-474-776-506	Sequence 506, App
C 305	91	6.4	2064	17	US-10-282-122A-11588	Sequence 11588, A	C 378	89.5	6.2	1527	17	US-10-425-114-5462	Sequence 5462, App
C 306	91	6.4	2088	18	US-10-425-115-46920	Sequence 46920, A	C 379	89.5	6.2	1590	17	US-08-961-527-184	Sequence 184, App
C 307	91	6.4	2367	17	US-10-104-047-1297	Sequence 1297, App	C 380	89.5	6.2	1624	18	US-10-158-844-184	Sequence 184, App
C 308	91	6.4	2997	13	US-10-106-534-3	Sequence 3, Appl	C 381	89.5	6.2	1637	19	US-10-425-115-28237	Sequence 28237, A
C 309	91	6.4	3144	18	US-10-437-963-82347	Sequence 82347, A	C 382	89.5	6.2	1637	18	US-10-211-028-20	Sequence 20, Appl
C 310	91	6.4	3158	13	US-10-106-534-1	Sequence 1, Appl	C 383	89.5	6.2	1767	18	US-10-437-963-4185	Sequence 4185, App
C 311	91	6.4	3241	17	US-10-108-260A-937	Sequence 937, App	C 384	89.5	6.2	3003	9	US-09-820-155-1	Sequence 1, Appl
C 312	91	6.4	3255	19	US-10-660-811A-17	Sequence 17, Appl	C 385	89.5	6.2	3054	18	US-10-437-963-82264	Sequence 82264, A
C 313	91	6.4	4257	15	US-10-161-403-30	Sequence 30, Appl	C 386	89.5	6.2	3117	17	US-10-188-248-39	Sequence 39, Appl
C 314	91	6.4	4257	18	US-10-161-408-22	Sequence 22, Appl	C 387	89.5	6.2	4320	15	US-10-156-761-595	Sequence 595, App
C 315	91	6.4	4346	15	US-10-161-403-113	Sequence 113, App	C 388	89.5	6.2	4320	15	US-10-161-403-88	Sequence 88, Appl
C 316	91	6.4	4346	18	US-10-161-408-26	Sequence 26, App	C 389	89.5	6.2	5754	18	US-10-437-963-59723	Sequence 59723, A
C 317	91	6.4	4608	17	US-10-172-118-14	Sequence 14, Appl	C 390	89.5	6.2	6280	18	US-10-672-764A-64	Sequence 64, Appl
C 318	91	6.4	4608	17	US-10-342-887-14	Sequence 14, Appl	C 391	89.5	6.2	6502	18	US-10-672-764A-41	Sequence 41, Appl
C 319	91	6.4	52101	16	US-10-132-134-13	Sequence 13, Appl	C 392	89.5	6.2	9249	17	US-10-389-120-2	Sequence 2, Appl
C 320	91	6.4	84830	19	US-10-132-134-1	Sequence 1, Appl	C 393	89.5	6.2	15120	17	US-10-458-201-1	Sequence 1, Appl
C 321	91	6.4	84830	19	US-10-660-811A-2	Sequence 2, Appl	C 394	89.5	6.2	26173	14	US-10-114-170-69	Sequence 69, Appl
C 322	90.5	6.3	1017	15	US-10-146-772-283	Sequence 283, App	C 395	89.5	6.2	53799	19	US-10-042-665A-3	Sequence 3, Appl
C 323	90.5	6.3	1017	17	US-10-241-742-283	Sequence 283, App	C 396	89.5	6.2	2162598	19	US-10-472-928-4979	Sequence 4979, App
C 324	90.5	6.3	1017	17	US-10-440-523-283	Sequence 283, App	C 397	89.5	6.2	2731748	18	US-10-297-465A-1	Sequence 1, Appl
C 325	90.5	6.3	1017	17	US-10-440-503-283	Sequence 283, App	C 398	89	6.2	1164	15	US-10-156-761-2298	Sequence 2298, App
C 326	90.5	6.3	1017	17	US-10-461-925-283	Sequence 283, App	C 399	89	6.2	1370	17	US-10-437-963-82464	Sequence 82464, A
C 327	90.5	6.3	1170	18	US-10-425-115-162747	Sequence 162747, A	C 400	89	6.2	1370	17	US-10-425-114-35579	Sequence 35579, A
C 328	90.5	6.3	1179	17	US-10-369-493-24240	Sequence 24240, A	C 401	89	6.2	1407	17	US-10-369-493-41593	Sequence 41593, A
C 329	90.5	6.3	1248	17	US-10-369-493-32441	Sequence 32441, A	C 402	89	6.2	1459	18	US-10-425-115-124308	Sequence 124308, A
C 330	90.5	6.3	1426	18	US-10-437-963-34832	Sequence 34832, A	C 403	89	6.2	1720	18	US-10-437-963-31539	Sequence 31539, A
C 331	90.5	6.3	2268	18	US-10-437-963-39626	Sequence 39626, A	C 404	89	6.2	1827	18	US-10-411-910A-211	Sequence 211, App
C 332	90.5	6.3	2853	18	US-10-425-115-172942	Sequence 172942, A	C 405	89	6.2	2193	18	US-10-425-115-114963	Sequence 114963, A
C 333	90.5	6.3	2960	18	US-10-483-512-71	Sequence 71, Appl	C 406	89	6.2	2351	17	US-10-425-114-2510	Sequence 2510, App
C 334	90.5	6.3	9272	18	US-10-723-860-1784	Sequence 1784, App	C 407	89	6.2	2407	18	US-10-437-963-59093	Sequence 59093, A
C 335	90.5	6.3	9287	10	US-09-960-706-633	Sequence 633, App	C 408	89	6.2	2684	18	US-10-425-115-137279	Sequence 137279, A
C 336	90.5	6.3	9287	10	US-09-873-319-396	Sequence 396, App	C 409	89	6.2	2713	17	US-10-015-115-17	Sequence 17, Appl
C 337	90.5	6.3	9456	18	US-10-723-860-6147	Sequence 6147, App	C 410	89	6.2	3318	17	US-10-369-493-44592	Sequence 44592, A
C 338	90.5	6.3	18435	15	US-10-156-761-412	Sequence 412, App	C 411	89	6.2	3438	17	US-10-312-352-60	Sequence 60, Appl
C 339	90.5	6.3	34875	18	US-10-775-169-316	Sequence 316, App	C 412	89	6.2	3470	16	US-10-209-059-25	Sequence 25, Appl
C 340	90.5	6.3	48908	14	US-10-114-170-137	Sequence 137, App	C 413	89	6.2	3470	17	US-10-627-132-25	Sequence 25, Appl
C 341	90.5	6.3	85915	18	US-10-647-196-1	Sequence 1, Appl	C 422	89	6.2	3476	14	US-10-237-535-51	Sequence 51, Appl
C 342	90.5	6.3	100000	15	US-10-156-761-15103	Sequence 15103, A	C 431	89	6.2	3476	14	US-10-239-196-51	Sequence 51, Appl
C 343	90.5	6.3	276820	17	US-10-271-416-9	Sequence 9, Appl	C 522	89	6.2	3699	17	US-10-362-571-7	Sequence 7, Appl
C 344	90	6.3	507	18	US-10-437-963-73604	Sequence 73604, A	C 523	89	6.2	5468	17	US-10-363-616-69	Sequence 69, Appl
C 345	90	6.3	813	18	US-10-425-115-104528	Sequence 104528, A	C 524	89	6.2	7095	15	US-10-156-761-7340	Sequence 7340, App
C 346	90	6.3	1097	17	US-10-425-115-12442	Sequence 12442, A	C 525	89	6.2	8009	10	US-09-373-658-34	Sequence 34, Appl
C 347	90	6.3	1099	17	US-10-425-114-1540	Sequence 1540, App	C 526	89	6.2	8009	11	US-09-989-687-34	Sequence 34, Appl
C 348	90	6.3	1188	18	US-10-437-963-48852	Sequence 48852, A	C 527	89	6.2	12951	17	US-10-282-122A-31678	Sequence 31678, A
C 349	90	6.3	1195	15	US-10-304-928-7	Sequence 7, Appl	C 528	89	6.2	73467	9	US-09-740-026-3	Sequence 3, Appl
C 350	90	6.3	1212	17	US-10-282-122A-11640	Sequence 11640, A	C 529	89	6.2	73467	14	US-10-237-859-3	Sequence 3, Appl
C 351	90	6.3	1240	18	US-10-425-115-43278	Sequence 43278, A	C 530	89	6.2	135638	16	US-10-314-657-1	Sequence 1, Appl
C 352	90	6.3	1422	17	US-10-389-647-347	Sequence 347, App	C 531	88.5	6.2	657	10	US-09-814-353-14012	Sequence 14012, A
C 353	90	6.3	1874	18	US-10-437-963-44429	Sequence 44429, A	C 532	88.5	6.2	918	17	US-10-369-493-44153	Sequence 44153, A
C 354	90	6.3	1976	17	US-10-425-114-660	Sequence 660, App	C 533	88.5	6.2	1123	18	US-10-425-115-70246	Sequence 70246, A

680	6.1	5465	10	US-09-965-738-81	Sequence 81, Appl	753	86.5	6.0	2388	18	US-10-425-115-114141	Sequence 114141,
681	6.1	5802	14	US-10-152-886-84	Sequence 84, Appl	c 754	86.5	6.0	2394	15	US-10-156-761-11	Sequence 11, Appl
682	6.1	5960	10	US-09-798-883B-14	Sequence 14, Appl	755	86.5	6.0	2484	17	US-10-264-049-752	Sequence 752, Appl
683	6.1	5960	10	US-09-326-885-14	Sequence 14, Appl	756	86.5	6.0	2486	15	US-10-106-698-11989	Sequence 1989, Appl
684	6.1	5967	17	US-10-120-988-405	Sequence 405, Appl	757	86.5	6.0	2655	17	US-10-369-493-31990	Sequence 31990, A
c 685	6.1	38764	11	US-09-997-722-286	Sequence 286, Appl	758	86.5	6.0	2655	18	US-10-723-860-5461	Sequence 5461, Appl
686	6.1	40668	18	US-10-450-826-57	Sequence 57, Appl	759	86.5	6.0	2709	9	US-09-922-199A-3	Sequence 3, Appl
687	6.1	57082	18	US-10-715-066-1	Sequence 1, Appl	760	86.5	6.0	2772	18	US-10-425-115-93681	Sequence 93681, A
688	6.1	66765	18	US-10-715-066-4	Sequence 4, Appl	761	86.5	6.0	2811	18	US-10-437-963-35886	Sequence 35886, A
689	6.1	117985	18	US-10-719-993-7053	Sequence 7053, Appl	c 762	86.5	6.0	3094	9	US-09-925-297-320	Sequence 290, Appl
c 690	6.1	158001	17	US-10-211-179-11	GENERAL INFORMATI	763	86.5	6.0	3189	9	US-09-815-242-4056	Sequence 4056, Appl
691	6.0	717	17	US-10-262-445-3	Sequence 3, Appl	764	86.5	6.0	3189	17	US-10-282-122A-7343	Sequence 7343, Appl
c 692	6.0	832	18	US-10-437-963-44583	Sequence 44583, A	765	86.5	6.0	3220	14	US-10-103-313-100	Sequence 100, Appl
c 693	6.0	1023	17	US-10-389-647-172	Sequence 172, Appl	766	86.5	6.0	3318	18	US-10-425-115-115973	Sequence 115973, A
c 694	6.0	1068	18	US-10-437-963-94656	Sequence 94656, A	767	86.5	6.0	3440	18	US-10-357-930-21306	Sequence 21306, A
695	6.0	1086	17	US-10-282-122A-40919	Sequence 40919, A	768	86.5	6.0	3440	18	US-10-357-930-22150	Sequence 22150, A
c 696	6.0	1098	17	US-10-282-122A-25587	Sequence 25587, A	769	86.5	6.0	3440	18	US-10-357-930-27148	Sequence 27148, A
c 697	6.0	1191	17	US-10-369-493-40731	Sequence 40731, A	770	86.5	6.0	3440	18	US-10-357-930-28011	Sequence 28011, A
c 698	6.0	1289	18	US-10-437-963-97181	Sequence 97181, A	c 771	86.5	6.0	3462	17	US-10-369-493-35433	Sequence 35433, A
699	6.0	1296	13	US-10-076-421-1	Sequence 1, Appl	772	86.5	6.0	3636	18	US-10-474-792-37	Sequence 37, Appl
c 700	6.0	1358	18	US-10-739-930-2535	Sequence 2535, Appl	773	86.5	6.0	3691	9	US-09-922-199A-1	Sequence 1, Appl
701	6.0	1475	9	US-09-735-705-122	Sequence 122, Appl	774	86.5	6.0	3729	17	US-10-671-403-86	Sequence 86, Appl
702	6.0	1475	9	US-09-850-716A-122	Sequence 122, Appl	775	86.5	6.0	3729	17	US-10-671-419-86	Sequence 86, Appl
703	6.0	1475	9	US-09-897-778-122	Sequence 122, Appl	776	86.5	6.0	3729	17	US-10-670-844-86	Sequence 86, Appl
704	6.0	1475	10	US-09-466-396A-122	Sequence 122, Appl	777	86.5	6.0	3729	17	US-10-671-134-86	Sequence 86, Appl
705	6.0	1475	14	US-10-007-700-122	Sequence 122, Appl	778	86.5	6.0	3729	17	US-10-673-120-86	Sequence 86, Appl
706	6.0	1475	15	US-10-117-982-122	Sequence 122, Appl	779	86.5	6.0	3729	17	US-10-673-120-86	Sequence 86, Appl
707	6.0	1475	15	US-10-101-510-159	Sequence 159, Appl	780	86.5	6.0	3729	17	US-10-673-120-86	Sequence 86, Appl
708	6.0	1475	17	US-10-313-986-122	Sequence 122, Appl	781	86.5	6.0	3729	18	US-10-673-120-86	Sequence 86, Appl
709	6.0	1475	17	US-10-411-037-33	Sequence 33, Appl	782	86.5	6.0	3729	18	US-10-673-120-86	Sequence 86, Appl
710	6.0	1475	17	US-10-411-026-33	Sequence 33, Appl	783	86.5	6.0	3729	18	US-10-673-120-86	Sequence 86, Appl
711	6.0	1475	17	US-10-410-962-33	Sequence 33, Appl	784	86.5	6.0	3729	19	US-10-673-120-86	Sequence 86, Appl
712	6.0	1475	17	US-10-411-049-33	Sequence 33, Appl	785	86.5	6.0	3729	19	US-10-673-120-86	Sequence 86, Appl
713	6.0	1475	18	US-10-410-930-33	Sequence 33, Appl	786	86.5	6.0	5871	14	US-10-152-886-24	Sequence 24, Appl
714	6.0	1475	18	US-10-410-937-33	Sequence 33, Appl	787	86.5	6.0	5871	14	US-10-152-886-24	Sequence 24, Appl
715	6.0	1475	18	US-10-410-937-33	Sequence 33, Appl	788	86.5	6.0	5871	14	US-10-152-886-24	Sequence 24, Appl
716	6.0	1475	18	US-10-411-012-33	Sequence 33, Appl	789	86.5	6.0	5871	14	US-10-152-886-24	Sequence 24, Appl
717	6.0	1475	18	US-10-287-394-33	Sequence 33, Appl	c 789	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
718	6.0	1475	18	US-10-410-913-33	Sequence 33, Appl	c 790	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
719	6.0	1475	18	US-10-775-972-122	Sequence 122, Appl	791	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
720	6.0	1884	19	US-10-041-080-33	Sequence 33, Appl	c 792	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
721	6.0	1884	19	US-10-041-080-33	Sequence 33, Appl	c 793	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
c 722	6.0	1896	18	US-10-181-174B-10	Sequence 10, Appl	c 794	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
723	6.0	1964	16	US-10-131-985-22	Sequence 22, Appl	795	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
724	6.0	1964	17	US-10-432-989-2	Sequence 2, Appl	796	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
725	6.0	2058	17	US-10-369-493-24298	Sequence 24298, A	797	86.5	6.0	10011	18	US-10-663-433-3	Sequence 3, Appl
726	6.0	2175	17	US-10-425-114-15621	Sequence 15621, A	c 798	86.5	6.0	174424	9	US-09-967-768A-314	Sequence 314, Appl
727	6.0	2211	17	US-10-425-114-1166	Sequence 1166, Appl	c 799	86.5	6.0	174424	9	US-09-967-768A-314	Sequence 314, Appl
728	6.0	2211	17	US-10-425-114-1166	Sequence 1166, Appl	c 800	86.5	6.0	174424	9	US-09-967-768A-314	Sequence 314, Appl
729	6.0	2294	9	US-09-735-705-123	Sequence 123, Appl	c 801	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
730	6.0	2294	9	US-09-850-716A-123	Sequence 123, Appl	c 802	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
731	6.0	2294	9	US-09-897-778-123	Sequence 123, Appl	c 803	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
732	6.0	2294	14	US-09-466-396A-123	Sequence 123, Appl	c 804	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
733	6.0	2294	14	US-10-007-700-123	Sequence 123, Appl	c 805	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
734	6.0	2294	15	US-10-117-982-123	Sequence 123, Appl	c 806	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
735	6.0	2294	17	US-10-313-986-123	Sequence 123, Appl	c 807	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
736	6.0	2294	17	US-10-641-643-1217	Sequence 1217, Appl	c 808	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
737	6.0	2294	18	US-10-775-972-123	Sequence 123, Appl	c 809	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
738	6.0	2297	13	US-10-087-192-593	Sequence 593, Appl	c 810	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
739	6.0	2304	14	US-10-171-311-183	Sequence 183, Appl	c 811	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
740	6.0	2304	15	US-10-301-822-160	Sequence 160, Appl	c 812	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
741	6.0	2304	17	US-10-388-360-335	Sequence 335, Appl	c 813	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
742	6.0	2304	17	US-10-295-027-413	Sequence 413, Appl	c 814	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
743	6.0	2304	17	US-10-295-027-413	Sequence 413, Appl	c 815	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
744	6.0	2304	17	US-10-159-563-121	Sequence 1058, Appl	c 816	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
745	6.0	2304	17	US-10-665-216-3	Sequence 121, Appl	c 817	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
746	6.0	2304	17	US-10-665-216-3	Sequence 3, Appl	c 818	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
747	6.0	2325	18	US-10-645-756-37	Sequence 37, Appl	c 819	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
748	6.0	2328	16	US-10-247-671-34	Sequence 34, Appl	c 820	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
749	6.0	2336	10	US-09-971-392-46	Sequence 46, Appl	c 821	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
750	6.0	2336	15	US-10-101-510-458	Sequence 458, Appl	c 822	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
751	6.0	2336	16	US-10-252-157-358	Sequence 157, Appl	c 823	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl
752	6.0	2341	14	US-10-116-802-163	Sequence 163, Appl	c 825	86.5	6.0	181343	18	US-10-723-860-2392	Sequence 2392, Appl

c 972	85	5.9	2679	17	US-10-104-047-1531	Sequence 1531, Ap	c1045	84.5	5.9	1666	14	US-10-208-408-2	Sequence 2, Appli
c 973	85	5.9	2758	17	US-10-094-749-1267	Sequence 1267, Ap	1046	84.5	5.9	1674	9	US-09-808-387-3	Sequence 3, Appli
c 974	85	5.9	2848	13	US-10-002-344-60	Sequence 60, Appl	1047	84.5	5.9	1677	9	US-10-369-493-34258	Sequence 34258, A
c 975	85	5.9	2848	17	US-10-958-862-60	Sequence 60, Appl	c1048	84.5	5.9	1679	13	US-10-044-090-316	Sequence 316, App
c 976	85	5.9	2929	17	US-10-425-114-11279	Sequence 11279, A	1049	84.5	5.9	1725	9	US-09-808-387-1	Sequence 1, Appli
c 977	85	5.9	2937	15	US-10-156-761-1581	Sequence 1581, Ap	c1050	84.5	5.9	1798	10	US-09-814-353-20589	Sequence 20589, A
c 978	85	5.9	3008	10	US-09-373-658-3	Sequence 3, Appli	1051	84.5	5.9	1826	18	US-10-437-963-100495	Sequence 100495, A
c 979	85	5.9	3008	11	US-09-989-687-3	Sequence 3, Appli	c1052	84.5	5.9	1833	10	US-09-971-392-91	Sequence 91, Appl
c 980	85	5.9	3033	18	US-10-425-115-113989	Sequence 113989, A	c1053	84.5	5.9	1833	16	US-10-240-965-50	Sequence 50, Appl
c 981	85	5.9	3033	18	US-10-437-963-80145	Sequence 80145, A	1054	84.5	5.9	1860	17	US-10-369-493-38468	Sequence 38468, A
c 982	85	5.9	3307	17	US-10-424-599-116102	Sequence 116102, A	c1055	84.5	5.9	1860	17	US-10-411-910A-124	Sequence 124, App
c 983	85	5.9	3404	17	US-10-602-494-70	Sequence 70, Appl	1056	84.5	5.9	1869	17	US-10-369-493-38622	Sequence 38622, A
c 984	85	5.9	3711	18	US-10-283-975A-398	Sequence 398, App	1057	84.5	5.9	1949	17	US-10-369-493-35060	Sequence 35060, A
c 985	85	5.9	3937	14	US-10-198-846-13985	Sequence 13985, A	1058	84.5	5.9	2184	17	US-10-282-122A-14290	Sequence 14290, A
c 986	85	5.9	4145	9	US-09-911-781-3	Sequence 3, Appli	1059	84.5	5.9	2377	18	US-10-425-115-176394	Sequence 176394, A
c 987	85	5.9	4145	10	US-09-976-800-82	Sequence 82, Appl	c1060	84.5	5.9	2463	18	US-10-425-115-170656	Sequence 170656, A
c 988	85	5.9	4145	14	US-10-138-838-82	Sequence 82, Appl	c1061	84.5	5.9	2478	18	US-10-322-281-381	Sequence 381, App
c 989	85	5.9	4145	14	US-10-139-031-82	Sequence 82, Appl	c1062	84.5	5.9	2550	18	US-10-425-115-111107	Sequence 111107, A
c 990	85	5.9	4145	14	US-10-138-905-82	Sequence 82, Appl	1063	84.5	5.9	2917	18	US-10-343-903-44	Sequence 44, Appl
c 991	85	5.9	4145	14	US-10-138-916-82	Sequence 82, Appl	1064	84.5	5.9	3096	18	US-10-476-597-70	Sequence 70, Appl
c 992	85	5.9	4145	15	US-10-139-296-82	Sequence 82, Appl	1065	84.5	5.9	3096	18	US-10-476-597-71	Sequence 71, Appl
c 993	85	5.9	4145	16	US-10-139-218-82	Sequence 82, Appl	c1066	84.5	5.9	3186	18	US-10-425-115-114129	Sequence 114129, A
c 994	85	5.9	4145	16	US-10-400-902-3	Sequence 3, Appli	1067	84.5	5.9	3291	18	US-10-723-860-1367	Sequence 1367, Ap
c 995	85	5.9	4145	16	US-10-405-660-82	Sequence 82, Appl	1068	84.5	5.9	3343	17	US-10-257-022-19	Sequence 19, Appl
c 996	85	5.9	4145	17	US-10-138-898-82	Sequence 82, Appl	1069	84.5	5.9	3408	9	US-09-795-693-16	Sequence 16, Appl
c 997	85	5.9	4212	13	US-10-194-163-39	Sequence 39, Appl	1070	84.5	5.9	3408	14	US-10-156-239-16	Sequence 16, Appl
c 998	85	5.9	4341	15	US-10-156-761-1074	Sequence 1074, Ap	1071	84.5	5.9	3408	14	US-10-199-485-16	Sequence 16, Appl
c 999	85	5.9	4512	10	US-09-792-616-2	Sequence 2, Appli	1072	84.5	5.9	3411	17	US-10-374-979-67	Sequence 67, Appl
1000	85	5.9	4512	18	US-10-764-328-2	Sequence 2, Appli	1073	84.5	5.9	3411	17	US-10-182-936A-67	Sequence 67, Appl
1001	85	5.9	4535	19	US-10-741-600-755	Sequence 755, App	1074	84.5	5.9	3411	18	US-10-477-238A-646	Sequence 646, App
c1002	85	5.9	4551	15	US-10-156-761-5715	Sequence 5715, Ap	1075	84.5	5.9	3414	18	US-10-680-287A-646	Sequence 646, App
c1003	85	5.9	5360	18	US-10-467-506A-13	Sequence 13, Appl	1076	84.5	5.9	3414	14	US-10-074-475-36	Sequence 36, Appl
c1004	85	5.9	5491	18	US-10-723-860-5914	Sequence 5914, Ap	1077	84.5	5.9	3512	13	US-10-072-621-1	Sequence 1, Appli
c1005	85	5.9	9320	18	US-10-471-065-20	Sequence 20, Appl	1078	84.5	5.9	3536	18	US-10-802-513-1	Sequence 1, Appli
1006	85	5.9	9369	16	US-10-200-562-190	Sequence 190, App	c1079	84.5	5.9	3575	9	US-09-796-858-41	Sequence 41, Appli
1007	85	5.9	9369	16	US-10-237-551-190	Sequence 190, App	c1080	84.5	5.9	3600	9	US-09-875-338-3	Sequence 3, Appli
c1008	85	5.9	9369	16	US-10-237-551-247	Sequence 247, App	c1081	84.5	5.9	3600	14	US-10-077-023-3	Sequence 3, Appli
c1009	85	5.9	71989	9	US-09-727-889-2	Sequence 2, Appli	c1082	84.5	5.9	3616	19	US-10-890-789-5	Sequence 5, Appli
1010	85	5.9	125746	15	US-10-849-462-2	Sequence 2, Appli	c1083	84.5	5.9	3660	10	US-09-814-353-19604	Sequence 19604, A
c1011	85	5.9	154746	10	US-10-156-761-15102	Sequence 15102, A	1084	84.5	5.9	4432	17	US-10-120-988-148	Sequence 148, App
c1012	85	5.9	593	16	US-10-029-386-5929	Sequence 8, Appli	1085	84.5	5.9	4548	15	US-10-156-761-6166	Sequence 6166, Ap
c1013	84.5	5.9	618	9	US-09-738-626-3423	Sequence 5929, Ap	c1086	84.5	5.9	4862	15	US-10-161-403-87	Sequence 87, Appl
c1014	84.5	5.9	688	18	US-10-437-963-59927	Sequence 5927, A	1087	84.5	5.9	5179	18	US-10-437-963-25554	Sequence 25554, A
c1015	84.5	5.9	867	18	US-10-425-115-48092	Sequence 48092, A	1088	84.5	5.9	5679	14	US-10-152-886-74	Sequence 74, Appl
c1016	84.5	5.9	870	19	US-10-890-789-2	Sequence 2, Appli	1089	84.5	5.9	6754	17	US-10-240-425-350	Sequence 350, App
c1017	84.5	5.9	873	9	US-09-910-174A-22	Sequence 22, Appl	1090	84.5	5.9	6754	18	US-10-473-974-118	Sequence 118, App
c1018	84.5	5.9	873	18	US-10-644-671-22	Sequence 22, Appl	1091	84.5	5.9	7080	17	US-10-276-774-729	Sequence 729, App
c1019	84.5	5.9	899	17	US-10-425-114-7134	Sequence 7134, Ap	1092	84.5	5.9	10846	9	US-09-923-109-5	Sequence 5, Appli
c1020	84.5	5.9	967	9	US-09-898-570-33	Sequence 33, Appl	1093	84.5	5.9	10846	15	US-10-164-204-5	Sequence 5, Appli
c1021	84.5	5.9	967	10	US-09-839-446-33	Sequence 33, Appl	1094	84.5	5.9	10846	17	US-10-705-430-5	Sequence 5, Appli
c1022	84.5	5.9	1161	18	US-10-425-115-3106	Sequence 3106, Ap	1095	84.5	5.9	10900	9	US-09-923-109-6	Sequence 6, Appli
c1023	84.5	5.9	1178	17	US-10-425-114-22293	Sequence 22293, Ap	1096	84.5	5.9	10900	15	US-10-164-204-6	Sequence 6, Appli
c1024	84.5	5.9	1179	17	US-10-282-122A-14447	Sequence 14447, A	1097	84.5	5.9	11606	18	US-10-602-475A-9	Sequence 9, Appli
c1025	84.5	5.9	1207	18	US-10-437-963-62054	Sequence 62054, A	1098	84.5	5.9	13116	17	US-10-499-406-2	Sequence 2, Appli
c1026	84.5	5.9	1286	14	US-10-132-829-3	Sequence 3, Appli	1099	84.5	5.9	14106	17	US-10-093-463-73	Sequence 73, Appl
c1027	84.5	5.9	1286	16	US-10-136-819-1	Sequence 1, Appli	c1100	84.5	5.9	14109	17	US-10-093-463-71	Sequence 71, Appl
c1028	84.5	5.9	1286	15	US-10-133-907-3	Sequence 3, Appli	c1101	84.5	5.9	45191	15	US-10-080-170-649	Sequence 649, App
c1029	84.5	5.9	1314	17	US-10-282-122A-30204	Sequence 30204, A	1102	84.5	5.9	45191	18	US-10-080-170-649	Sequence 649, App
c1030	84.5	5.9	1323	17	US-10-369-493-44491	Sequence 44491, A	1103	84.5	5.9	45191	18	US-10-080-170-649	Sequence 649, App
c1031	84.5	5.9	1406	18	US-10-726-699-56	Sequence 56, Appl	1104	84.5	5.9	45191	18	US-10-468-356-649	Sequence 649, App
c1032	84.5	5.9	1413	17	US-10-369-493-40672	Sequence 40672, A	1105	84.5	5.9	71292	13	US-10-087-192-1942	Sequence 1942, Ap
c1033	84.5	5.9	1364	15	US-10-437-963-32627	Sequence 32627, A	c1106	84.5	5.9	74868	14	US-10-175-523-67	Sequence 67, Appl
c1034	84.5	5.9	1366	15	US-10-156-761-6572	Sequence 6572, Ap	1107	84.5	5.9	98474	13	US-10-087-192-175	Sequence 175, App
c1035	84.5	5.9	1395	18	US-10-723-860-8124	Sequence 8124, Ap	1108	84.5	5.9	101209	18	US-10-087-192-460	Sequence 460, App
c1036	84.5	5.9	1406	18	US-10-726-699-27	Sequence 27, Appl	c1109	84.5	5.9	104729	13	US-10-723-860-1434	Sequence 1434, Ap
c1037	84.5	5.9	1406	18	US-10-726-699-56	Sequence 56, Appl	1110	84	5.9	714	17	US-10-282-122A-26405	Sequence 26405, A
c1038	84.5	5.9	1545	17	US-10-369-493-40672	Sequence 40672, A	1111	84	5.9	750	17	US-10-282-122A-28206	Sequence 28206, A
c1039	84.5	5.9	1545	17	US-10-282-122A-14095	Sequence 14095, A	1112	84	5.9	765	18	US-10-425-115-58352	Sequence 58352, A
c1040	84.5	5.9	1553	13	US-10-002-775-3	Sequence 3, Appli	1113	84	5.9	831	17	US-10-437-963-41149	Sequence 41149, A
c1041	84.5	5.9	1553	14	US-10-115-615-3	Sequence 3, Appli	1114	84	5.9	876	18	US-10-369-493-32649	Sequence 32649, A
c1042	84.5	5.9	1604	9	US-09-875-338-1	Sequence 1, Appli	c1115	84	5.9	947	16	US-10-425-115-13959	Sequence 13959, A
c1043	84.5	5.9	1604	14	US-10-077-023-1	Sequence 1, Appli	1116	84	5.9	1117	18	US-10-437-963-46167	Sequence 46167, A
c1044	84.5	5.9	1662	10	US-09-292-862-1	Sequence 1, Appli	c1117	84	5.9	1132	18	US-10-425-115-48054	Sequence 48054, A

c1118	84	5.9	1296	18	US-10-739-930-4335	Sequence 4335, Ap	1191	83.5	5.8	1240	11	US-09-729-821-2	Sequence 2, Appli
c1119	84	5.9	1299	18	US-10-739-930-2323	Sequence 2323, Ap	1192	83.5	5.8	1240	15	US-10-734-282-2	Sequence 2, Appli
c1120	84	5.9	1352	18	US-10-425-115-64812	Sequence 64812, A	1193	83.5	5.8	1265	15	US-10-037-270-892	Sequence 892, App
c1121	84	5.9	1388	17	US-10-282-122A-25610	Sequence 25610, A	1194	83.5	5.8	1265	17	US-10-117-722-892	Sequence 213, App
c1122	84	5.9	1497	17	US-10-282-122A-25610	Sequence 11595, A	1195	83.5	5.8	1339	11	US-09-997-722-213	Sequence 2995, A
c1123	84	5.9	1589	18	US-10-767-701-12146	Sequence 12146, A	1196	83.5	5.8	1446	17	US-10-369-493-35956	Sequence 35956, A
c1124	84	5.9	1602	18	US-10-425-115-124288	Sequence 124288, A	1197	83.5	5.8	1480	17	US-10-369-493-35956	Sequence 29943, A
c1125	84	5.9	1609	14	US-10-082-830-48	Sequence 48, Appl	1198	83.5	5.8	1525	17	US-10-369-493-35956	Sequence 66, Appl
c1126	84	5.9	1629	17	US-10-282-122A-14919	Sequence 14919, A	1199	83.5	5.8	1525	17	US-10-369-493-35956	Sequence 66, Appl
c1127	84	5.9	1746	15	US-10-156-761-4695	Sequence 4695, Ap	1200	83.5	5.8	1557	15	US-10-119-926-18	Sequence 18, Appl
c1128	84	5.9	1827	18	US-10-411-910A-104	Sequence 104, App	1201	83.5	5.8	1613	15	US-10-425-115-166627	Sequence 166627, A
c1129	84	5.9	2028	18	US-10-425-115-94597	Sequence 94597, A	1202	83.5	5.8	1613	15	US-10-425-115-166627	Sequence 1, Appli
c1130	84	5.9	2291	17	US-10-094-749-218	Sequence 218, App	1203	83.5	5.8	1649	18	US-10-378-945-1	Sequence 96353, A
c1131	84	5.9	2436	17	US-10-260-238-1510	Sequence 1510, Ap	1204	83.5	5.8	1678	18	US-10-425-115-96353	Sequence 16419, A
c1132	84	5.9	2601	17	US-10-369-493-33730	Sequence 33730, A	1205	83.5	5.8	1772	17	US-10-425-114-16419	Sequence 28363, A
c1133	84	5.9	2667	10	US-09-895-298-12	Sequence 12, Appl	1206	83.5	5.8	1811	17	US-10-425-114-16419	Sequence 17717, A
c1134	84	5.9	2667	18	US-10-885-039-12	Sequence 12, Appl	1207	83.5	5.8	1914	18	US-10-441-949-60	Sequence 60, Appl
c1135	84	5.9	2780	9	US-09-864-864-318	Sequence 318, App	1208	83.5	5.8	1923	10	US-09-746-660A-105	Sequence 105, App
c1136	84	5.9	2788	18	US-10-723-860-6037	Sequence 6037, Ap	1209	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1137	84	5.9	2828	18	US-10-723-860-6037	Sequence 6037, Ap	1210	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1138	84	5.9	2919	17	US-10-369-493-44751	Sequence 44751, A	1211	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1139	84	5.9	2961	18	US-10-425-115-93677	Sequence 93677, A	1212	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1140	84	5.9	3008	17	US-10-108-260A-1736	Sequence 1736, Ap	1213	83.5	5.8	1923	18	US-10-441-949-61	Sequence 61, Appl
c1141	84	5.9	3336	15	US-10-156-761-376	Sequence 376, App	1214	83.5	5.8	1929	17	US-10-425-114-25324	Sequence 5578, Ap
c1142	84	5.9	3831	17	US-10-282-122A-30485	Sequence 30485, A	1215	83.5	5.8	2020	17	US-10-425-114-25324	Sequence 5578, Ap
c1143	84	5.9	4248	17	US-10-282-122A-13146	Sequence 13146, A	1216	83.5	5.8	2088	18	US-10-425-115-22868	Sequence 22868, A
c1144	84	5.9	4818	17	US-10-282-122A-26430	Sequence 26430, A	1217	83.5	5.8	2103	18	US-10-425-115-22868	Sequence 177617
c1145	84	5.9	5470	18	US-10-723-860-7477	Sequence 7477, Ap	1218	83.5	5.8	2106	18	US-10-437-963-39568	Sequence 39568, A
c1146	84	5.9	6816	16	US-10-021-660-12	Sequence 12, Appl	1219	83.5	5.8	2235	9	US-09-738-860-678	Sequence 678, App
c1147	84	5.9	6816	17	US-10-211-462-31	Sequence 31, Appl	1220	83.5	5.8	2235	9	US-09-738-860-678	Sequence 1261, App
c1148	84	5.9	6822	18	US-10-437-963-82458	Sequence 82458, A	1221	83.5	5.8	2261	13	US-10-425-115-35617	Sequence 35617, A
c1149	84	5.9	6901	19	US-10-780-002-31	Sequence 31, Appl	1222	83.5	5.8	2328	13	US-10-087-192-935	Sequence 935, App
c1150	84	5.9	7068	18	US-10-437-963-86105	Sequence 86105, A	1223	83.5	5.8	2358	10	US-09-746-660A-103	Sequence 103, App
c1151	84	5.9	7536	17	US-10-282-122A-26585	Sequence 26585, A	1224	83.5	5.8	2393	18	US-10-739-930-5492	Sequence 5492, App
c1152	84	5.9	7539	17	US-10-282-122A-26585	Sequence 26585, A	1225	83.5	5.8	2402	17	US-10-405-877-116	Sequence 116, App
c1153	84	5.9	8010	17	US-10-016-248-3	Sequence 3, Appli	1226	83.5	5.8	2430	15	US-10-157-031-396	Sequence 396, App
c1154	84	5.9	9748	17	US-10-282-122A-31388	Sequence 31388, A	1227	83.5	5.8	2479	18	US-10-723-860-5318	Sequence 5318, App
c1155	84	5.9	10136	17	US-10-016-248-1	Sequence 1, Appli	1228	83.5	5.8	2574	14	US-10-167-749-101	Sequence 101, App
c1156	84	5.9	10296	17	US-10-282-122A-33665	Sequence 33665, A	1229	83.5	5.8	2574	17	US-10-170-481A-101	Sequence 101, App
c1157	84	5.9	14227	15	US-10-156-761-1540	Sequence 1540, Ap	1230	83.5	5.8	2574	17	US-10-102-028-101	Sequence 101, App
c1158	84	5.9	59554	17	US-10-052-482-202	Sequence 202, App	1231	83.5	5.8	2574	17	US-10-162-521A-101	Sequence 101, App
c1159	84	5.9	60196	15	US-10-205-032-1	Sequence 1, Appli	1232	83.5	5.8	2574	17	US-10-162-521A-101	Sequence 101, App
c1160	84	5.9	86114	15	US-10-080-170-648	Sequence 648, App	1233	83.5	5.8	2574	19	US-10-162-521A-101	Sequence 101, App
c1161	84	5.9	86114	18	US-10-080-170-648	Sequence 648, App	1234	83.5	5.8	2574	19	US-10-162-521A-101	Sequence 101, App
c1162	84	5.9	86114	18	US-10-468-356-648	Sequence 648, App	1235	83.5	5.8	2574	19	US-10-162-521A-101	Sequence 101, App
c1163	84	5.9	176080	17	US-10-235-192A-43	Sequence 43, Appl	1236	83.5	5.8	2589	15	US-10-242-576-1	Sequence 1, Appli
c1164	84	5.9	347001	18	US-10-319-908-16	Sequence 16, Appl	1237	83.5	5.8	2772	17	US-10-108-260A-169	Sequence 169, App
c1165	83.5	5.8	576	15	US-10-156-761-205	Sequence 205, App	1238	83.5	5.8	2772	9	US-09-738-860-678	Sequence 2944, Ap
c1166	83.5	5.8	579	14	US-10-198-846-9350	Sequence 9350, Ap	1239	83.5	5.8	2810	9	US-09-738-860-678	Sequence 1, Appli
c1167	83.5	5.8	688	18	US-10-767-701-768	Sequence 768, App	1240	83.5	5.8	2810	9	US-09-738-860-678	Sequence 1, Appli
c1168	83.5	5.8	706	18	US-10-425-115-120383	Sequence 120383, A	1241	83.5	5.8	2824	18	US-10-322-281-339	Sequence 339, App
c1169	83.5	5.8	747	9	US-09-764-877-2387	Sequence 2387, Ap	1242	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1170	83.5	5.8	747	17	US-10-242-515-2387	Sequence 2387, Ap	1243	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1171	83.5	5.8	770	9	US-09-974-300-2057	Sequence 2057, Ap	1244	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1172	83.5	5.8	834	18	US-10-425-115-176763	Sequence 176763, A	1245	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1173	83.5	5.8	874	9	US-09-925-301-191	Sequence 191, App	1246	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1174	83.5	5.8	897	17	US-10-424-599-127609	Sequence 127609, A	1247	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1175	83.5	5.8	972	15	US-10-156-761-6533	Sequence 6533, Ap	1248	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1176	83.5	5.8	976	18	US-10-425-115-177697	Sequence 177697, A	1249	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1177	83.5	5.8	990	17	US-10-260-238-4176	Sequence 4176, Ap	1250	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1178	83.5	5.8	991	17	US-10-114-270-135	Sequence 135, App	1251	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1179	83.5	5.8	991	17	US-10-114-270-137	Sequence 137, App	1252	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1180	83.5	5.8	991	9	US-09-876-216-1	Sequence 1, Appli	1253	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1181	83.5	5.8	993	15	US-10-359-076-1	Sequence 1, Appli	1254	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1182	83.5	5.8	1004	17	US-10-425-114-15631	Sequence 15631, A	1255	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1183	83.5	5.8	1080	9	US-09-815-242-4061	Sequence 4061, Ap	1256	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1184	83.5	5.8	1080	17	US-10-282-122A-7305	Sequence 7305, Ap	1257	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1185	83.5	5.8	1116	15	US-10-156-761-1283	Sequence 1283, Ap	1258	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1186	83.5	5.8	1162	18	US-10-437-963-73894	Sequence 73894, A	1259	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1187	83.5	5.8	1216	18	US-10-767-701-7988	Sequence 7988, Ap	1260	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1188	83.5	5.8	1224	17	US-10-282-122A-27529	Sequence 27529, A	1261	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1189	83.5	5.8	1239	18	US-10-425-115-162441	Sequence 162441, A	1262	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App
c1190	83.5	5.8	1240	9	US-09-729-821-2	Sequence 2, Appli	1263	83.5	5.8	2824	18	US-10-322-281-339	Sequence 287, App

c1348	83.5	5.8	4694	18	US-10-723-860-5310	Sequence 5310, Ap	83	1614	17	US-10-616-187-45	Sequence 45, Appl
c1349	83.5	5.8	4719	17	US-10-258-106-25	Sequence 25, Appl	83	1614	17	US-10-671-242-45	Sequence 45, Appl
c1350	83.5	5.8	4837	17	US-10-062-674-1978	Sequence 1978, Ap	83	1832	18	US-10-437-963-76365	Sequence 76365, A
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c1375	83.5	5.8	59394	11	US-09-997-722-235	Sequence 235, App	83	4162	17	US-10-112-944-47	Sequence 47, Appl
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c1394	83	5.8	1068	17	US-10-282-122A-30125	Sequence 30125, A	83	125401	18	US-10-203-295-35	Sequence 35, Appl
c1395	83	5.8	1194	17	US-10-369-493-24835	Sequence 24835, A	83	125401	18	US-10-322-281-158	Sequence 158, App
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c1416	83	5.8	1523	17	US-10-468-333-3	Sequence 3, Appl	83	1101	18	US-10-461-925-155	Sequence 155, App
c1417	83	5.8	1602	15	US-10-156-761-2697	Sequence 2697, Ap	83	1106	17	US-10-437-963-37652	Sequence 37652, A
c1418	83	5.8	1614	9	US-09-976-740-45	Sequence 45, Appl	83	1178	18	US-10-425-114-186	Sequence 186, App
c1419	83	5.8	1614	13	US-10-023-529-45	Sequence 45, Appl	83	1189	18	US-10-425-115-46339	Sequence 46339, A
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Sequence 122825,
Sequence 19, Appl
Sequence 64780, A
Sequence 30235, A
Sequence 12528, A

Search completed: March 29, 2005, 13:35:50
Job time : 626 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2005, 04:18:08 ; Search time 3093 Seconds
(without alignments)
3445.844 Million cell updates/sec

Title: US-10-015-388a-54

Perfect score: 1432

Sequence: 1 MCFINKLLALLAVLWLFQIP.....LRAQGPAPARGERRGCSRA 280

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:

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-DB=EST -QFMT=fastcap -SURF1=rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
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Database :

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8: gb_gse1:*
9: gb_gse2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1168	81.6	3688	3 AK034144	Mus muscu
2	1024	71.5	673	2 BB626090	BB626090
3	915	63.9	603	7 CN722464	E0842C03-
4	870	60.8	576	7 CN718045	E0757H05-
5	845	59.0	528	2 BF075771	225066 MA
6	796	55.6	541	5 BQ82104	K-EST0054
7	753	52.6	589	4 B1344908	B1344908
8	710.5	49.6	727	6 CD578927	UI-N-FY0-
9	672.5	47.0	743	7 CF724147	UI-N-GZ0-

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11	527	36.8	567	4	B1541289	454959 MA
12	502	35.1	1165	5	BQ715935	AGENCOURT
13	462	32.3	476	6	CB286548	CMD39_G03
14	457	31.9	288	2	AW478789	21675 MAR
15	448	31.3	298	7	CN723141	E0854H11-
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17	418	29.2	542	7	CF897764	A0229E12-
18	414	28.9	938	5	BQ952171	AGENCOURT
19	375.5	26.2	756	2	BF160178	601767886
20	373	26.0	835	5	BP684628	BP684628
21	343	24.0	204	7	CN717279	E0741H10-
22	316	22.1	834	9	CNS03RKA	Tetraodon
23	300.5	21.0	1189	9	CL641240	CH213-7N1
24	249.5	17.4	858	6	CA986932	AGENCOURT
25	240	16.8	813	1	AI557159	PT2_1_14_
26	202.5	14.1	1014	9	CNS02C0U	Tetraodon
27	178	12.4	1220	8	CC212415	CH261-186
28	166	11.6	602	7	CN668727	A0871A06-
29	160.5	11.2	870	9	CNS03EM3	Tetraodon
30	157	11.0	854	9	CL122296	ISB1-8102
31	151	10.5	757	5	BM138380	BM138380
32	147.5	10.3	380	5	BX866129	BX866129
33	137.5	9.6	565	2	AV977502	AV977502
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35	135.5	9.5	606	5	BW257047	BW257047
36	123.5	8.6	268	8	BZ834183	CH240_202
37	118	8.2	784	5	BW081796	BW081796
38	114.5	8.0	899	5	BUI123269	603148305
39	114	8.0	1271	3	CR634092	Tetraodon
40	113	7.9	1280	3	CR652652	Tetraodon
41	112	7.8	876	4	B1950567	HVSMEL002
42	111.5	7.8	1173	3	CR652074	Tetraodon
43	111	7.8	826	5	BM127780	BM127780
44	110.5	7.7	476	5	BX548759	BX548759
45	109.5	7.6	970	5	BQ921283	AGENCOURT
46	109	7.6	795	9	BX240656	Danio rer
47	109	7.6	827	9	BX135541	Danio rer
48	109	7.6	1307	3	CR639820	Tetraodon
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50	108	7.5	904	9	CG2211398	OG3DY12TV
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52	107	7.5	736	6	CA432624	UI-H-FLL-
53	105.5	7.4	794	5	BUI133809	603119121
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56	105.5	7.4	2220	9	CL945674	OsIFSB005
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58	105	7.3	796	4	BG871126	602790323
59	104.5	7.3	925	5	BQ918952	AGENCOURT
60	103	7.2	941	8	CC124481	NDL_78F14
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62	102	7.1	891	6	CB196308	AGENCOURT
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79	99.5	6.9	603	4	BG384948	306489 MA
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C 231	94	6.6	673	4	BI960378	HVSMEM002	C 304	93	6.5	2121	9	CL969972	OiFCC019
C 232	94	6.6	674	7	CK962937	4077615 B	C 305	93	6.5	3642	9	CL978063	OiFCC031
C 233	94	6.6	682	7	CK963478	4076160 B	C 306	92.5	6.5	458	7	CF732839	UI-N-HB0-
C 234	94	6.6	683	6	BY747887	BY747887	C 307	92.5	6.5	622	6	CA197731	SCAGAD107
C 235	94	6.6	683	7	CK965556	4080546 B	C 308	92.5	6.5	651	6	CA094082	SCCCL400
C 236	94	6.6	684	7	CK967503	4083019 B	C 309	92.5	6.5	672	4	BI955459	HVSMEM002
C 237	94	6.6	684	7	CK982840	4072199 B	C 310	92.5	6.5	684	4	BG274868	WHE2118 C
C 238	94	6.6	685	7	CK977695	4109059 B	C 311	92.5	6.5	726	4	BG231184	BG923184
C 239	94	6.6	686	7	CK963769	4078138 B	C 312	92.5	6.5	728	6	CD908518	G468.110C
C 240	94	6.6	686	7	CK976981	4108149 B	C 313	92.5	6.5	759	2	BF627397	HVSMEM000
C 241	94	6.6	686	7	CK982973	4107710 B	C 314	92.5	6.5	774	6	CB955159	AGENCOURT
C 242	94	6.6	687	7	CK977860	4108947 B	C 315	92.5	6.5	809	5	BX337592	BX337592
C 243	94	6.6	688	7	CK940248	4113805 B	C 316	92.5	6.5	816	4	BI952395	HVSMEM000
C 244	94	6.6	688	7	CK978955	4110694 B	C 317	92.5	6.5	876	9	CG607156	QGMWFO47H
C 245	94	6.6	688	7	CK979852	4111376 B	C 318	92.5	6.5	876	9	CG281803	CG281803
C 246	94	6.6	690	7	CK968289	4083636 B	C 319	92.5	6.5	948	4	BI462234	603205552
C 247	94	6.6	690	7	CK976266	4107326 B	C 320	92.5	6.5	951	2	BE214936	HV_CEB000
C 248	94	6.6	700	7	CK981811	4114501 B	C 321	92.5	6.5	953	4	BI456794	603174688
C 249	94	6.6	720	7	CK968952	4084506 B	C 322	92.5	6.5	1000	4	BM552624	AGENCOURT
C 250	94	6.6	727	7	CK966403	4081494 B	C 323	92.5	6.5	1008	4	BI670332	603292701
C 251	94	6.6	766	7	CK973716	4104380 B	C 324	92.5	6.5	1029	9	CG211302	QG1DK33TV
C 252	94	6.6	781	3	CR641149	Tetraodon	C 325	92.5	6.5	1097	3	AK047780	Mus muscu
C 253	94	6.6	838	4	BI952373	HVSMEM000	C 326	92.5	6.5	3597	3	AK085684	Mus muscu
C 254	94	6.6	846	7	CK974254	4105208 B	C 327	92	6.4	452	2	AW013240	Sp190f W1
C 255	94	6.6	870	5	BU225793	603946725	C 328	92	6.4	643	9	CC478416	CH240 304
C 256	94	6.6	891	2	BF3112847	601896991	C 329	92	6.4	649	4	BI955246	HVSMEM002
C 257	94	6.6	906	5	BU155418	AGENCOURT	C 330	92	6.4	667	1	AV910604	AV910604
C 258	94	6.6	912	5	BX334692	BX334692	C 331	92	6.4	682	3	CR648452	Tetraodon
C 259	94	6.6	934	5	BQ680655	BQ680655	C 332	92	6.4	686	8	BZ415333	if54a12.9
C 260	94	6.6	934	5	BU179046	AGENCOURT	C 333	92	6.4	690	5	BQ257892	NISC kp07
C 261	94	6.6	1357	8	BZ548495	pacs1-60	C 334	92	6.4	693	2	BE216255	BE216255
C 262	94	6.6	2682	9	CL969033	OiFCC017	C 335	92	6.4	698	5	BU397697	603536254
C 263	94	6.6	3735	3	AK043669	Mus muscu	C 336	92	6.4	713	2	BF628666	HVSMEM000
C 264	93.5	6.5	604	5	BU092442	946130F07	C 337	92	6.4	746	7	CO517983	3530 1.11
C 265	93.5	6.5	629	1	AV609635	AV609635	C 338	92	6.4	756	2	BF266955	HV_CEA001
C 266	93.5	6.5	714	4	BG328765	602427047	C 339	92	6.4	760	2	BF627589	HVSMEM000
C 267	93.5	6.5	774	4	BI762380	603049047	C 340	92	6.4	809	7	CO799872	AGENCOURT
C 268	93.5	6.5	837	5	CB659131	OSJNEC15N	C 341	92	6.4	811	6	CA243740	SCQGF407
C 269	93.5	6.5	856	8	BH702422	BH702422	C 342	92	6.4	814	7	CF132151	UI-HF-F00
C 270	93.5	6.5	844	8	CC344924	OGTAM21TV	C 343	92	6.4	820	2	BF624789	HVSMEM001
C 271	93.5	6.5	861	4	BG751793	602730727	C 344	92	6.4	827	2	BF264782	HV_CEA001
C 272	93.5	6.5	866	8	BH702422	BOMMQ06TF	C 345	92	6.4	827	2	BF267532	HV_CEA001
C 273	93.5	6.5	889	6	CD358942	AGENCOURT	C 346	92	6.4	829	2	BF263229	HV_CEA000
C 274	93.5	6.5	892	2	BF623079	HVSMEM001	C 347	92	6.4	834	5	BX438268	BX438268
C 275	93.5	6.5	918	5	BU554267	AGENCOURT	C 348	92	6.4	900	5	BX357722	BX357722
C 276	93.5	6.5	975	5	BU197207	AGENCOURT	C 349	92	6.4	920	4	BM013414	60363165
C 277	93.5	6.5	1049	5	BM919417	BM919417	C 350	92	6.4	922	2	BF066038	HV_CEB001
C 278	93.5	6.5	3153	9	CL982154	OiFSC046	C 351	92	6.4	973	2	BE548456	601076021
C 279	93	6.5	594	2	BF090297	BF090297	C 352	92	6.4	1117	2	BE620421	601483628
C 280	93	6.5	618	1	AL507561	AL507561	C 353	92	6.4	1219	8	BZ579066	msb2 6164
C 281	93	6.5	620	1	AV557154	AV557154	C 354	92	6.4	1252	4	BM556363	AGENCOURT
C 282	93	6.5	626	6	CB840366	M15B-0644	C 355	92	6.4	2472	3	HSM804344	Homo sapi
C 283	93	6.5	653	6	CB518630	CB518630	C 356	91.5	6.4	481	2	BF702235	MI-P-AL-a
C 284	93	6.5	661	7	CK597927	AGENCOURT	C 357	91.5	6.4	538	2	BE759652	BB759652
C 285	93	6.5	670	7	CK266010	170005316	C 358	91.5	6.4	541	8	BZ580999	3590 1.36
C 286	93	6.5	677	4	BJ482168	BJ482168	C 359	91.5	6.4	568	6	CA624151	w11n.pk01
C 287	93	6.5	783	4	BM018953	603646907	C 360	91.5	6.4	595	6	CD661366	CD661366
C 288	93	6.5	797	5	BU009027	BU009027	C 361	91.5	6.4	619	4	BI134742	UI-M-BH3-
C 289	93	6.5	797	6	CB900781	tr1c024xd	C 362	91.5	6.4	634	7	CF115309	Shultzomi
C 290	93	6.5	797	7	CF870590	tr1c024xd	C 363	91.5	6.4	640	4	BI953782	HVSMEM001
C 291	93	6.5	813	7	CK76543	CK76543	C 364	91.5	6.4	660	8	BZ895801	NARP2 019
C 292	93	6.5	831	2	BF628948	BF628948	C 365	91.5	6.4	663	6	CA320541	UI-N-FW0-
C 293	93	6.5	863	4	BI118103	BI118103	C 366	91.5	6.4	678	4	BI716214	1031007H0
C 294	93	6.5	886	5	BU186573	AGENCOURT	C 367	91.5	6.4	688	5	BU400273	BU400273
C 295	93	6.5	887	4	BI655389	BI655389	C 368	91.5	6.4	741	5	BX862108	BX862108
C 296	93	6.5	891	5	BQ690378	BQ690378	C 369	91.5	6.4	748	5	BU265787	BU265787
C 297	93	6.5	917	6	CA984114	CA984114	C 370	91.5	6.4	773	9	CG198048	CG198048
C 298	93	6.5	960	5	BX423119	BX423119	C 371	91.5	6.4	786	9	CL980410	CL980410
C 299	93	6.5	972	9	CHS040VA	Tetraodon	C 372	91.5	6.4	876	8	CC332343	CC332343
C 300	93	6.5	992	7	CF880802	tr1c024xe	C 373	91.5	6.4	877	4	BG865243	BG865243
C 301	93	6.5	1077	8	BZ551827	pacs1-60	C 374	91.5	6.4	877	9	CG259213	CG259213

C 375	91.5	6.4	908	4	BI150114	602849342	448	90.5	6.3	696	4	BM608888	170006870
376	91.5	6.4	931	3	AY106485	Zea mays	449	90.5	6.3	697	6	CB055230	NISC gm08
377	91.5	6.4	932	4	BM561466	AGENCOURT	C 450	90.5	6.3	698	6	CB222421	UI-R-DV0-
378	91.5	6.4	1063	5	BM903637	AGENCOURT	C 451	90.5	6.3	711	6	CN237338	RJB132C02
C 379	91.5	6.4	1095	3	BC006189	Mus muscu	452	90.5	6.3	741	7	CV114366	AGENCOURT
380	91.5	6.4	1182	3	AY108490	Zea mays	453	90.5	6.3	754	7	CV0402970	AGENCOURT
C 381	91.5	6.4	1206	3	BC028330	Mus muscu	454	90.5	6.3	774	7	CO388439	AGENCOURT
382	91.5	6.4	1224	9	CL965137	OsIFCC011	455	90.5	6.3	782	7	BI767295	603057986
C 383	91.5	6.4	1501	3	CR617424	full-leng	456	90.5	6.3	786	4	BI767295	603057986
C 384	91.5	6.4	1550	3	CR601928	full-leng	457	90.5	6.3	818	7	CO554206	AGENCOURT
C 385	91.5	6.4	1868	3	BC012904	Homo sapi	458	90.5	6.3	822	7	CO395878	AGENCOURT
C 386	91.5	6.4	3750	9	AY414005	Mus muscu	459	90.5	6.3	829	7	CK773115	961720 MA
C 387	91.5	6.4	438	4	BM746010	K-EST0019	460	90.5	6.3	847	4	BG541318	602569821
C 388	91.5	6.4	499	6	CB878764	AGENCOURT	461	90.5	6.3	863	7	CO388794	AGENCOURT
C 389	91.5	6.4	507	8	BZ580639	3590_1_39	462	90.5	6.3	868	5	BX929045	602569821
C 390	91.5	6.4	585	4	BM501813	952036C08	463	90.5	6.3	871	5	BUI23191	603003133
C 391	91.5	6.4	615	4	BG369112	HVMEB1002	464	90.5	6.3	885	9	CG373673	OG4BK51TC
C 392	91.5	6.4	643	9	CG246867	OG0AB73TV	C 465	90.5	6.3	886	5	BQ882836	AGENCOURT
C 393	91.5	6.4	672	8	CG396334	PUHP171TB	C 466	90.5	6.3	906	2	AW982788	HVMEG0000
C 394	91.5	6.4	687	7	CK975303	4106527 B	467	90.5	6.3	908	5	BQ432053	AGENCOURT
C 395	91.5	6.4	690	7	CN161339	950622 MA	468	90.5	6.3	915	4	BG335095	602403573
C 396	91.5	6.4	706	6	CA122120	SCJFLR107	C 469	90.5	6.3	950	5	BQ641398	AGENCOURT
C 397	91.5	6.4	729	5	BX456257	BX456257	C 470	90.5	6.3	963	9	CC631613	OGUIG81TV
398	91.5	6.4	738	9	CG246859	OG0AB73TV	C 471	90.5	6.3	974	5	BUI23191	603003133
399	91.5	6.4	758	5	BUI249423	603592154	C 472	90.5	6.3	986	3	CR694341	Tetraodon
400	91.5	6.4	779	6	CA512710	UI-R-FJ0-	473	90.5	6.3	999	5	BX334546	603003133
401	91.5	6.4	795	9	CG734191	OGUME20TV	474	90.5	6.3	1056	5	BM922613	AGENCOURT
402	91.5	6.4	796	2	BF859402	963002C07	475	90.5	6.3	1070	9	CNS06821	T7 end of
C 403	91.5	6.4	817	2	BF264482	HV_CEA000	476	90.5	6.3	1088	4	BM544272	AGENCOURT
C 404	91.5	6.4	836	9	CG247683	OG1CV91TH	C 477	90.5	6.3	1089	9	CL944703	AGENCOURT
405	91.5	6.4	847	2	BE908929	601497867	478	90.5	6.3	1170	5	BQ896744	AGENCOURT
406	91.5	6.4	852	5	BQ890164	AGENCOURT	479	90.5	6.3	1214	2	BE422245	602403573
407	91.5	6.4	856	7	CN162742	952158 MA	C 480	90.5	6.3	1303	8	BZ570288	602403573
408	91.5	6.4	890	9	CG370784	OGYCH50TV	C 481	90.5	6.3	1363	3	CR653497	Tetraodon
409	91.5	6.4	898	9	CG680929	OGYCH50TV	C 482	90.5	6.3	1464	3	CR653497	Tetraodon
410	91.5	6.4	914	9	CG250633	CG250633	C 483	90.5	6.3	1577	3	CR694327	Tetraodon
411	91.5	6.4	920	7	CF580423	AGENCOURT	484	90.5	6.3	1623	3	AK043787	Mus muscu
C 412	91.5	6.4	964	4	BG023947	602303640	485	90.5	6.3	1717	3	CR620892	full-leng
C 413	91.5	6.4	972	5	BQ619005	RNOSEQ2E1	C 486	90.5	6.3	1774	4	BG743567	602633914
C 414	91.5	6.4	981	8	BZ570784	msb2_1534	C 487	90.5	6.3	1810	3	CR623164	full-leng
C 415	91.5	6.4	1005	9	CL970274	OsIFCC041	C 488	90.5	6.3	1843	3	BC032475	Homo sapi
416	91.5	6.4	1027	9	BM458216	AGENCOURT	C 489	90.5	6.3	1894	3	CR621766	full-leng
C 417	91.5	6.4	1039	5	BQ060881	AGENCOURT	C 490	90.5	6.3	2004	9	AY407914	Pan trogl
418	91.5	6.4	1103	4	BM558891	AGENCOURT	C 491	90.5	6.3	2127	9	CL504232	SAIL 734
419	91.5	6.4	1110	8	CG305860	CH261-113	C 492	90.5	6.3	2730	3	AK030866	Mus muscu
420	91.5	6.4	1350	9	CL970977	OsIFCC020	C 493	90.5	6.3	3042	9	CL960537	OsIFCC004
C 421	91.5	6.4	1476	3	CNSLTI1AK	human ful	C 494	90.5	6.3	3784	9	AY420498	Homo sapi
C 422	91.5	6.4	1492	3	CR621008	full-leng	495	90.5	6.3	505	5	BQ326397	CM3-CN009
C 423	91.5	6.4	1503	3	CR623408	full-leng	496	90.5	6.3	568	4	BI682896	464093 MA
C 424	91.5	6.4	1530	3	CNSLTI1AJ	human ful	497	90.5	6.3	577	6	CB249755	UI-M-EX0-
C 425	91.5	6.4	1551	3	CNSLTI1AL	human ful	498	90.5	6.3	582	5	BP297132	BP297132
C 426	91.5	6.4	1574	3	CR616658	full-leng	C 499	90.5	6.3	608	2	BE452945	602403573
C 427	91.5	6.4	1630	3	CR623931	full-leng	C 500	90.5	6.3	611	2	BP251191	BP251191
C 428	91.5	6.4	1639	3	CR602316	full-leng	C 501	90.5	6.3	616	9	CG348471	OGOCF72TV
C 429	91.5	6.4	1647	3	CR618931	full-leng	C 502	90.5	6.3	627	7	CN788353	602403573
C 430	91.5	6.4	1664	3	CR601083	full-leng	C 503	90.5	6.3	650	7	CN366219	170004706
C 431	91.5	6.4	1763	3	CR626376	full-leng	504	90.5	6.3	654	2	BF863865	602403573
C 432	91.5	6.4	1784	3	CNSLTI1AM	human ful	505	90.5	6.3	677	3	CR655376	Tetraodon
C 433	91.5	6.4	1845	3	CR621976	full-leng	C 506	90.5	6.3	678	7	CN157469	946180 MA
434	91.5	6.4	2340	9	CL972081	OsIFCC022	507	90.5	6.3	678	7	CN159412	946180 MA
C 435	91.5	6.4	2345	3	BC008814	Homo sapi	508	90.5	6.3	679	3	CR649445	Tetraodon
C 436	91.5	6.4	2348	3	BC062565	Homo sapi	509	90.5	6.3	683	3	CR652460	Tetraodon
C 437	91.5	6.4	2848	3	AK016522	602403573	510	90.5	6.3	684	3	CR642393	Tetraodon
C 438	91.5	6.4	2994	9	CL972758	OsIFCC023	511	90.5	6.3	688	3	CR634043	Tetraodon
C 439	91.5	6.4	3051	3	CNS0ALP6	Arabisops	512	90.5	6.3	688	3	CR651789	Tetraodon
C 440	91.5	6.4	3231	3	AY724521	Rattus no	513	90.5	6.3	689	3	CR642553	Tetraodon
C 441	91.5	6.4	4930	3	CR749837	Homo sapi	514	90.5	6.3	690	3	CR647097	Tetraodon
C 442	90.5	6.3	647	9	CO513881	s13dSG73F	515	90.5	6.3	692	3	CR640044	Tetraodon
C 443	90.5	6.3	647	9	CO513881	s13dSG73F	516	90.5	6.3	693	3	CR637526	Tetraodon
C 444	90.5	6.3	651	4	BM388938	UI-R-D20-	517	90.5	6.3	694	3	CR645308	Tetraodon
C 445	90.5	6.3	657	5	BQ208529	UI-R-DX1-	518	90.5	6.3	694	3	CR652067	Tetraodon
C 446	90.5	6.3	666	6	CA225062	SCCARM2C0	519	90.5	6.3	695	3	CR638115	Tetraodon
C 447	90.5	6.3	677	4	BI285583	UI-R-CW08	520	90.5	6.3	695	3	CR652304	Tetraodon

C 521	521	90	6.3	597	3	CR652825	Tetraodon	594	89.5	6.2	833	6	CB652492	OSJNEC021
C 522	522	90	6.3	707	6	CA283389	SCBGSD105	595	89.5	6.2	862	2	BF104612	BF104612 601647621
523	523	90	6.3	717	3	CR649811	Tetraodon	596	89.5	6.2	867	2	CO543777	LYS8T1143
524	524	90	6.3	730	3	CR650904	Tetraodon	C 597	89.5	6.2	870	5	BQ233203	AGENCOURT
525	525	90	6.3	737	8	AO631350	RPCI-11-4	598	89.5	6.2	886	5	BX424410	BX424410
526	526	90	6.3	748	9	CC664692	OGWEA07TV	599	89.5	6.2	893	9	CG338878	OG2BZ40TH
527	527	90	6.3	754	5	BZ271251	603508354	600	89.5	6.2	911	2	BF692621	603248980
528	528	90	6.3	761	3	CR634795	Tetraodon	C 601	89.5	6.2	922	5	BX328285	BX328285
529	529	90	6.3	761	3	CR646944	Tetraodon	602	89.5	6.2	930	6	CA976041	AGENCOURT
530	530	90	6.3	762	3	CR644580	Tetraodon	603	89.5	6.2	930	6	CA976041	AGENCOURT
531	531	90	6.3	764	6	CR523440	UI-M-GH0-	604	89.5	6.2	953	6	BY716393	BY716393
532	532	90	6.3	765	6	CB312195	AGENCOURT	C 605	89.5	6.2	956	6	BY716393	BY716393
C 533	533	90	6.3	766	2	BZ265921	HV_CEA001	C 606	89.5	6.2	1042	6	CD507684	CD507684
C 534	534	90	6.3	768	7	CNI41776	WOUND1_1	607	89.5	6.2	1051	1	AL564056	AL564056
535	535	90	6.3	773	4	BI818555	603033078	608	89.5	6.2	1102	5	BM908109	BM908109
536	536	90	6.3	776	3	CR638058	Tetraodon	C 609	89.5	6.2	1128	6	CD498522	CD498522
537	537	90	6.3	777	3	CR638828	Tetraodon	610	89.5	6.2	1206	3	AK011926	AK011926
538	538	90	6.3	777	3	CR640383	Tetraodon	611	89.5	6.2	1423	9	CL460782	CL460782
C 539	539	90	6.3	777	7	CNI48568	WOUND1_57	C 612	89.5	6.2	1484	3	CR603169	full-lang
540	540	90	6.3	778	3	CR636585	Tetraodon	613	89.5	6.2	2198	3	AK038734	Mus muscu
541	541	90	6.3	778	3	CR638807	Tetraodon	614	89.5	6.2	3098	3	AK044016	Mus muscu
542	542	90	6.3	778	3	CR654110	Tetraodon	615	89.5	6.2	3127	3	AK084631	Mus muscu
543	543	90	6.3	779	3	CR649270	Tetraodon	616	89.5	6.2	3358	3	AK048691	Mus muscu
544	544	90	6.3	779	3	CR651938	Tetraodon	617	89	6.2	375	7	CN031190	UMC-PGYO2
545	545	90	6.3	782	3	CR636544	Tetraodon	618	89	6.2	405	7	CN300678	170006008
546	546	90	6.3	782	3	CR647795	Tetraodon	619	89	6.2	485	1	AI634694	AI634694
C 547	547	90	6.3	786	6	CR629660	OSIIEB06B	620	89	6.2	514	5	EX280101	EX280101
548	548	90	6.3	787	3	CR636642	Tetraodon	621	89	6.2	550	8	BZ580996	BZ580996
549	549	90	6.3	789	3	CR651423	Tetraodon	C 622	89	6.2	562	8	BZ917191	CH240_102
C 550	550	90	6.3	792	4	BI193608	602946501	C 623	89	6.2	581	5	BP365751	BP365751
551	551	90	6.3	794	3	CR644935	Tetraodon	C 624	89	6.2	596	5	BQ463683	HG01B18r
552	552	90	6.3	794	3	CR646272	Tetraodon	C 625	89	6.2	606	9	AY408969	AY408969
553	553	90	6.3	794	3	CR649219	Tetraodon	C 626	89	6.2	609	4	BG705699	602668929
554	554	90	6.3	811	4	BG537371	602566561	627	89	6.2	611	9	CC526396	CH240_401
C 555	555	90	6.3	820	7	CO883041	BoVGen_11	C 628	89	6.2	616	6	CB878361	HP08E09T
C 556	556	90	6.3	822	7	CR948885	4074105_B	C 629	89	6.2	620	5	BQ468275	HP01K22T
557	557	90	6.3	856	4	BI768085	603056396	630	89	6.2	621	7	CN481338	hw06d04.Y
C 558	558	90	6.3	880	9	CS522797	CH240_371	C 631	89	6.2	624	1	AV924399	AV924399
559	559	90	6.3	886	7	CV212131	EST871841	C 632	89	6.2	631	6	CB877867	HP06H12T
C 560	560	90	6.3	932	4	BI771877	603055278	C 633	89	6.2	635	6	CB879862	HP02P01T
561	561	90	6.3	935	2	BF533003	602073530	C 634	89	6.2	637	6	CB877021	HP03E14T
C 562	562	90	6.3	953	6	BY717668	BY717668	C 635	89	6.2	648	9	CL156955	CL156955
C 563	563	90	6.3	979	5	BQ961288	AGENCOURT	C 636	89	6.2	654	7	CF789740	867039_MA
C 564	564	90	6.3	1044	5	BX337023	BX337023	C 637	89	6.2	665	4	BG280961	BG280961
C 565	565	90	6.3	1139	8	BZ563497	pacs2-164	C 638	89	6.2	667	9	CC559311	CH240_468
566	566	90	6.3	1179	2	BF307229	601891393	639	89	6.2	683	2	BE949497	UI-M-CCO-
C 567	567	90	6.3	1285	3	BC023209	Homo sapi	C 640	89	6.2	695	2	BF621894	HVSMEO000
C 568	568	90	6.3	1395	3	BC029348	Homo sapi	C 641	89	6.2	714	3	CR646145	Tetraodon
C 569	569	90	6.3	1491	1	AA424076	AA424076	C 642	89	6.2	716	7	CN135400	OX1_32_CO
C 570	570	89.5	6.2	491	1	AI807514	wf48f05.x	C 643	89	6.2	718	2	BE519877	HV_CEB002
C 571	571	89.5	6.2	549	1	AI807514	ic57d08_b	C 644	89	6.2	728	7	CV479233	CS_hyp_45
C 572	572	89.5	6.2	573	8	BZ310697	ic57d08_b	645	89	6.2	730	2	BE274037	601104335
C 573	573	89.5	6.2	576	2	BE357931	DG1_23_BO	C 646	89	6.2	748	7	CN139561	OX1_22_GO
C 574	574	89.5	6.2	581	9	CC674595	OGWCUT9TH	C 647	89	6.2	764	5	BUS95554	AGENCOURT
C 575	575	89.5	6.2	589	4	BJ769002	BJ769002	C 648	89	6.2	765	4	BI836384	603082901
576	576	89.5	6.2	589	4	BJ806535	BJ806535	C 649	89	6.2	765	7	CN134141	OX1_20_BO
C 577	577	89.5	6.2	662	9	CE171457	tigr-g88-	C 650	89	6.2	766	7	CN138735	OX1_13_D0
C 578	578	89.5	6.2	664	1	AV609758	AV609758	C 651	89	6.2	780	8	BZ577903	msh2_5629
C 579	579	89.5	6.2	670	9	CC533960	CH240_412	C 652	89	6.2	784	9	CG017514	ZUACH49TV
580	580	89.5	6.2	674	9	CC572653	CH240_449	C 653	89	6.2	799	4	BI772181	603056121
C 581	581	89.5	6.2	675	4	BI955087	HVSMEO02	C 654	89	6.2	803	9	CG318499	CG318499
C 582	582	89.5	6.2	689	7	CN134142	OX1_17_F0	C 655	89	6.2	806	9	CC482572	CH240_311
C 583	583	89.5	6.2	695	7	CN133695	OX1_17_F0	C 656	89	6.2	819	9	CC482572	CH240_311
584	584	89.5	6.2	707	8	AZ569578	262FvH05	657	89	6.2	823	5	BQ425155	AGENCOURT
585	585	89.5	6.2	732	7	CN060788	A06_Ag2_P	C 658	89	6.2	827	2	BF623285	HVSMEO001
586	586	89.5	6.2	733	7	CK433144	UI-D-GC1_P	C 659	89	6.2	832	4	BI949179	HVSMEO001
C 587	587	89.5	6.2	796	4	BG911734	602808202	C 660	89	6.2	837	4	BG571235	602592177
C 588	588	89.5	6.2	796	9	CC690766	OGUKB63TH	C 661	89	6.2	839	2	BF262287	BF262287
589	589	89.5	6.2	797	6	CB650217	OSJNEB141	C 662	89	6.2	844	9	CL526997	80E08rp42
C 590	590	89.5	6.2	801	4	BG367903	HVSMEO001	C 663	89	6.2	856	4	BI952488	HVSMEO000
C 591	591	89.5	6.2	820	8	BZ655107	OGCCS57TM	C 664	89	6.2	858	7	CN163976	994087_MA
C 592	592	89.5	6.2	825	5	BM944207	UI-M-EHOP	C 665	89	6.2	869	2	BF033230	601454485
C 593	593	89.5	6.2	830	6	CB630998	OSIIEB08E	C 666	89	6.2	869	4	BG968296	602834717

C 667	89	6.2	870	5	BX336730	BX336730	BX336730	740	88.5	6.2	1803	3	AK009709	Mus muscu
C 668	89	6.2	878	8	CG337734	CGPBE18TH	CG337734	C 741	88.5	6.2	1884	9	CI487289	SAIL 44 G
C 669	89	6.2	880	4	B1550580	603197828	B1550580	C 742	88.5	6.2	2327	7	CV068894	F2_new_ch
C 670	89	6.2	891	5	BUI61097	AGENCOURT	BUI61097	C 743	88.5	6.2	2538	9	CU980030	OSIFCC034
C 671	89	6.2	891	7	CV069595	WPAEHUX15	CV069595	C 744	88.5	6.2	3454	3	AK028441	Mus muscu
C 672	89	6.2	892	5	BQ441122	AGENCOURT	BQ441122	C 745	88.5	6.2	5262	9	CL967637	OsIFCC015
C 673	89	6.2	892	9	BQ894222	AGENCOURT	BQ894222	C 746	88.5	6.2	10655	3	AK090136	Mus muscu
C 674	89	6.2	923	9	CG702023	OGGAC07TM	CG702023	C 747	88	6.1	388	2	BF441044	257114 MA
C 675	89	6.2	937	8	BZ561320	pacs2-164	BZ561320	C 748	88	6.1	463	2	BF063267	7h87c12.x
C 676	89	6.2	940	4	B1770311	603056215	B1770311	C 749	88	6.1	463	2	BI057918	PM4-GN049
C 677	89	6.2	947	8	BZ571199	msb2 1773	BZ571199	C 750	88	6.1	575	6	CA186190	SCSGT311
C 678	89	6.2	968	9	CG881640	ZMMEB049	CG881640	C 751	88	6.1	579	4	BI407794	602919167
C 679	89	6.2	977	5	BX327801	BX327801	BX327801	C 752	88	6.1	595	5	BU648465	111206900
C 680	89	6.2	990	8	BZ564269	pacs2-164	BZ564269	C 753	88	6.1	597	6	CD887832	G118.106G
C 681	89	6.2	1006	4	BG425099	602452679	BG425099	C 754	88	6.1	620	4	EG300930	HVSNB001
C 682	89	6.2	1032	6	CD105894	AGENCOURT	CD105894	C 755	88	6.1	630	4	EM601221	170006870
C 683	89	6.2	1051	2	BF384507	602046471	BF384507	C 756	88	6.1	631	4	BJ453452	BJ453452
C 684	89	6.2	1078	8	BZ563432	pacs2-164	BZ563432	C 757	88	6.1	632	1	AA511080	vh61d05.r
C 685	89	6.2	1107	5	BX377454	BX377454	BX377454	C 758	88	6.1	635	6	CD898877	G174.110F
C 686	89	6.2	1119	5	BQ681628	AGENCOURT	BQ681628	C 759	88	6.1	638	4	BI953729	HVSNB001
C 687	89	6.2	1128	8	BZ558882	pacs2-164	BZ558882	C 760	88	6.1	638	6	CD898686	G174.109M
C 688	89	6.2	1168	8	BZ562536	pacs2-164	BZ562536	C 761	88	6.1	643	6	CD886350	G118.102B
C 689	89	6.2	1168	4	BI951926	HVSNB000	BI951926	C 762	88	6.1	655	7	CK979040	4110528 B
C 690	89	6.2	1211	5	BUS10035	AGENCOURT	BUS10035	C 763	88	6.1	660	5	BU647624	1112060A0
C 691	89	6.2	1220	3	CR662193	Tetraodon	CR662193	C 764	88	6.1	669	7	CV434385	CS hyp 33
C 692	89	6.2	1221	5	BM926108	AGENCOURT	BM926108	C 765	88	6.1	671	5	BM114846	EX114846
C 693	89	6.2	1267	3	CR677011	Tetraodon	CR677011	C 766	88	6.1	672	5	BM949540	UI-M-EGOP
C 694	89	6.2	1361	8	BZ580081	msb2_928	BZ580081	C 767	88	6.1	673	6	CA118767	SCBGLR111
C 695	89	6.2	1409	3	CR727990	Tetraodon	CR727990	C 768	88	6.1	685	8	BZ872430	CH240_192
C 696	89	6.2	1616	9	AG075498	Pan trogl	AG075498	C 769	88	6.1	685	9	CC562085	CH240_472
C 697	89	6.2	1750	9	AV415784	Mus muscu	AV415784	C 770	88	6.1	690	3	CR656616	Tetraodon
C 698	89	6.2	1759	3	BC029313	Homo sapi	BC029313	C 771	88	6.1	695	7	CK581028	IST W15 3
C 699	89	6.2	3270	3	BC035457	Homo sapi	BC035457	C 772	88	6.1	702	5	BM445000	BM445000
C 700	88.5	6.2	573	4	BJ104203	BJ104203	BJ104203	C 773	88	6.1	708	7	CV303090	CS_hyp_28
C 701	88.5	6.2	590	9	CG302675	OG3AX81TV	CG302675	C 774	88	6.1	710	3	CR654957	Tetraodon
C 702	88.5	6.2	600	4	BI799827	H14IG02 E	BI799827	C 775	88	6.1	711	7	CN149436	WOUNDI_62
C 703	88.5	6.2	623	8	BZ885549	CH240_244	BZ885549	C 776	88	6.1	711	7	CV463384	CS hyp 57
C 704	88.5	6.2	628	7	CO662703	CS_hyp_40	CO662703	C 777	88	6.1	718	5	BM444963	BM444963
C 705	88.5	6.2	678	7	CV479788	CS_hyp_40	CV479788	C 778	88	6.1	742	4	BM177866	BM177866
C 706	88.5	6.2	694	7	CN133843	OXI_18_D1	CN133843	C 779	88	6.1	764	9	CM506871	OP_Ba000
C 707	88.5	6.2	768	8	BH529737	BOGXF2TF	BH529737	C 780	88	6.1	765	4	BU583378	BU583378
C 708	88.5	6.2	783	8	BH564792	BOHFX19TF	BH564792	C 781	88	6.1	793	7	CK193516	CK193516
C 709	88.5	6.2	792	4	BM046604	603626685	BM046604	C 782	88	6.1	796	6	CA214548	SCSPB110
C 710	88.5	6.2	800	8	BZ574638	msb2 3762	BZ574638	C 783	88	6.1	802	7	CO063690	est_k_bre
C 711	88.5	6.2	812	4	BG417631	HVSNB001	BG417631	C 784	88	6.1	815	2	BF267926	HV_CEA001
C 712	88.5	6.2	831	7	CR635363	UI-M-HNO	CR635363	C 785	88	6.1	818	9	CG281398	OGWJ03TV
C 713	88.5	6.2	841	4	BI258457	602972447	BI258457	C 786	88	6.1	824	4	BG345164	HVSNB001
C 714	88.5	6.2	843	2	BF264360	HV_CEA000	BF264360	C 787	88	6.1	825	2	BF267638	HV_CEA001
C 715	88.5	6.2	849	4	BG751460	602730038	BG751460	C 788	88	6.1	825	9	CG324936	OG0BJ87TV
C 716	88.5	6.2	877	4	BM015034	603640995	BM015034	C 789	88	6.1	864	8	BZ863664	CH240_210
C 717	88.5	6.2	885	2	BE747335	601580329	BE747335	C 790	88	6.1	864	8	BZ559802	pacs2-164
C 718	88.5	6.2	888	4	BF984969	602308492	BF984969	C 791	88	6.1	871	6	CB960458	AGENCOURT
C 719	88.5	6.2	888	5	BQ687705	AGENCOURT	BQ687705	C 792	88	6.1	894	4	BF979661	602287964
C 720	88.5	6.2	894	5	BQ685576	AGENCOURT	BQ685576	C 793	88	6.1	909	5	BQ956203	AGENCOURT
C 721	88.5	6.2	899	4	BI909673	603070624	BI909673	C 794	88	6.1	916	9	CG281070	OG3AU02TH
C 722	88.5	6.2	906	9	CL963217	OsIFCC008	CL963217	C 795	88	6.1	926	9	CG625298	OGUKO53TV
C 723	88.5	6.2	915	6	CB589793	AGENCOURT	CB589793	C 796	88	6.1	929	5	BU528425	AGENCOURT
C 724	88.5	6.2	932	9	CC649322	OGUP11TV	CC649322	C 797	88	6.1	930	4	BU519939	603071721
C 725	88.5	6.2	950	8	BZ549147	pacs1-60	BZ549147	C 798	88	6.1	942	4	BG030352	602297468
C 726	88.5	6.2	951	9	CNS060JO	T7 end of	AL421289	C 799	88	6.1	972	5	EX375933	EX375933
C 727	88.5	6.2	956	5	BUS03920	AGENCOURT	BUS03920	C 800	88	6.1	977	8	CC199125	ZMMEB032
C 728	88.5	6.2	970	2	BE792500	601584964	BE792500	C 801	88	6.1	991	9	CNS03MTR	Tetraodon
C 729	88.5	6.2	999	9	CL949374	OsIFB005	CL949374	C 802	88	6.1	992	5	BM404307	BM404307
C 730	88.5	6.2	1000	1	AL524279	AL524279	AL524279	C 803	88	6.1	1042	7	CK211974	FGAS02383
C 731	88.5	6.2	1012	5	BUI46208	AGENCOURT	BUI46208	C 804	88	6.1	1062	4	BI410932	BI410932
C 732	88.5	6.2	1023	5	EX438826	EX438826	EX438826	C 805	88	6.1	1098	5	BQ880280	AGENCOURT
C 733	88.5	6.2	1029	5	BM919894	AGENCOURT	BM919894	C 806	88	6.1	1136	3	CR623119	full-len
C 734	88.5	6.2	1037	4	BG519654	602578771	BG519654	C 807	88	6.1	1136	3	BU163413	AGENCOURT
C 735	88.5	6.2	1044	3	AK020150	Mus muscu	AK020150	C 808	88	6.1	1202	3	CR725876	Tetraodon
C 736	88.5	6.2	1046	5	BQ056949	AGENCOURT	BQ056949	C 809	88	6.1	1226	4	BI411327	602964426
C 737	88.5	6.2	1076	5	BX359507	EX359507	BX359507	C 810	88	6.1	1234	5	BU856206	AGENCOURT
C 738	88.5	6.2	1158	2	BF578719	602093215	BF578719	C 811	88	6.1	1262	8	BZ578229	msb2_5755
C 739	88.5	6.2	1724	3	AK077751	Mus muscu	AK077751	C 812	88	6.1	1276	2	BF337756	602037535

C 813	88	6.1	1452	9	CL968968	CL968968	OsIFCC017	886	87.5	6.1	2901	3	AK031120	Mus muscu
C 814	88	6.1	1462	4	BG032875	BG032875	602300458	887	87.5	6.1	3104	3	AK044719	Mus muscu
C 815	88	6.1	1535	9	AG065661	AG065661	Pan trogl	888	87.5	6.1	3251	3	AK039337	Mus muscu
C 816	88	6.1	1578	9	CL945954	CL945954	OsIFSB001	889	87	6.1	402	5	BX102955	BX102955
C 817	88	6.1	2253	9	CL980455	CL980455	OsIFCC034	890	87	6.1	409	5	CG045303	CG045303
C 818	87.5	6.1	503	8	BZ781911	BZ781911	i132e06.g	891	87	6.1	413	5	BP614180	BP614180
C 819	87.5	6.1	538	4	BN258866	BN258866	523800.MA	892	87	6.1	418	5	AI620687	AI620687
C 820	87.5	6.1	597	9	CE056928	CE056928	tigr-g88-	893	87	6.1	564	5	BP742257	BP742257
C 821	87.5	6.1	614	4	BJ096164	BJ096164	BU096164	894	87	6.1	597	8	CN788819	CN788819
C 822	87.5	6.1	636	9	CE504464	CE504464	CH240.344	895	87	6.1	597	8	AQ689304	AQ689304
C 823	87.5	6.1	641	5	BP766024	BP766024	DG1.62.A0	896	87	6.1	600	4	BI986557	BI986557
C 824	87.5	6.1	650	2	BE360349	BE360349	DG1.62.A0	897	87	6.1	604	9	CL743745	CL743745
C 825	87.5	6.1	656	5	BU287394	BU287394	604163285	898	87	6.1	611	4	EG300690	EG300690
C 826	87.5	6.1	667	4	BI279634	BI279634	UI-R-DE0-	899	87	6.1	616	4	BM669774	BM669774
C 827	87.5	6.1	671	6	CD761542	CD761542	GGEZSM101	900	87	6.1	622	9	CC473143	CC473143
C 828	87.5	6.1	674	6	CA070113	CA070113	SCSGAD100	901	87	6.1	624	7	CN134980	CN134980
C 829	87.5	6.1	683	7	CN848704	CN848704	000520AAC	902	87	6.1	624	7	CD442675	CD442675
C 830	87.5	6.1	684	7	CN133868	CN133868	OX1.18.G0	903	87	6.1	631	6	BQ257103	BQ257103
C 831	87.5	6.1	697	9	CG695668	CG695668	CG695668	904	87	6.1	651	5	BQ257103	BQ257103
C 832	87.5	6.1	712	5	BQ865793	BQ865793	QGC5011.Y	905	87	6.1	651	5	CK972541	CK972541
C 833	87.5	6.1	716	6	CB247533	CB247533	UI-M-F10-	906	87	6.1	655	2	AW757596	AW757596
C 834	87.5	6.1	719	8	BZ858386	BZ858386	CH240.283	907	87	6.1	655	4	BI959218	BI959218
C 835	87.5	6.1	721	6	CA212718	CA212718	SCCST3C1	908	87	6.1	665	4	BI765133	BI765133
C 836	87.5	6.1	724	4	BI908181	BI908181	603067493	909	87	6.1	667	7	CK982658	CK982658
C 837	87.5	6.1	736	8	BZ634998	BZ634998	OGCC134TC	910	87	6.1	679	4	BI939098	BI939098
C 838	87.5	6.1	745	5	BI139755	BI139755	BP139755	911	87	6.1	679	7	CK947889	CK947889
C 839	87.5	6.1	755	4	BI836321	BI836321	603083012	912	87	6.1	679	7	CN853814	CN853814
C 840	87.5	6.1	762	4	BI768197	BI768197	6020356647	913	87	6.1	683	9	CG436783	CG436783
C 841	87.5	6.1	765	4	BG765688	BG765688	602739704	914	87	6.1	688	6	CA156029	CA156029
C 842	87.5	6.1	766	4	BI149125	BI149125	602913964	915	87	6.1	705	3	CK648705	CK648705
C 843	87.5	6.1	775	9	CNS02852	CNS02852	Tetraodon	916	87	6.1	706	7	CN144154	CN144154
C 844	87.5	6.1	776	5	BU408345	BU408345	603405184	917	87	6.1	729	6	CA231656	CA231656
C 845	87.5	6.1	785	8	BH383930	BH383930	AG-ND-172	918	87	6.1	730	8	BZ520704	BZ520704
C 846	87.5	6.1	788	9	CG631607	CG631607	OGULG81TH	919	87	6.1	731	5	CN150983	CN150983
C 847	87.5	6.1	796	9	CG244005	CG244005	OGHAA26TV	920	87	6.1	731	5	BX922736	BX922736
C 848	87.5	6.1	800	7	C0386693	C0386693	AGENCOURT	921	87	6.1	749	7	CN137496	CN137496
C 849	87.5	6.1	803	4	BI770839	BI770839	603058326	922	87	6.1	760	7	CN134678	CN134678
C 850	87.5	6.1	840	9	CE514203	CE514203	CH240.359	923	87	6.1	762	2	BF265661	BF265661
C 851	87.5	6.1	854	5	BU171653	BU171653	AGENCOURT	924	87	6.1	763	6	CA237471	CA237471
C 852	87.5	6.1	862	8	BZ799254	BZ799254	PUGBN13TD	925	87	6.1	767	9	CG436790	CG436790
C 853	87.5	6.1	868	2	BZ788300	BZ788300	601480103	926	87	6.1	769	8	BZ458224	BZ458224
C 854	87.5	6.1	868	6	CA291678	CA291678	SCQFL801	927	87	6.1	772	7	CN132717	CN132717
C 855	87.5	6.1	885	6	CD244547	CD244547	AGENCOURT	928	87	6.1	778	7	CN144331	CN144331
C 856	87.5	6.1	887	5	BQ731339	BQ731339	AGENCOURT	929	87	6.1	785	3	CR641779	CR641779
C 857	87.5	6.1	898	8	CG333766	CG333766	OG4BA10TC	930	87	6.1	788	3	CR644268	CR644268
C 858	87.5	6.1	902	8	CG376684	CG376684	PUHLU55TB	931	87	6.1	791	8	BZ853044	BZ853044
C 859	87.5	6.1	907	7	CF593730	CF593730	AGENCOURT	932	87	6.1	832	7	CF752360	CF752360
C 860	87.5	6.1	908	5	BQ645604	BQ645604	AGENCOURT	933	87	6.1	841	9	CC630803	CC630803
C 861	87.5	6.1	909	2	BE797774	BE797774	601586337	934	87	6.1	846	6	CB995082	CB995082
C 862	87.5	6.1	920	9	CG683070	CG683070	ZMHBBC015	935	87	6.1	849	9	CG674894	CG674894
C 863	87.5	6.1	930	2	BE732984	BE732984	601569754	936	87	6.1	851	8	BZ704179	BZ704179
C 864	87.5	6.1	938	9	CG445765	CG445765	OGTBJ19TV	937	87	6.1	856	5	BX916091	BX916091
C 865	87.5	6.1	939	2	BF300876	BF300876	602028876	938	87	6.1	872	6	CD050939	CD050939
C 866	87.5	6.1	940	8	BZ556971	BZ556971	pacel-60	940	87	6.1	887	7	CF585066	CF585066
C 867	87.5	6.1	948	8	CG665915	CG665915	OGLRG41TV	941	87	6.1	888	4	BG682602	BG682602
C 868	87.5	6.1	1012	4	BM550191	BM550191	AGENCOURT	942	87	6.1	891	2	BF663980	BF663980
C 869	87.5	6.1	1015	5	BQ888762	BQ888762	AGENCOURT	943	87	6.1	894	4	BF62140	BF62140
C 870	87.5	6.1	1024	5	BQ582226	BQ582226	AGENCOURT	944	87	6.1	928	5	BX396548	BX396548
C 871	87.5	6.1	1037	5	BQ900677	BQ900677	AGENCOURT	945	87	6.1	929	9	CG117193	CG117193
C 872	87.5	6.1	1059	9	CL991800	CL991800	ZMHBH000	946	87	6.1	933	9	CG297832	CG297832
C 873	87.5	6.1	1061	5	BM920114	BM920114	AGENCOURT	947	87	6.1	950	5	BQ918792	BQ918792
C 874	87.5	6.1	1067	5	BM920114	BM920114	AGENCOURT	948	87	6.1	953	5	BX336948	BX336948
C 875	87.5	6.1	1135	4	BM803335	BM803335	AGENCOURT	949	87	6.1	960	5	BM903732	BM903732
C 876	87.5	6.1	1174	5	BM914761	BM914761	AGENCOURT	950	87	6.1	973	5	BQ073527	BQ073527
C 877	87.5	6.1	1311	3	CR607553	CR607553	full_leng	951	87	6.1	996	9	CL961407	CL961407
C 878	87.5	6.1	1419	9	CL973598	CL973598	OsIFCC024	952	87	6.1	1029	4	BM544473	BM544473
C 879	87.5	6.1	1479	4	BG862470	BG862470	602796008	953	87	6.1	1031	5	BUS02796	BUS02796
C 880	87.5	6.1	1510	9	AG356852	AG356852	Mus muscu	954	87	6.1	1045	5	CL471991	CL471991
C 881	87.5	6.1	1524	3	AK077719	AK077719	Mus muscu	955	87	6.1	1072	5	BQ217632	BQ217632
C 882	87.5	6.1	1670	4	BF975317	BF975317	60245736	956	87	6.1	1073	1	AL519958	AL519958
C 883	87.5	6.1	2259	9	CL965071	CL965071	OsIFCC011	957	87	6.1	1098	5	BUS27314	BUS27314
C 884	87.5	6.1	2305	3	BC044627	BC044627	Homo sapi	958	87	6.1	1122	6	CD507271	CD507271
C 885	87.5	6.1												
C 886	87.5	6.1												
C 887	87.5	6.1												
C 888	87.5	6.1												
C 889	87.5	6.1												
C 890	87.5	6.1												
C 891	87.5	6.1												
C 892	87.5	6.1												
C 893	87.5	6.1												
C 894	87.5	6.1												
C 895	87.5	6.1												
C 896	87.5	6.1												
C 897	87.5	6.1												
C 898	87.5	6.1												
C 899	87.5	6.1												
C 900	87.5	6.1												
C 901	87.5	6.1												
C 902	87.5	6.1												
C 903	87.5	6.1												
C 904	87.5	6.1												
C 905	87.5	6.1												
C 906	87.5	6.1												
C 907	87.5	6.1												
C 908	87.5	6.1												
C 909	87.5	6.1												
C 910	87.5	6.1												
C 911	87.5	6.1												
C 912	87.5	6.1	</											

c 959	87	6.1	1257	9	AG066326	Pan trogl	AG066326	86.5	6.0	1403	9	AG186950	AG186950	Pan trogl
960	87	6.1	1337	7	CO635720	AGENCOURT	CO635720	86.5	6.0	1563	3	CNS0A6QF	AX824382	Arabidops
961	87	6.1	1360	4	BM552690	AGENCOURT	BM552690	86.5	6.0	1679	3	AK011229	Mus muscu	AX824382
962	87	6.1	1414	3	CR643446	Tetraodon	CR643446	86.5	6.0	1823	3	CR633902	Tetraodon	CR633902
963	87	6.1	1506	9	CL961254	OsifCC005	CL961254	86.5	6.0	1870	9	CG758664	P051-4-D0	CG758664
c 964	87	6.1	1733	3	BC024308	Homo sapi	BC024308	86.5	6.0	1923	9	CL979626	OsifCC033	CL979626
965	87	6.1	1811	5	BU103687	SCERT102	BU103687	86.5	6.0	1933	7	CO635679	Contig976	CL979626
c 966	87	6.1	2841	3	AK044765	Mus muscu	AK044765	86.5	6.0	2415	9	CL944530	OsifSB004	CL944530
967	87	6.1	3167	3	BC024102	Homo sapi	BC024102	86.5	6.0	3289	3	AK029933	Mus muscu	AK029933
c 968	87	6.1	3860	3	CR749395	Homo sapi	CR749395	86.5	6.0	3791	9	AY400807	Pan trogl	AY400807
969	87	6.1	6285	3	CR749818	Homo sapi	CR749818	86.5	6.0	3823	3	AK031712	Mus muscu	AK031712
c 970	86.5	6.0	369	7	CG342275	AGENCOURT	CG342275	86.5	6.0	3947	3	BC048169	AG622698	np36509.8
c 971	86.5	6.0	404	4	BG945069	RC6-AN006	BG945069	86	6.0	299	1	AA622698	np36509.8	AG622698
972	86.5	6.0	491	4	BM255549	517317 MA	BM255549	86	6.0	409	5	BY419748	BY419748	BY419748
973	86.5	6.0	514	6	CD051515	ds159 P	CD051515	86	6.0	434	1	AA188733	3P78C07.1	AA188733
974	86.5	6.0	541	6	CA830804	1117009C1	CA830804	86	6.0	434	7	CK465159	936237 MA	CK465159
975	86.5	6.0	542	4	BU121236	BU121236	BU121236	86	6.0	434	7	CK465159	936237 MA	CK465159
976	86.5	6.0	548	7	CO219787	WS0107.B2	CO219787	86	6.0	469	6	CA616905	938541 MA	CA616905
c 977	86.5	6.0	573	5	BP214058	BP214058	BP214058	86	6.0	486	6	CB726880	AMGNNUC.N	CB726880
c 978	86.5	6.0	595	2	BF622001	HVSNEA000	BF622001	86	6.0	493	1	AV396713	AV396713	AV396713
c 979	86.5	6.0	600	9	CG767568	CH240.134	CG767568	86	6.0	520	4	BI5339757	452547 MA	BI5339757
c 980	86.5	6.0	605	6	CB469226	sn04_G10	CB469226	86	6.0	520	9	CW011396	ZMBELC000	CW011396
c 981	86.5	6.0	617	9	CW012740	ZMBELC000	CW012740	86	6.0	561	7	CR287289	CR287289	CR287289
c 982	86.5	6.0	638	4	BI873687	963110E05	BI873687	86	6.0	561	8	BZ866306	CH240.235	BZ866306
c 983	86.5	6.0	638	7	CO517169	sl3GSG33D	CO517169	86	6.0	566	5	BU579630	im88C01.X	BU579630
c 984	86.5	6.0	647	7	CN141013	OX1.48.F1	CN141013	86	6.0	579	1	AV592949	AV592949	AV592949
985	86.5	6.0	670	5	BP460698	BP460698	BP460698	86	6.0	594	1	AI655373	ts98A09.X	AI655373
c 986	86.5	6.0	670	7	CN217818	RJA018F09	CN217818	86	6.0	600	4	BI340290	365514 MA	BI340290
c 987	86.5	6.0	684	8	BZ395719	EINEOI16TR	BZ395719	86	6.0	605	5	BU619355	UI-H-FU1-	BU619355
c 988	86.5	6.0	690	4	BM684639	UI-E-EO1-	BM684639	86	6.0	605	8	BZ832394	CH240.222	BZ832394
c 989	86.5	6.0	699	7	CR835304	4059703 B	CR835304	86	6.0	609	5	BU644968	mgnb017XM	BU644968
c 990	86.5	6.0	699	7	CN220142	WLA013D03	CN220142	86	6.0	616	5	BU571866	946185F12	BU571866
c 991	86.5	6.0	705	2	BZ214076	HV.CEB000	BZ214076	86	6.0	623	9	CC489668	CH240.322	CC489668
c 992	86.5	6.0	712	8	BZ528091	OGAJR28TM	BZ528091	86	6.0	625	2	BE532956	601234369	BE532956
993	86.5	6.0	715	5	BM943102	UI-M-CG0P	BM943102	86	6.0	636	4	BI910072	603067905	BI910072
c 994	86.5	6.0	715	7	CK782207	UI-M-H30-	CK782207	86	6.0	641	9	CC762973	CH240.234	CC762973
c 995	86.5	6.0	720	7	CN432579	BE030002A	CN432579	86	6.0	641	9	CC762973	CH240.3E1	CC762973
996	86.5	6.0	728	9	CG198051	PUIAY67TV	CG198051	86	6.0	642	9	CC563308	CH240.474	CC563308
c 997	86.5	6.0	729	9	CG630762	OGUIG71TV	CG630762	86	6.0	644	4	BM001090	103105380	BM001090
c 998	86.5	6.0	730	7	CO217178	WS0047.B2	CO217178	86	6.0	656	9	CR831075	GR0AA63C	CR831075
c 999	86.5	6.0	731	9	CS569846	CH240.445	CS569846	86	6.0	658	3	CR648458	Tetraodon	CR648458
1000	86.5	6.0	732	5	BM950513	UI-M-EHOP	BM950513	86	6.0	675	4	BI954151	HVSNEA001	BI954151
c1001	86.5	6.0	734	6	CA468398	AGENCOURT	CA468398	86	6.0	677	5	BM973798	UI-CF-EC1	BM973798
1002	86.5	6.0	734	7	CN225286	WLA069H10	CN225286	86	6.0	681	9	CC500845	CH240.338	CC500845
1003	86.5	6.0	737	6	CN225286	WLA069H10	CN225286	86	6.0	682	2	BE280853	601155421	BE280853
1004	86.5	6.0	766	7	CO730199	UI-H-FU1-	CO730199	86	6.0	682	2	BE280853	601155421	BE280853
c1005	86.5	6.0	766	7	CO740445	SLL07827	CO740445	86	6.0	685	9	CC589126	CH240.387	CC589126
c1006	86.5	6.0	773	4	BM008340	603617316	BM008340	86	6.0	691	7	CN137459	OX1.57.A0	CN137459
c1007	86.5	6.0	776	5	BU122625	603149251	BU122625	86	6.0	692	4	BI252769	602952833	BI252769
c1008	86.5	6.0	791	5	BX352322	BX352322	BX352322	86	6.0	694	7	CN140375	OX1.35.F0	CN140375
c1009	86.5	6.0	801	6	CF066352	Ac3912.AM	CF066352	86	6.0	694	9	CC511731	CH240.355	CC511731
c1010	86.5	6.0	819	7	CP745353	UI-M-GVO-	CP745353	86	6.0	695	7	CN149557	WOUND1.63	CN149557
c1011	86.5	6.0	824	6	CD439604	EL01N0526	CD439604	86	6.0	698	7	CN145724	WOUND1.34	CN145724
c1012	86.5	6.0	830	6	CB670497	OSUNEEO3J	CB670497	86	6.0	698	9	CL154052	104.338.1	CL154052
c1013	86.5	6.0	864	6	CL109938	AGENCOURT	CL109938	86	6.0	702	9	CC585519	CH240.382	CC585519
c1014	86.5	6.0	867	9	CL415688	ZMBBB042	CL415688	86	6.0	703	4	BU167897	BU167897	BU167897
c1015	86.5	6.0	894	6	CA185212	SCSBST309	CA185212	86	6.0	705	9	CC587560	CH240.385	CC587560
c1016	86.5	6.0	895	5	BQ232886	AGENCOURT	BQ232886	86	6.0	707	7	CN139895	OX1.24.G0	CN139895
c1017	86.5	6.0	925	5	BQ883149	AGENCOURT	BQ883149	86	6.0	707	7	CN140336	OX1.35.C0	CN140336
c1018	86.5	6.0	925	2	BQ960337	AGENCOURT	BQ960337	86	6.0	707	7	CN399921	170005321	CN399921
c1019	86.5	6.0	926	2	BQ970559	601679765	BQ970559	86	6.0	711	7	CN147983	WOUND1.53	CN147983
c1020	86.5	6.0	926	6	CB204967	AGENCOURT	CB204967	86	6.0	713	8	BG678096	602625839	BG678096
c1021	86.5	6.0	930	1	AL566821	AL566821	AL566821	86	6.0	714	7	CR559093	CH240.221	CR559093
c1022	86.5	6.0	963	9	CL970133	OsifCC019	CL970133	86	6.0	714	7	CR559093	DXP2P468J	CR559093
c1023	86.5	6.0	972	5	BQ925595	AGENCOURT	BQ925595	86	6.0	716	7	CN146525	WOUND1.41	CN146525
c1024	86.5	6.0	976	7	CF546891	AGENCOURT	CF546891	86	6.0	718	1	AA983446	Oq9B06.8	AA983446
c1025	86.5	6.0	1020	9	CL018874	CH216-4D1	CL018874	86	6.0	719	7	CN144341	WOUND1.21	CN144341
c1026	86.5	6.0	1023	5	BQ680487	AGENCOURT	BQ680487	86	6.0	724	9	CC554192	CH240.460	CC554192
c1027	86.5	6.0	1080	5	BX334929	BX334929	BX334929	86	6.0	725	7	CN138867	OX1.14.B1	CN138867
c1028	86.5	6.0	1085	4	BM805302	AGENCOURT	BM805302	86	6.0	726	7	CN147855	WOUND1.52	CN147855
c1029	86.5	6.0	1121	6	CB995357	AGENCOURT	CB995357	86	6.0	726	7	CN143327	WOUND1.15	CN143327
c1030	86.5	6.0	1161	8	BZ579434	msH2.6353	BZ579434	86	6.0	726	9	CC592505	CH240.393	CC592505
c1031	86.5	6.0	1238	9	CG746469	P039-3-H0	CG746469	86	6.0	730	6	CA158440	SCEZR2309	CA158440

1105	86	6.0	732	4	BJ171151	BJ171151	86	6.0	816	7	CN134585	CN134585	OX1_27_F0
1106	86	6.0	733	9	CC586672	CH240_384	86	6.0	816	9	CC589396	CH240_388	CC589396
1107	86	6.0	734	9	CC509659	CH240_352	86	6.0	818	4	BG702456	CH202456	BG702456
1108	86	6.0	735	9	CE221501	tigr-G8a-	86	6.0	819	7	CK791519	AGENCOURT	CK791519
1109	86	6.0	735	9	CN148623	WOUND1_57	86	6.0	824	7	CN140221	OX1_34_G0	CN140221
1110	86	6.0	735	7	CN151158	WOUND1_73	86	6.0	826	7	CK794617	AGENCOURT	CK794617
1111	86	6.0	738	5	BQ45468	UI-CF-ENI	86	6.0	832	9	CC536103	CH240_415	CC536103
1112	86	6.0	738	5	BQ45468	UI-CF-ENI	86	6.0	832	9	CC536103	CH240_415	CC536103
1113	86	6.0	739	7	CN147720	WOUND1_51	86	6.0	834	7	CN148634	WOUND1_57	CN148634
1114	86	6.0	740	7	CN148459	WOUND1_56	86	6.0	837	7	CN152355	WOUND1_81	CN152355
1115	86	6.0	740	7	CN147623	WOUND1_50	86	6.0	841	7	CN148754	WOUND1_58	CN148754
1116	86	6.0	741	7	CN148202	WOUND1_54	86	6.0	841	9	CG367567	CGXBH14TH	CG367567
1117	86	6.0	741	7	CN150970	WOUND1_72	86	6.0	842	7	CK193475	FGAS00188	CK193475
1118	86	6.0	742	1	AUI32766	AUI32766	86	6.0	842	9	CG251566	CGZBG11TH	CG251566
1119	86	6.0	742	7	CN132887	OX1_8_G05	86	6.0	844	9	CN135725	OX1_38_D0	CN135725
1120	86	6.0	742	7	CN137824	OX1_59_H0	86	6.0	844	9	CC520507	CH240_367	CC520507
1121	86	6.0	742	9	CC507175	CH240_348	86	6.0	851	2	BF583262	602101725	BF583262
1122	86	6.0	742	9	CC981727	ZUACD45TH	86	6.0	854	7	CN132986	OX1_9_A07	CN132986
1123	86	6.0	743	4	BJ167473	BJ167473	86	6.0	855	9	CNS03XN2	Tet-raodon	AL465223
1124	86	6.0	743	4	BJ171757	BJ171757	86	6.0	857	9	CC474906	CH240_300	CC474906
1125	86	6.0	743	4	BJ602382	BJ602382	86	6.0	861	9	CC593836	CH240_395	CC593836
1126	86	6.0	744	9	CC489586	CH240_322	86	6.0	862	5	BP172130	BP172130	BP172130
1127	86	6.0	745	9	CC478230	CH240_304	86	6.0	862	7	CN148954	WOUND1_59	CN148954
1128	86	6.0	749	7	CN147043	WOUND1_46	86	6.0	865	9	CG249561	OGYBW01TH	CG249561
1129	86	6.0	750	7	CN145375	WOUND1_28	86	6.0	866	4	BG334285	602461790	BG334285
1130	86	6.0	751	7	CN147603	WOUND1_50	86	6.0	866	5	BUS29044	AGENCOURT	BUS29044
1131	86	6.0	752	7	CN148219	WOUND1_54	86	6.0	869	9	CC484829	CH240_314	CC484829
1132	86	6.0	753	4	BG684048	602635658	86	6.0	870	5	BQ641748	AGENCOURT	BQ641748
1133	86	6.0	753	7	CN144666	WOUND1_23	86	6.0	872	7	CN136367	OX1_42_C0	CN136367
1134	86	6.0	754	8	BZ859977	CH240_286	86	6.0	874	4	BG747965	602705632	BG747965
1135	86	6.0	756	7	CN140474	OX1_36_B0	86	6.0	883	7	CN136692	OX1_44_F0	CN136692
1136	86	6.0	757	2	BF630737	HVSMB001	86	6.0	887	7	CO063216	est_k_bre	CO063216
1137	86	6.0	759	7	CN140032	OX1_33_D0	86	6.0	891	4	BG293666	OG3CV94TV	BG293666
1138	86	6.0	760	7	CN134692	OX1_27_H0	86	6.0	907	5	BX347595	OG3CV94TV	BX347595
1139	86	6.0	761	5	BX840232	BX840232	86	6.0	911	7	CN148961	WOUND1_59	CN148961
1140	86	6.0	762	6	CD432729	ETH1_25_H	86	6.0	928	5	BQ674900	AGENCOURT	BQ674900
1141	86	6.0	764	2	BE277913	601120290	86	6.0	933	6	CB181809	AGENCOURT	CB181809
1142	86	6.0	764	7	CN137689	OX1_58_H1	86	6.0	935	5	BQ647364	AGENCOURT	BQ647364
1143	86	6.0	767	7	CN135930	OX1_39_G0	86	6.0	940	5	BQ920746	AGENCOURT	BQ920746
1144	86	6.0	768	7	CN138408	OX1_63_D0	86	6.0	949	7	CO581053	ILLUMIGN	CO581053
1145	86	6.0	768	7	CN150683	WOUND1_70	86	6.0	953	5	BQ721531	AGENCOURT	BQ721531
1146	86	6.0	771	7	CN149388	WOUND1_62	86	6.0	955	7	CK182866	EST772181	CK182866
1147	86	6.0	772	7	CN140057	OX1_33_F0	86	6.0	969	6	BY716204	BY716204	BY716204
1148	86	6.0	773	7	CF132245	UI-HF-FQ0	86	6.0	969	6	CC650477	OGUAZ10TV	CC650477
1149	86	6.0	775	7	CN149412	WOUND1_62	86	6.0	975	5	BQ945751	AGENCOURT	BQ945751
1150	86	6.0	776	7	CN134505	OX1_26_F0	86	6.0	982	5	BX331859	BX331859	BX331859
1151	86	6.0	776	7	CN136997	OX1_54_C0	86	6.0	989	3	CF5652848	Tet-raodon	CF5652848
1152	86	6.0	778	2	BF866617	963068E12	86	6.0	990	9	CC710075	OGUHN69TV	CC710075
1153	86	6.0	778	7	CN145718	WOUND1_34	86	6.0	990	9	CU198217	ZMMBBC024	CU198217
1154	86	6.0	780	7	CN148894	WOUND1_59	86	6.0	1020	5	BX343348	BX343348	BX343348
1155	86	6.0	781	4	B1520385	603071863	86	6.0	1035	3	CR726723	Tet-raodon	CR726723
1156	86	6.0	783	7	CN136864	OX1_53_F0	86	6.0	1036	9	CG434327	ZMMBBC005	CG434327
1157	86	6.0	785	7	CN136402	OX1_42_G0	86	6.0	1040	4	BM559574	AGENCOURT	BM559574
1158	86	6.0	785	7	CN144467	WOUND1_22	86	6.0	1048	5	BX438346	BX438346	BX438346
1159	86	6.0	788	7	CF932223	TrEST-B25	86	6.0	1068	5	BUI77863	AGENCOURT	BUI77863
1160	86	6.0	789	7	CN133059	OX1_9_H05	86	6.0	1093	4	BM560965	AGENCOURT	BM560965
1161	86	6.0	790	7	CN136056	OX1_40_C0	86	6.0	1098	4	BI912745	603176136	BI912745
1162	86	6.0	791	8	BZ870305	CH240_248	86	6.0	1098	5	BX337038	BX337038	BX337038
1163	86	6.0	793	7	CN151320	WOUND1_74	86	6.0	1119	3	CF5640777	Tet-raodon	CF5640777
1164	86	6.0	796	9	CG285423	CG5AU01TC	86	6.0	1125	4	BM551740	AGENCOURT	BM551740
1165	86	6.0	797	9	CC536552	CH240_415	86	6.0	1125	4	BM551740	AGENCOURT	BM551740
1166	86	6.0	798	7	CN148345	WOUND1_55	86	6.0	1150	5	B0839187	AGENCOURT	B0839187
1167	86	6.0	801	7	CV463060	CS_hyp_49	86	6.0	1243	5	B0721351	AGENCOURT	B0721351
1168	86	6.0	802	7	CN136880	OX1_53_G1	86	6.0	1330	4	BM811176	AGENCOURT	BM811176
1169	86	6.0	804	7	CN143629	WOUND1_17	86	6.0	1600	3	CNS0ARAC0	AGENCOURT	CNS0ARAC0
1170	86	6.0	806	7	CN145867	WOUND1_35	86	6.0	1784	2	BF312396	601898936	BF312396
1171	86	6.0	807	9	CC581438	CH240_376	86	6.0	1879	9	CU969921	OG1FCC019	CU969921
1172	86	6.0	808	7	CN134423	BI413618	86	6.0	1894	4	BG328291	602427267	BG328291
1173	86	6.0	811	4	BI413618	OX1_26_F0	86	6.0	2091	3	AK017844	Mus muscu	AK017844
1174	86	6.0	812	7	CN134514	OX1_26_G0	86	6.0	2283	3	AK011533	Mus muscu	AK011533
1175	86	6.0	812	7	CN136294	OX1_42_C0	86	6.0	3598	3	AK030410	Mus muscu	AK030410
1176	86	6.0	812	7	CN136609	OX1_44_F0	86	6.0	4532	3	AK090093	Mus muscu	AK090093
1177	86	6.0	813	9	CC521671	CH240_369	86	6.0	491	1	AL039275	DKF2p434A	AL039275

1251	85.5	6.0	514	4	BJ803040	BJ803040	BJ803040	BJ803040	85.5	6.0	1324	85.5	6.0	957	3	CR708534	CR708534	Tetraodon
1252	85.5	6.0	530	8	BZ566382	pac82-164	BZ566382	pac82-164	85.5	6.0	1325	85.5	6.0	969	5	BUL93436	BUL93436	AGENCY
1253	85.5	6.0	536	8	AZ089498	RPC1-23-4	AZ089498	RPC1-23-4	85.5	6.0	1326	85.5	6.0	970	4	B1597080	B1597080	AGENCY
1254	85.5	6.0	559	1	AI871505	w167h03.x	AI871505	w167h03.x	85.5	6.0	1327	85.5	6.0	973	4	B1226777	B1226777	AGENCY
1255	85.5	6.0	560	4	BI528759	1024093C0	BI528759	1024093C0	85.5	6.0	1328	85.5	6.0	976	5	BM926289	BM926289	AGENCY
1256	85.5	6.0	600	7	CF182341	UI-N-EXO-	CF182341	UI-N-EXO-	85.5	6.0	1329	85.5	6.0	975	5	BM940398	BM940398	AGENCY
1257	85.5	6.0	601	4	BI991853	1020053F0	BI991853	1020053F0	85.5	6.0	1330	85.5	6.0	981	2	BE793251	BE793251	AGENCY
1258	85.5	6.0	631	7	CF909004	A0530F03-	CF909004	A0530F03-	85.5	6.0	1331	85.5	6.0	990	5	BO960405	BO960405	AGENCY
1259	85.5	6.0	638	4	BM749316	K-EST0024	BM749316	K-EST0024	85.5	6.0	1332	85.5	6.0	992	3	CR711939	CR711939	Tetraodon
1260	85.5	6.0	639	6	CB469855	snl1_H07.	CB469855	snl1_H07.	85.5	6.0	1333	85.5	6.0	998	5	EX342369	EX342369	Tetraodon
1261	85.5	6.0	643	1	AA391499	ld10174.5	AA391499	ld10174.5	85.5	6.0	1334	85.5	6.0	1001	2	BE548710	BE548710	AGENCY
1262	85.5	6.0	648	4	BG043738	sv27e08.Y	BG043738	sv27e08.Y	85.5	6.0	1335	85.5	6.0	1001	4	BG395869	BG395869	AGENCY
1263	85.5	6.0	658	2	BB642617	BB642617	BB642617	BB642617	85.5	6.0	1336	85.5	6.0	1006	3	CR716042	CR716042	Tetraodon
1264	85.5	6.0	663	9	CG016859	ZUAB32TH	CG016859	ZUAB32TH	85.5	6.0	1337	85.5	6.0	1007	3	CR716928	CR716928	Tetraodon
1265	85.5	6.0	668	7	CK947906	4072583.B	CK947906	4072583.B	85.5	6.0	1338	85.5	6.0	1008	9	CNS03CVT	CNS03CVT	Tetraodon
1266	85.5	6.0	675	9	CC480869	CH240.308	CC480869	CH240.308	85.5	6.0	1339	85.5	6.0	1039	2	BF125415	BF125415	AGENCY
1267	85.5	6.0	687	4	BG340132	602437713	BG340132	602437713	85.5	6.0	1340	85.5	6.0	1049	4	BM561005	BM561005	AGENCY
1268	85.5	6.0	697	7	CN142676	WOUND1.11	CN142676	WOUND1.11	85.5	6.0	1341	85.5	6.0	1059	5	BQ691667	BQ691667	AGENCY
1269	85.5	6.0	698	4	BG859559	1024064A1	BG859559	1024064A1	85.5	6.0	1342	85.5	6.0	1083	5	BQ879397	BQ879397	AGENCY
1270	85.5	6.0	700	6	CD053874	HO03D24S	CD053874	HO03D24S	85.5	6.0	1343	85.5	6.0	1089	5	BM925969	BM925969	AGENCY
1271	85.5	6.0	700	7	CN142583	WOUND1.10	CN142583	WOUND1.10	85.5	6.0	1344	85.5	6.0	1096	4	BG746209	BG746209	AGENCY
1272	85.5	6.0	704	1	AA790552	w17h03.r	AA790552	w17h03.r	85.5	6.0	1345	85.5	6.0	1098	7	CK210787	CK210787	AGENCY
1273	85.5	6.0	717	6	CA243627	SCQFL407	CA243627	SCQFL407	85.5	6.0	1346	85.5	6.0	1107	5	BQ686727	BQ686727	AGENCY
1274	85.5	6.0	719	2	BF220330	601296987	BF220330	601296987	85.5	6.0	1347	85.5	6.0	1120	5	BM922869	BM922869	AGENCY
1275	85.5	6.0	731	8	BZ342449	ic83e12.b	BZ342449	ic83e12.b	85.5	6.0	1348	85.5	6.0	1126	4	BG293989	BG293989	AGENCY
1276	85.5	6.0	739	7	CO001589	EST789924	CO001589	EST789924	85.5	6.0	1349	85.5	6.0	1161	4	BG403494	BG403494	AGENCY
1277	85.5	6.0	741	6	CD430898	ETH1.5.A0	CD430898	ETH1.5.A0	85.5	6.0	1350	85.5	6.0	1204	8	B2556358	B2556358	AGENCY
1278	85.5	6.0	748	7	CN136253	OX1_41.G0	CN136253	OX1_41.G0	85.5	6.0	1351	85.5	6.0	1248	5	BM913610	BM913610	AGENCY
1279	85.5	6.0	750	9	CL542158	OB_Ba006	CL542158	OB_Ba006	85.5	6.0	1352	85.5	6.0	1296	5	CL972919	CL972919	AGENCY
1280	85.5	6.0	754	7	CF748814	UI-N-HJ0-	CF748814	UI-N-HJ0-	85.5	6.0	1353	85.5	6.0	1485	9	CL981424	CL981424	AGENCY
1281	85.5	6.0	759	5	BQ572373	UI-N-PD0-	BQ572373	UI-N-PD0-	85.5	6.0	1354	85.5	6.0	1713	3	AK044604	AK044604	AGENCY
1282	85.5	6.0	760	2	BF616953	HVMEC001	BF616953	HVMEC001	85.5	6.0	1355	85.5	6.0	1803	2	BE962810	BE962810	AGENCY
1283	85.5	6.0	760	7	CF429971	PH1.25.G0	CF429971	PH1.25.G0	85.5	6.0	1356	85.5	6.0	2216	3	BC051962	BC051962	AGENCY
1284	85.5	6.0	770	7	CV463398	CS_FVD_53	CV463398	CS_FVD_53	85.5	6.0	1357	85.5	6.0	2225	3	CF625324	CF625324	AGENCY
1285	85.5	6.0	771	9	CG439436	CG8AE41IV	CG439436	CG8AE41IV	85.5	6.0	1358	85.5	6.0	2836	3	AK078023	AK078023	AGENCY
1286	85.5	6.0	773	9	CG325677	OGYARS1TH	CG325677	OGYARS1TH	85.5	6.0	1359	85.5	6.0	2931	9	CL974984	CL974984	AGENCY
1287	85.5	6.0	779	4	BG294850	602391675	BG294850	602391675	85.5	6.0	1360	85.5	6.0	3097	3	AK035712	AK035712	AGENCY
1288	85.5	6.0	785	4	BF826410	EST703792	BF826410	EST703792	85.5	6.0	1361	85.5	6.0	3209	3	AK046771	AK046771	AGENCY
1289	85.5	6.0	791	4	BI544438	603241951	BI544438	603241951	85.5	6.0	1362	85.5	6.0	4659	3	AK031271	AK031271	AGENCY
1290	85.5	6.0	803	2	BF568250	602184626	BF568250	602184626	85.5	6.0	1363	85.5	6.0	347	5	BY398894	BY398894	AGENCY
1291	85.5	6.0	809	5	EX329628	EX329628	EX329628	EX329628	85.5	6.0	1364	85.5	6.0	347	5	BY412973	BY412973	AGENCY
1292	85.5	6.0	810	7	CF822687	EST700069	CF822687	EST700069	85.5	6.0	1365	85.5	6.0	387	5	BY412973	BY412973	AGENCY
1293	85.5	6.0	826	5	EX888923	EX888923	EX888923	EX888923	85.5	6.0	1366	85.5	6.0	387	5	BY412973	BY412973	AGENCY
1294	85.5	6.0	832	4	CF823744	EST701126	CF823744	EST701126	85.5	6.0	1367	85.5	6.0	447	2	BF563485	BF563485	AGENCY
1295	85.5	6.0	833	5	EX881366	EX881366	EX881366	EX881366	85.5	6.0	1368	85.5	6.0	455	8	AO847973	AO847973	AGENCY
1296	85.5	6.0	837	4	BI820511	603036140	BI820511	603036140	85.5	6.0	1369	85.5	6.0	516	8	AO847973	AO847973	AGENCY
1297	85.5	6.0	840	4	BG294497	602391821	BG294497	602391821	85.5	6.0	1370	85.5	6.0	517	6	CD345223	CD345223	AGENCY
1298	85.5	6.0	841	7	CN138409	OX1_63_D0	CN138409	OX1_63_D0	85.5	6.0	1371	85.5	6.0	522	8	BZ594941	BZ594941	AGENCY
1299	85.5	6.0	847	5	BU128145	603115136	BU128145	603115136	85.5	6.0	1372	85.5	6.0	523	8	BZ594941	BZ594941	AGENCY
1300	85.5	6.0	848	7	CO812913	AGENCY	CO812913	AGENCY	85.5	6.0	1373	85.5	6.0	539	2	AW786079	AW786079	AGENCY
1301	85.5	6.0	851	7	CF446415	EST682760	CF446415	EST682760	85.5	6.0	1374	85.5	6.0	581	5	BP226156	BP226156	AGENCY
1302	85.5	6.0	855	4	BG855139	1024041H0	BG855139	1024041H0	85.5	6.0	1375	85.5	6.0	581	5	BP226156	BP226156	AGENCY
1303	85.5	6.0	858	7	CF240894	AGENCY	CF240894	AGENCY	85.5	6.0	1376	85.5	6.0	600	9	CC680905	CC680905	AGENCY
1304	85.5	6.0	862	7	CO009250	EST797585	CO009250	EST797585	85.5	6.0	1377	85.5	6.0	602	6	CB878893	CB878893	AGENCY
1305	85.5	6.0	864	5	BU122872	603148285	BU122872	603148285	85.5	6.0	1378	85.5	6.0	611	6	CB877026	CB877026	AGENCY
1306	85.5	6.0	865	4	BI462355	603203712	BI462355	603203712	85.5	6.0	1379	85.5	6.0	613	6	CB877756	CB877756	AGENCY
1307	85.5	6.0	867	7	CN201023	Tor10693	CN201023	Tor10693	85.5	6.0	1380	85.5	6.0	621	7	CK371597	CK371597	AGENCY
1308	85.5	6.0	869	5	BU169535	AGENCY	BU169535	AGENCY	85.5	6.0	1381	85.5	6.0	632	9	CL543778	CL543778	AGENCY
1309	85.5	6.0	879	9	CG248450	OGWB82TH	CG248450	OGWB82TH	85.5	6.0	1382	85.5	6.0	639	5	BU439505	BU439505	AGENCY
1310	85.5	6.0	887	7	CF826159	EST703541	CF826159	EST703541	85.5	6.0	1383	85.5	6.0	649	2	BE645367	BE645367	AGENCY
1311	85.5	6.0	890	7	CO030670	EST809054	CO030670	EST809054	85.5	6.0	1384	85.5	6.0	650	6	BY749456	BY749456	AGENCY
1312	85.5	6.0	891	5	BQ233574	AGENCY	BQ233574	AGENCY	85.5	6.0	1385	85.5	6.0	651	5	BM205784	BM205784	AGENCY
1313	85.5	6.0	897	7	CO009288	EST797623	CO009288	EST797623	85.5	6.0	1386	85.5	6.0	654	2	BE985566	BE985566	AGENCY
1314	85.5	6.0	897	9	CG620871	OGUFW82TV	CG620871	OGUFW82TV	85.5	6.0	1387	85.5	6.0	659	6	BY735116	BY735116	AGENCY
1315	85.5	6.0	900	9	CG439069	OGF1A123TV	CG439069	OGF1A123TV	85.5	6.0	1388	85.5	6.0	668	7	CK434506	CK434506	AGENCY
1316	85.5	6.0	909	5	BU169499	AGENCY	BU169499	AGENCY	85.5	6.0	1389	85.5	6.0	670	2	BF430820	BF430820	AGENCY
1317	85.5	6.0	925	5	BQ366377	EST700677	BQ366377	EST700677	85.5	6.0	1390	85.5	6.0	685	6	CA283181	CA283181	AGENCY
1318	85.5	6.0	932	7	CF823295	EST700677	CF823295	EST700677	85.5	6.0	1391	85.5	6.0	690	6	CD763439	CD763439	AGENCY

1397	85	5.9	705	8	BH240868	ATXQA57TR	1470	85	5.9	883	9	CC699717	OGUHD39TV
1398	85	5.9	707	8	BZ863360	CH240_198	1471	85	5.9	888	6	CD380658	PTM005827
1399	85	5.9	708	4	BM625358	170006974	C1472	85	5.9	889	4	BI413581	602987037
1400	85	5.9	712	5	BU624312	UI-H-FG1-	C1473	85	5.9	890	4	BI407927	602919373
1401	85	5.9	713	4	BM653219	170006873	C1474	85	5.9	890	4	BZ560396	pacs1-164
1402	85	5.9	714	2	BF628531	HVSNED000	1475	85	5.9	893	8	BZ551286	pacs1-60
1403	85	5.9	716	2	BF502996	AT18879.5	1476	85	5.9	895	5	BU113025	603129791
1404	85	5.9	716	5	BM986267	EST531721	C1477	85	5.9	899	9	CG318029	OGWFT46TV
1405	85	5.9	717	4	BG967679	602833484	C1478	85	5.9	902	5	BU528634	AGENCOURT
1406	85	5.9	717	7	CN149571	WOUND1_63	C1479	85	5.9	903	2	BE798767	601585794
1407	85	5.9	719	9	CG437156	OGTAI20TV	C1480	85	5.9	903	5	BQ879327	AGENCOURT
1408	85	5.9	722	9	CG437146	OGTAI20TH	C1481	85	5.9	905	1	AL961556	AL961556
1409	85	5.9	738	4	BG705967	602669291	C1482	85	5.9	906	6	CD556373	AGENCOURT
1410	85	5.9	739	9	CG259164	OGWKD80TH	1483	85	5.9	910	2	BF680343	602154124
1411	85	5.9	740	7	CF730613	UI-M-GD20	1484	85	5.9	922	7	CN509062	AGENCOURT
1412	85	5.9	741	9	CG487158	CH240_318	1485	85	5.9	922	9	CG836429	ZM8B8C021
1413	85	5.9	745	2	BF382943	601817012	1486	85	5.9	923	9	CG089526	PUFL702TB
1414	85	5.9	746	9	CG318023	CG318023	C1487	85	5.9	924	5	EX354149	EX354149
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ALIGNMENTS

RESULT 1	AKO34144	3688 bp	linear	HTC 03-APR-2004
AKO34144	Mus musculus adult male diencerphalon cDNA, RIKEN full-length			
LOCUS	enriched library, clone:9330159116			
DEFINITION	full insert sequence.			
ACCESSION	AKO34144.1	GI:26329732		
VERSION	AKO34144.1	GI:26329732		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Math. Enzymol. 303, 19-44 (1999)			
MEDLINE	93279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to			
JOURNAL	Prepare full-length cDNA libraries for rapid discovery of new genes			
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)			
PUBMED	20499374			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kutsuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			

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20530913
MEDLINE
PUBMED
11076861
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 6,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
REFERENCE
AUTHORS
6 (bases 1 to 3688)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
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ORIGIN
Alignment Scores:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Mus.

Pred. No.: 9,22e-103 Length: 3688
Score: 1168.00 Matches: 231
Percent Similarity: 93.00% Conservative: 8
Best Local Similarity: 89.88% Mismatches: 18
Query Match: 81.56% Indels: 0
DB: 3 Gaps: 0
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Db 302 CCCTCCCTGGCAGAGCTGTAGAAATTTGTGCAGAAAGAAATTTGATCAAACTGTGTCAA 361
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QY 164 GlnLeuValThrGlnGlyGluGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 183
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RESULT 2
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LOCUS
DEFINITION BB626090 RIKEN full-length enriched, adult male diencephalon Mus
musculus cDNA clone 9330159116 5', mRNA sequence.
ACCESSION BB626090
VERSION BB626090.1
KEYWORDS GI:15398717
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (bases 1 to 603)
REFERENCE
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE Transcriptional analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0842 row: C column: 03
Seq primer: M13 Reverse
High quality sequence stop: 603
POLYA=No.

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(Long)"
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Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The
mRNAs were extracted from a pool of 360 embryos at 4-cell
stage. Double-stranded cDNAs were synthesized with an
Oligo (dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGCGAGCGCCCTTTT-3'] from
10.8ng of mRNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker Li-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2Kb. The library was
constructed by Yulan Piao."

ORIGIN
Alignment Scores:
Pred. No.: 3 78e-79 Length: 603
Score: 915.00 Matches: 180
Percent Similarity: 93.94% Conservative: 6
Best Local Similarity: 90.91% Mismatches: 12
Query Match: 63.90% Indels: 0
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US-10-015-388A-54 (1-280) x CN722464 (1-603)

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Db 8 GCCTTTGAGTGACTACACTGCTTCAGAGCATGTTGGACAGTGTACCTGTTGGAC 67
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Qy 116 GlnAlaPhePheHisAsnGlnProProSerLeuArgArgThrValGlnPheValAlaGlu 135
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SOURCE EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 576)
AUTHORS Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.
TITLE Transcriptional analysis of mouse stem cells and early embryos
JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0757 row: H column: 05
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Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The
mRNAs were extracted from a pool of 360 embryos at 4-cell
stage. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen]:
5'-PGACTAGTCTAGATCGGAGCGCCCTTTT-3' from
10.8ng of mRNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker Lu-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2Kb. The library was
constructed by Yulan Piao."

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ORIGIN

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Alignment Scores:
Pred. No.:      8.94e-75      Length:      576
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US-10-015-388A-54 (1-280) x CN718045 (1-576)

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Qy 76 TrpValSerGlySerSerGlyArgSerGlyPheMetArgLysIleThrProThrThr 95
Db 128 TGGGTTTCAGAGACGATGGCGGAGTGGAGCTTTGTGAGAGAAATCACTCCCACTACC 187
Qy 96 ThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAla 115
Db 188 ACCAGCAGCTGGGAGCGCTCCCTCTCCAGACCAAGCCAGCGGCTCGAGGCTCAACTTGCT 247
Qy 116 GlnAlaPhePheHisAsnGlnProSerLeuArgArgThrValGluPheValAlaGlu 135
Db 248 GAGGCCCTTTTCCACAAACAGCCACCTCCCTCGCGAGGACTGTAGAAATTTGTGGCAGAA 307
Qy 136 ArgIleGlySerAsnCysValLysHisIleLysAlaThrLeuValAlaAspLeuValArg 155
Db 308 AGNATTGGATCAAACTGTGTCAACACATCAAGGGCAGCTGTTAACAGATTTGTTGCAT 367
Qy 156 GlnAlaGluSerLeuLeuGlnGlnLeuValThrGlnGlyGluGluGlyAspPro 175
Db 368 CAAGCAGAGTCACTTCTTCAGAGCAGCTGTTGGCAGCGGGACAGGAGGGGAGATCCA 427
Qy 176 AlaGlnLeuLeuGluIleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAla 195
Db 428 GCACAGCTTTTGGGAATCCTTGTGTCTCAACTCTGCCCCCAATGGGGGCCCAAGCATTGACC 487

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Qy 196 LeuGlyArgGluPheCysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGlu 215
Db 488 CAGGGCGGGAGTCTCTCCAAAGAGAGAGCCGCCCGCTGTGCGAGCACTGTACCAGAG 547
Qy 216 GluThrProAlaAlaValLeuSerSer 224
Db 548 GAGACCCCGAGCTGCTGTTCTAAGCAGT 574
RESULT 5
LOCUS      BF075771
DEFINITION 250666 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  BF075771
VERSION     BF075771.1 GI:10869282
KEYWORDS   EST.
SOURCE      Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 528)
AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
TITLE      Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
JOURNAL    Mamm. Genome 13 (8), 475-478 (2002)
MEDLINE    22213789
PUBMED     12226715
COMMENT    Contact: Smith TPL
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCACGATCAGCAGC
            Plate: 42 row: H column: 9
            Seq primer: ATTAGGTGACACTATAG.
            Location/Qualifiers
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                    /mol_type="mRNA"
                    /db_xref="taxon:9823"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /clone_lib="MARC 2PIG"
                    /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                    Library made from pooled tissue from testis, ovary,
                    endometrium, hypothalamus, pituitary, and placenta."

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FEATURES

source

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Alignment Scores:
Pred. No.:      2.2e-72      Length:      528
Score:          845.00      Matches:      164
Percent Similarity: 97.14%      Conservative: 6
Best Local Similarity: 93.71%      Mismatches: 5
Query Match:     59.01%      Indels:      0
DB:              2          Gaps:      0

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US-10-015-388A-54 (1-280) x BF075771 (1-528)

```

Qy 59 LeuTyThrCysCysProTyrlleGlyGluLeuArgLysLeuLeuAlaSerTrpValSer 78
Db 2 CTCTACACCTGCTGCCCTATATTGGAGAGCTCCGAAACTGCTGGTTCATGGGTATCA 61
Qy 79 GlySerSerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSer 98
Db 62 GGCAGCAGTGGCGGAGTGGGGGCTTCTGTAGGAAATACCCCAACACCACCACTGGG 121

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Qy	99	LeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGlnAlaPhe	118
Db	122	CTGGGGGCCACGCTCCCGGACCACCGAGGGCTGCAGGCACAGCTGGCCCAAGCCTTC	181
Qy	119	PheHisGlnProProSerLeuArgArgThrValGluPheValAlaGluArgIleGly	138
Db	182	TTCCACAACACGCGCCATCCCTGCGCAGGACTGTGGAGTTGTGGCAGAGAAATTGGC	241
Qy	139	SerAsnCysValIysHisIleLeuAlaThrLeuValAlaAspLeuValArgGlnAlaGlu	158
Db	242	TCTAACTGTGTCAAGCATATCAAGGCCACACTGGTAGCAGATCTGGTGGCCAGCAGAG	301
Qy	159	SerLeuLeuGlnGluGlnLeuValThrGlnGlyGluGluGlyGlyAspProAlaGlnLeu	178
Db	302	TCGCTTCTTCAGGAGCAGCTGTGTACGCAGGAGCAGAGAAGGGGGAGACCAGCCAGCTG	361
Qy	179	LeuGluIleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArg	198
Db	362	TTGAGATCTTGTGTCCAGCTGTGTGCCCCACGGGGGCCATGCATTAACCTGGGGGGG	421
Qy	199	GluPheCysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGluGluThrPro	218
Db	422	GAGTTCTGCCAAAGAGAGAGCCAGGTGCGGTGCAGGCATTGCTCTCTGAGGAGACCCCG	481
Qy	219	AlaAlaValLeuSerSerAlaGluAsnIleAlaValGlyLeuAla	233
Db	482	GCAGCCGTTCTGAGCAGTGCAGATAAATTGCGGTGGGGCTTGCA	526

RESULT 6				
BQ082104				
LOCUS	BQ082104	541 bp	mRNA	linear EST 04-APR-2002
DEFINITION	K-EST0054026 S7SNU719s1 Homo sapiens cDNA clone S7SNU719s1-14-C09 5', mRNA sequence.			

FEATURES	SOURCE
1. The first two columns of the table are labeled 'FEATURES' and 'SOURCE' respectively.	

ORIGIN

Alignment Scores:	
Pred. No.:	1,428-67
Score:	796.00
Percent Similarity:	98.77%
Best Local Similarity:	98.79%
Query Match:	55.59%
DB:	5
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	5
	Gaps:
	0
	Indels:
	0
	Mismatches:
	2
	Conservative:
	0
	Matches:
	163
	Length:
	541

US-10-015-388A-54 (1-280) x B0082104 (1-541)

Qy	116	GlnAlaPhePheHisAsnGlnProProSerLeuArgA-gThrValGluPheValAlaGlu	135
Db	15	CAGGCCCTTTTCCAAACACAGCCGCCCTCTCTGGCGCGAGCGTA-GAGTTCTGTCGAGAA	73
Qy	136	ArgIleGlySerAsnCysValLysHisIstIleLysAlaThrLeuValAlaAspLeuValArg	155
Db	74	AGATTGGATCAAACTGTGTCAACACATATCAAGGCTACACTGGTGGCAGATCTGGTGGC	133
Qy	156	GlnAlaGluSerLeuLeuGlnGluGlnLeuValThrGlnGlyGluGluGlyGlyAspPro	175
Db	134	CAGCGAGAGTCACTTCTCCAAAGCAGCTGTGTGCACACAGGAAGAGAAAGGGGAGACCCA	193
Qy	176	AlaGlnLeuLeuGluIleLeuCysSerGlnLeuCysProHisGlyAlaGlnAlaLeuAla	195
Db	194	GCCACAGCTGTGGAGATCTTGTTGCCAGCTGTGGCCCTCACGGGGCCCGCCGATTTGGC	253
Qy	196	LeuGlyArgGluPheCysGlnArgLysSerProGlyAlaValArgAlaLeuLeuProGlu	215
Db	254	CTGGGGCGGAGATTCTGTCAAAGAAAGAGCCCTGGGGCTGTGGCGGCGCTGTTCCAGAG	313
Qy	216	GluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValGlyLeuAlaThrGlu	235
Db	314	GAGACCCCGGACCGCTTCTGAGCAGGTGCAGAGAACATTCCTGTGGGGCTTGCAACAGAG	373
Qy	236	LysAlaCysAlaTrpLeuSerAlaAsnIleThrAlaLeuIleArgArgGluValLysAla	255
Db	374	AAAGCCCTGTGCTTGGCTGTACGCCAAACATCACAGCACTGATCAGGAGGAGGTGAAGACA	433
Qy	256	AlaValSerArgThrLeuArgAlaGlnGlyProGluProAlaAlaArgGlyGluArgArg	275
Db	434	GCAGTGAGTGCACACTTCGAGGCCACGGGTCTGAACTGTGCCCGGGGGAGCGGAGG	493
Qy	276	GlyCysSerArgAla	280
Db	494	GGCTGTCTCCCGCGCC	508

RESULT 7

BI344908
 LOCUS 373541 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 30-JUL-2001
 DEFINITION
 ACCESSION BI344908
 VERSION BI344908.1 GI:15038197
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 589)
 Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
 Vallet, J., Wise, T., Rohrer, G.A., Perte, G., Sultana, R.,
 Quackenbush, J., and Keele, J.W.
 Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly
 Mamm. Genome 13 (8), 475-478 (2002)
 2213789
 12226715
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel.: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCT
 BACKWARD: GTTTCACGTCACGAGG
 Plate: 120 row: B column: 22
 Seq primer: ATTAGGTGACACTATAG.
 Seq primer: Location/Qualifiers
 1..589
 /organism="Sus scrofa"
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 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 2P1G"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."
 FEATURES
 source
 Alignment Scores:
 Pred. No.: 2.6e-63 Length: 589
 Score: 753.00 Matches: 145
 Percent Similarity: 96.13% Conservative: 4
 Best Local Similarity: 93.55% Mismatches: 6
 Query Match: 52.58% Indels: 0
 Gaps: 0
 DB:
 US-10-015-388A-54 (1-280) x BI344908 (1-589)
 Qy 45 GluHisGlyLeuAspAlaProValValAspGlnGlnLeuLeuThrCysCysPro 64
 Db 5 GAGCATGCTGGACAGCATGCTGCTGGACACGACCTGCTTACACTGTCGCC 64
 Qy 65 TyrLeuGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySerSerGlyArgSer 84
 Db 65 TATATTGAGAGCTCCGAACTGCTGCTTCATGGGTATCAGGACAGTGGCGGAGT 124
 Qy 85 GlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGlyAlaGlnProSer 104
 Db 125 GGGGCTCTGTCAGAGAAATCACCACCCACCTGCTGGGCTGGGGGCCAGCTCCC 184
 Qy 105 GlnThrSerGlnGlyGlnAlaGlnLeuAlaGlnAlaPhePheHisAsnGlnProPro 124
 Db 185 CGGACACCCAGGGGCTGACGACAGCTGGCCCAAGCTTCTTCCAAACACCGCGCA 244
 Qy 125 SerLeuArgArgThrValGluPheValAlaGluArgIleGlySerAsnCysValLysHis 144

Db 245 TCCCTGGCGCAGGACTGGAGTTTGTGGCAGAGAAATTGGCTCTAACTGTGTCAAGCAT 304
 Qy 145 IleLysAlaThrLeuValAlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGln 164
 Db 305 ATCAAGGCCACACCTGGTAGCAGATCTGGTGGCCAGGACAGAGTGGCTTCTTCAGGAGCAG 364
 Qy 165 LeuValThrGlnGlyGluGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 184
 Db 365 CTGGTGACGCGAGGACGAGAAGGGGAGACCCAGCCAGCTGTGGAGATCTTGTGTTC 424
 Qy 185 GlnLeuCysProHisGlyAlaGlnAlaLeuAlaLeuGlyArgGlu 199
 Db 425 CAGTGTGCCCCCAGGGGCCAGGCATTGACCTGGGGCGGGAG 469
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 CD578927 727 bp mRNA linear EST 15-JUL-2003
 LOCUS UI-M-FY0-cgn-d-08-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 DEFINITION IMAGE:30354991 5', mRNA sequence.
 ACCESSION CD578927
 VERSION CD578927
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 727)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..727
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30354991"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: NotI; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGCAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:

Score:

5.09e-59

Length:

710.50

Matches:

727

154

Percent Similarity: 68.35% Conservatives: 8
 Best Local Similarity: 64.98% Mismatches: 16
 Query Match: 49.62% Indels: 60
 DB: 6 Gaps: 2

US-10-015-388A-54 (1-280) x CD578927 (1-727)

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Qy 71 LysLeuLeuAlaSerTrpValSerGlySerGlyArgSerGlyGlyPheMetArgLys 90
Db 1 AAATGCTTCTCTCTGGGTTTCAGGAAGCAGTGGCGGAGTGGAGGCTTTGTGAGGAA 60
Qy 91 lleThrProThrThrThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeu 110
Db 61 ATCACTCCCACTACACAGCAGCCTGGAGCCCTCTCTCCAGACAGCCAGCGGGCTG 120
Qy 111 GlnAlaGlnLeuAlaGlnAlaPhePheHisGlnGlnProProSerLeuArgArgThrVal 130
Db 121 CAGGCTCAACTGCTGGCCCTTTTCACACAGCAGCCCTCTCTGGAGGAGTGT 180
Qy 131 GluPheValAlaGluArgGlySerAsnCysValHisHisLeuAlaThrLeuVal 150
Db 181 GAATTTGTGGCAGAAAGAAATGGATCAAACTGTGTCAACACATCAAGCGCAGACTGTA 240
Qy 151 AlaAspLeuValArgGlnAlaGluSerLeuLeuGlnGlnLeuValThrGlnGlyGlu 170
Db 241 GCAGATTTGGTGCATCAAGCAGAGTCACTTCTTCAGGAGCAGCTGGTGGCAGCGGACAG 300
Qy 171 GluGlyGlyAspProAlaGlnLeuGluLeuLeuCysSerGlnLeuCysProHisGly 190
Db 301 GAAGGGGAGATCCAGCAGCTTTTGAATCTGTGTCTCAACTCTGCCCATGG 360
Qy 191 AlaGlnAlaLeuAlaLeuGlyArgGluPheCysGlnArgLysSerProGlyAlaValArg 210
Db 361 GCCCAAGCATTTGACCCAGCGGGCGGAGTTCTGCCAAGGAGAGAGCCCAAGCGCTGTGGA 420
Qy 211 AlaLeuLeuProGluGluThrProAlaVal 221
Db 421 GCACGTGTACAGAGGAGACCCAGCTCTGTACTAGGAAGAGAGCCTGCAGCTAGCAA 480
Qy 221 ----- 221
Db 481 GCCAGTAGCAGGAGGATGTACATGTGTACATGTGCACATGTGTGAGGCTGTGTA 540
Qy 221 ----- 221
Db 541 GGGTGGTTCGACTGTAGATCAATCACTGTACTACCTGCTTCCCAAGTCCCTGACT 600
Qy 222 -----LeuSerSerAlaGluAsnIleAlaValGlyLeuAla 233
Db 601 CAGCAGTCTCTGTGTGCCAGAGTTCTAAGCAGTGCAGAGAAATGTCTGTGGGGCTTGC 660
Qy 234 ThrGluLysAlaCysAlaTrpLeuSerAlaAsnIleThrAlaLeuIleArg 250
Db 661 ACAGAGAAGC-TGCTCTGTGTGTACGCC-----ACATCACAGGTGAGG 704

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RESULT 9

CF724147

LOCUS

DEFINITION UI-M-G20-C1j-n-07-0-UI.r1 NIH_BMAP_G20 Mus musculus cDNA clone

ACCESSION

CF724147

VERSION

CF724147.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

743 bp mRNA linear EST 09-OCT-2003
 IMAGE:30605790 5', mRNA sequence.
 CF724147
 CF724147.1 GI:37598315
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (Bases 1 to 743)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: PYX-5.

Location/Qualifiers

1. .743

source

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30605790"

/tissue_type="whole eye"

/dev_stage="embryo 12.5,13.5,14.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP G20"

/note="Organ: Eye; Vector: PYX- Asc; Site 1: Ecor I;

Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction; ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into PYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TTAATGAGT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 2,75e-55 Length: 743

Score: 672.50 Matches: 132

Percent Similarity: 90.26% Conservatives: 7

Best Local Similarity: 85.71% Mismatches: 14

Query Match: 46.96% Indels: 1

DB: 7 Gaps: 1

US-10-015-388A-54 (1-280) x CF724147 (1-743)

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Qy 1 MetCysPheLeuAsnLysLeuLeuLeuAlaValLeuGlyTrpLeuPheGlnIlePro 20
Db 281 ATGTGCTTCTCGAATAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340
Qy 21 ThrValProGluAspLeuPheLeuGluGlyProSerTyrAlaPheGluValAsp 40
Db 341 ACAGTTCTGAGGACTTATTTCTTCTAGAGATGCTCAGGTAGATGCTTTGAGGTGACT 400
Qy 41 ThrValAlaProGluHisGlyLeuAspAsnAlaProValValAspGlnLeuLeuTyr 60
Db 401 ACAACTGCTTCAGAGCATGTTTGGACAGTGTACCTGTTGTGGACACGACGCTGTATAT 460
Qy 61 ThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSerTrpValSerGlySer 80
Db 461 ACCTGTTGCCCTTACATTGGAGAGCTCCGGAACCTGCTTCTCTGGTTCAGGAAGC 520
Qy 81 SerGlyArgSerGlyGlyPheMetArgLysIleThrProThrThrThrSerLeuGly 100
Db 521 AGTGGGGAGTGGAGGCTTTGTGAGAGAAATCACTCCACTACACAGCAGGCTGGGA 580
Qy 101 AlaGlnProSerGlnThrSerGlnGlnAlaGlnLeuAlaGlnAlaPhePheHis 120
Db 581 GCCCTGCTCTCCAGACAGCAGCGGGCTGCAGGCTCAACTGTGTGAGGCTTTTTCAC 640
Qy 121 AsnGlnProProSerLeuArgArgThrValGluPheValAlaGluArgIleGlySerAsn 140

```


[illegible]

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 3100 and 3700 capillary sequencers. Raw sequence data was batch
 processed, analyzed, groomed and submitted by the Animal
 Biotechnology Center (URL:
<http://primer.ansci.umn.edu/software.html>), University of
 Minnesota. Trace files have been submitted to the NCBI trace
 archive (<http://www.ncbi.nlm.nih.gov/Traces/trace.cgi>).
 Chromatograms were analyzed with Phred version: 0.00925.c. Vector
 (pCMV SPORT6, Invitrogen), Sus scrofa mitochondrion
 (gi|535862|ref|NC_000845.1|), Escherichia coli K12 (gi|5835862|
 ref|NC_000913.1|), Porcine reproductive and respiratory syndrome
 virus (gi|11878202|gb|AF303357.1|AF303357), Altheromonas sp.16S rRNA
 gene (gi|4218471|emb|Y15322.1|Y15322), Sus scrofa 28S ribosomal
 RNA (gi|3388170|gb|AF080393.1|AF080393), and Sus scrofa 18S ribosomal
 RNA (gi|3388592|gb|AF102857.1|AF102857). Sequences were identified
 and masked by Crossmatch -minscore=20, -mismatch=12, -penalty=-8.
 SWAR alignment scores were set to match score=1, gap initial
 penalty=-3 and gap extension penalty=-2. A continuous stretch of at
 least 50 bases of a PHRED quality 20 were required for
 submission. 5' and 3' TERMINI were defined by a continuous stretch
 of 10 nucleotides with a PHRED quality not less than 20. A terminal
 stretch of at most 40 un-masked bases were automatically trimmed
 when flanking masked sequence. Sequences with an INTERNAL continuous
 stretch of at most 20 bases with PHRED quality less than 20 were
 automatically prepared for submission. HIQUAL_START and HIQUAL_STOP
 refer to the coordinates on CLIP_QUALITY and CLIP_VECTOR at the
 NCBI trace archive.
 Plate: 24 row: G column: 03
 Seq primer: SP6 primer
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 High quality sequence stop: 417.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="PPSUBLIB_24G03"
 /tissue_type="Peyer's patch"
 /clone_lib="UNMMPM3"
 /notes="Organ: small intestine, jejunum; Vector:
 pCMVSPORT6; Site 1: NotI; Site 2: SalI; Jejunal Peyer's
 patches were isolated from healthy, 4-6 week old
 cross-bred pigs. RNA was extracted either immediately or
 after 3 hours stimulation in an Using chamber with one of
 the following treatments: 1) no treatment, 2) Salmonella
 choleraesuis vaccine strain SC-54, 3) phorbol myristate
 acetate, concanavalin A, and 8-bromo-cyclic AMP, and 4)
 lipopolysaccharide and cholera toxin. Each treatment was
 performed in the presence and absence of cycloheximide.
 Purified poly A+ RNA from each of the treated tissues
 (2-4) was combined together, reverse transcribed, and
 cloned in to pCMVSPORT6 to make a library of approximately

530,000 recombinant clones with an average insert size of
 1.0 kbp. Poly A+ RNA from freshly isolated and non-treated
 tissue from an Using chamber (treatment 1) was cloned in
 the same manner to produce an unstimulated cDNA library of
 approximately 900,000 clones with an average insert size
 of 1.5 kbp. Equal portions of the two libraries were
 pooled and then subtracted with porcine SI fibroblast RNA
 to create a subtracted porcine Peyer's SI fibroblast RNA
 approximately 6,000 clones with an average insert size of
 1.0 kbp."

ORIGIN

Alignment Scores: 5.7e-35 Length: 476
 Pred. No.: 462.00 Matches: 96
 Score: 462.00
 Percent Similarity: 95.15% Conservative: 2
 Best Local Similarity: 93.20% Mismatches: 5
 Query Match: 32.26% Indels: 1
 DB: 6 Gaps: 0

US-10-015-388A-54 (1-280) x CB286548 (1-476)

Qy 97 ThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAlaGln 116
 Db 3 ACTGGCTGGGGGCCAGCCCTCCCGGACACCCAGGGGCTGCAGGCGCAGCTGGCCCAA 62
 Qy 117 AlaPhePheHisAsnGlnProProSerLeuArgThrValGluPheValAlaGluArg 136
 Db 63 GCCTTCTTCCC-AACCCAGCGCCATCTCCGCGAGGACTGTGGAGTTTGTGCAGAGAGA 121
 Qy 137 IleGlySerAsnGlyValLeuHisIleLeuAlaThrLeuValAlaAspLeuValArgGln 156
 Db 122 ATTGGCTTAACCTGTGCAAGCATATCAAGGCCACACTGGTAGCAGATCTGTGGCCAG 181
 Qy 157 AlaGluSerLeuLeuGlnGlnLeuValThrGlnGlyGluGlyGlyValAspProAla 176
 Db 182 GCAGAGTCGCTTCTTCAGGAGCAGCTGTGACGAGGACGAGAGGGGGAGACCCAGCC 241
 Qy 177 GlnLeuLeuGluIleLeuLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGln 196
 Db 242 CAGCTGTGGAGATCTTGTGTTCCTCCAGCTGTGCCCCCAGCGGGCCAGGACCTGACCTG 301
 Qy 197 GlyArgGlu 199
 Db 302 GGGCGGGAG 310

RESULT 14

AW478789 288 bp mRNA linear EST 25-APR-2001
 LOCUS 21675 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION AW478789
 VERSION AW478789.1 GI:7048895
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE 1 (bases 1 to 288)
 AUTHORS Smith, R.P., L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Pertea, G., Holt, I., Kazamychewa, S., Liang, F.,
 Quackenbush, J. and Keele, J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013
 PUBMED 11282978
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366

Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTITCCCAGTCACGACG
Plate: 12 row: M column: 3
Seq primer: ATTTAGGTGACACTATAG.

FEATURES

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/lab_host="DH10B"
/clone_lib="MARC PROV"
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/note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN

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Pred. No.:	8.46e-35	Length:
Score:	457.00	Matches:
Percent Similarity:	96.84%	Conservative:
Best Local Similarity:	95.79%	Mismatches:
Query Match:	31.91%	Indels:
DB:	2	Gaps:
		288

US-10-015-388A-54 (1-280) x AW478789 (1-288)

QY	173	GlyAspProAlaGlnLeuLeuGluLeuLeuCysSerGlnLeuCysProHisGlyAlaGln	192
Db	3	GCGCATCCAGCCCACGCTGTGGAGATCTTGTGTTCACGAGTGTCCTCACGGGGCCAG	62
QY	193	AlaLeuAlaLeuGlyValTrpGluPheCysGlnArgIysSerProGlyAlaValArgAlaLeu	212
Db	63	GGTTTGACCCAGGGCGGAGATTCTGCCAAGAAGAGTCCAGGTGCCGTGAGGGCACTG	122
QY	213	LeuProGluGluThrProAlaAlaValLeuSerSerAlaGluAsnIleAlaValGlyLeu	232
Db	123	CTTCTGAGGAGACC CGCGGACCGCTTCTAAGCAGTCGAGAAACATTGCTGTGACCTT	182
QY	233	AlaThrGluLysAlaCysAlaTrpLeuSerAlaAsnIleThrAlaLeuIleArgArgGlu	252
Db	183	GCACACAGAGAAGCCTGTGCATGTGTTCAGCCAACATCATCAGCATGTATCAGAAGGAG	242

Qy 253 ValLysAlaAlaValSerArgThrLeuArgAlaGlnGlyProGlu 267
Db 243 GTGAAAGCGGCCGTGAGTCGCACGCTTCGCGCCCAAGGTCTCTGAG 287

RESULT 15
CN723141
LOCUS CN723141 298 bp mRNA linear EST 18-MAY-2004
E0854H11-5 NIA Mouse four-cell-Embryo cDNA library (Long) Mus
musculus cDNA clone NIA:E0854H11 IMAGE:30910846 5' mRNA sequence.

ACCESSION CN723141
VERSION CN723141.1
GI:47492526

EST.
Mus musculus (house mouse)

ORGANISM	Mus musculus
BOOKC	Mus musculus

Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 298)
 REFERENCE

AUTHORS

Sharov, A.A., Fido, I., Matcoba, K.R., Dudekula, D.B., Qian, Y., VanBurken, V., Falco, G., Matton, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelseo, G., Umegawa, A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelsso, J., Hide, W. and KO, M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
Plate: E0854 row: H column: 11
Seq primer: M13 Reverse
High quality sequence stop: 298
POLYA=No.

FEATURES
SOURCE

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/dev_stage="4-cell"
/lab_pos="rrv108"

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/c:\ncbi\pub\mice\4-cell-embryo\cdna library
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 (\long")
 [Note=Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
 Site_2: NotI; Mouse cdna project by the Laboratory of
 Genetics, National Institute on Aging (NIA), Intramural
 Research Program, NIH (<http://leguun.grc.nia.nih.gov/cDNA>).
 This is a long-transcript enriched cdna library (Ref.
 Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). The
 mRNAs were extracted from a pool of 360 embryos at 4-cell
 stage. Double-stranded cDNAs were synthesized with an
 oligo(dT) primer [Invitrogen].
 5'-pGACATGTTGTAGATCGAGCGCGCCCTTTTTTTTTTTT-3'] from
 1.0 ng of mRNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to Loxe-linker LL-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
 vector. The DH10B E. coli host was transformed with the
 ligation mixture by the standard chemical method. The
 average insert size is about 2.2Kb. The library was
 constructed by vulan. Biao."

ORIGIN

Alignment Scores:		
Pred. No.:	6.75e-34	Length: 298
Score:	448.00	Matches: 86
Percent Similarity:	93.75%	Conservative: 4
Best Local Similarity:	89.58%	Mismatches: 6
Query Match:	31.28%	Indels: 0
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US-10-015-388A-54 (1-280) x CN723141 (1-298)

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Qy		
9	GCCTTTGGTGACACAACTGCTTCAGAGCATGGTTTGGACAGTGCACCTGTTGTGGAC	68
Db		
56	GlnGlnLeuLeuTyrThrCysCysProTyrIleGlyGluLeuArgLysLeuLeuAlaSer	75
Qy		
69	CAGCAGCTGTTATATACCTGTTGCCCTTACATTCGAGAGCTCCGAAACTGCTTGCCTTC	128
Db		
76	TrpValSerGlySerSerGlyArgSerGlyGlyPheMetArgLysIleLeuThrProThr	95
Qy		
129	TGGGTTTCAGAAAGCAGTGGCGAGTGGAGCTTTGTGAGAAATCACTCTCCCACTACC	188
Db		

Qy	96	ThrThrSerLeuGlyAlaGlnProSerGlnThrSerGlnGlyLeuGlnAlaGlnLeuAla	115
Db	189	ACCAGCAGCCTGGGAGCCCTGCCTCTCCAGACCAGCCAGGGGCTGCAGGCTCAACTTGCT	248
Qy	116	GlnAlaPhePheHisAsnGlnProProSerLeuArgArgThrValGlu	131
Db	249	GAGGCTTTTTCACACACAGCCACCTCCCTGCGCAGGACTGTAGAA	296

Search completed: March 29, 2005, 10:59:04
 Job time : 3276 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 20:47:38 ; Search time 14744 Seconds
(without alignments)
11765.442 Million cell updates/sec

Title: US-10-015-388A-53

Perfect score: 3580

Sequence: 1 gaccggtccctccggtcctg.....cacgaacagcgggtgcgcct 3580

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
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6: gb.pat.*
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8: gb.pl.*
9: gb.pr.*
10: gb.to.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3580	100.0	3580	6	AX696985 Sequence
2	3580	100.0	3580	9	AY358467 Homo sapi
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4	1534	42.8	3212	9	BC008333 Homo sapi
5	1534	42.8	3212	9	BC008334 Homo sapi
6	1515	42.3	4725	9	AF252398 Homo sapi
7	1214	33.9	4350	9	BC066640 Homo sapi
8	1214	33.9	4354	9	BC052568 Homo sapi
9	1073	30.0	2145	9	HSM801358 Homo sapi
10	1056	29.5	129517	2	AC016400 Homo sapi
11	1056	29.5	148295	9	AC090510 Homo sapi
12	871	24.3	209157	9	CNS01094 Human chr
13	725	20.3	2315	9	AC026092 Homo sapi
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15	725	20.3	3589	6	C0851120 Sequence
16	725	20.3	3589	9	AK128338 Homo sapi
17	718	20.1	3617	9	BC070062 Homo sapi
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19	656	18.3	110000	2	AC106723_2 Continuation (3 of

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23	346	9.7	985	6	C0729264	Sequence
24	314	8.8	357	6	AX778901	Sequence
25	203	5.7	2958	9	AB081753	Homo sapi
26	178	5.0	753	6	CQ719078	Sequence
27	173	4.8	177	6	AX411242	Sequence
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29	169	4.7	110000	2	AC106723_0	Sequence
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34	65	1.8	334051	2	AC123374	Rattus no
35	64	1.8	86363	9	HSJ539E24	Human DNA
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39	64	1.8	164699	2	AC015678	Homo sapi
40	64	1.8	171375	9	CNS01DSX	Human chr
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44	64	1.8	198402	9	AC069546	Homo sapi
45	64	1.8	219821	9	AC008738	Homo sapi
46	64	1.8	233231	2	AC022220	Homo sapi
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58	59	1.6	1746	9	HSM800208	Homo sapi
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69	59	1.6	181322	9	AC027018	Homo sapi
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79	58	1.6	554	6	AX364312	Sequence
80	58	1.6	568	6	AX421562	Sequence
81	58	1.6	703	6	BD276320	MOLSCULES
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85	58	1.6	943	6	AX098202	Sequence
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92	58	1.6	1057	6	AR409284	Sequence

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C 94	BD275148	48 Human	C 167	57	1.6	1454	6	AR177955	Sequence
C 95	AX098194	Sequence	C 168	57	1.6	1464	6	BD270355	50 human
C 96	AX040958	Sequence	C 169	57	1.6	1485	6	AR177965	Sequence
C 97	BC073962	Homo sapi	C 170	57	1.6	1576	9	AL133070	Homo sapi
C 98	AX098191	Sequence	C 171	57	1.6	1621	6	BD107842	36 human
C 99	BD107881	36 human	C 172	57	1.6	1734	6	BD275139	48 Human
C 100	BD223128	98 human	C 173	57	1.6	2000	6	BD252089	47 secret
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C 104	BD223130	98 human	C 177	57	1.6	2581	6	AR339790	Sequence
C 105	BD223130	Sequence	C 178	57	1.6	2581	6	BD131136	45 human
C 106	BD260828	49 human	C 179	57	1.6	2584	6	BD140660	36 human
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C 113	AR374729	Sequence	C 186	57	1.6	138417	9	AC007254	Homo sapi
C 114	BD062047	Novel tum	C 187	57	1.6	156788	2	AC150449	Pan trogl
C 115	CQ838245	Sequence	C 188	57	1.6	240864	2	AC006510	Homo sapi
C 116	BD130999	67 Human	C 189	56	1.6	72	6	AX381283	Sequence
C 117	AX251708	Sequence	C 190	56	1.6	73	6	AX381604	Sequence
C 118	AR339750	Sequence	C 191	56	1.6	74	6	AX381324	Sequence
C 119	BD131096	45 human	C 192	56	1.6	74	6	AX381456	Sequence
C 120	AX098200	Sequence	C 193	56	1.6	77	6	AX381197	Sequence
C 121	BD244702	Novel mol	C 194	56	1.6	81	6	AX381268	Sequence
C 122	AX350867	Sequence	C 195	56	1.6	82	6	AX381282	Sequence
C 123	AX074222	Sequence	C 196	56	1.6	82	6	AX381340	Sequence
C 124	AX040974	Sequence	C 197	56	1.6	90	6	AX381219	Sequence
C 125	AX048730	Sequence	C 198	56	1.6	90	6	AX381308	Sequence
C 126	BD249844	33 human	C 199	56	1.6	95	6	AX381490	Sequence
C 127	BD249845	33 human	C 200	56	1.6	100	6	AX381490	Sequence
C 128	AX127529	Sequence	C 201	56	1.6	117	6	AX381824	Sequence
C 129	AX675184	Sequence	C 202	56	1.6	154	6	AX381214	Sequence
C 130	AX573129	Sequence	C 203	56	1.6	161	6	AX381305	Sequence
C 131	BD276443	143 Human	C 204	56	1.6	485	6	CQ523774	Sequence
C 132	AX098198	Sequence	C 205	56	1.6	487	6	BD266698	29 human
C 133	AX098203	Sequence	C 206	56	1.6	487	6	AR216197	Sequence
C 134	AR301767	Sequence	C 207	56	1.6	639	6	AX766155	Sequence
C 135	CQ412293	Sequence	C 208	56	1.6	639	9	BC004336	Homo sapi
C 136	CQ490721	Sequence	C 209	56	1.6	824	6	BD072967	70 human
C 137	CQ496562	Sequence	C 210	56	1.6	931	6	BD218549	71 human
C 138	AX048774	Sequence	C 211	56	1.6	980	6	CQ848996	Sequence
C 139	BD260167	50 human	C 212	56	1.6	980	6	BD078436	101 human
C 140	BD192851	Plant fat	C 213	56	1.6	1058	6	BD275398	50 Human
C 141	AR438050	Sequence	C 214	56	1.6	1138	6	AR374744	Sequence
C 142	CQ489398	Sequence	C 215	56	1.6	1261	6	BD194910	86 human
C 143	CQ495240	Sequence	C 216	56	1.6	1261	6	CQ855238	Sequence
C 144	AX098201	Sequence	C 217	56	1.6	1362	6	BD249153	27 human
C 145	AX474240	Sequence	C 218	56	1.6	1367	6	BD074331	50 human
C 146	AX474270	Sequence	C 219	56	1.6	1407	6	AX127526	Sequence
C 147	AX474271	Sequence	C 220	56	1.6	1421	6	BD074318	50 human
C 148	AX474272	Sequence	C 221	56	1.6	1722	6	BD218620	71 human
C 149	AX474273	Sequence	C 222	56	1.6	1779	6	BD205730	97 human
C 150	AR117332	Sequence	C 223	56	1.6	2122	6	BD252054	47 secret
C 151	AR117332	Sequence	C 224	56	1.6	4773	6	CQ412935	Sequence
C 152	AX117525	Sequence	C 225	56	1.6	128999	9	AL391139	Human DNA
C 153	AX127525	Sequence	C 226	56	1.6	136901	2	AC041036	Homo sapi
C 154	AX247632	Sequence	C 227	56	1.6	166173	2	AC023060	Homo sapi
C 155	AR564552	Sequence	C 228	56	1.6	166317	9	AL157895	Human DNA
C 156	BD275441	50 Human	C 229	56	1.6	169247	9	AL669970	Human DNA
C 157	BD232172	Novel sec	C 230	56	1.6	174210	2	EX005241	Homo sapi
C 158	BD249815	33 human	C 231	56	1.6	220000	2	AC108707	Homo sapi
C 159	BD249815	33 human	C 232	56	1.6	243558	9	AC010310	Rattus no
C 160	AX643010	Sequence	C 233	56	1.6	283951	2	AC109383	Rattus no
C 161	AC006077	Homo sapi	C 234	56	1.6	291762	2	AC125887	Rattus no
C 162	AC008670	Homo sapi	C 235	56	1.6	343504	2	AL158031	Homo sapi
C 163	CNS051E5	Human chr	C 236	55	1.5	129	6	AX901537	Sequence
C 164	AL122075	Rattus no	C 237	55	1.5	129	6	BD037070	Sequence
C 165	AR177949	Sequence	C 238	55	1.5	131	6	AX902861	Sequence
	AR162252	Sequence							

C 239	55	1.5	131	6	BD038394	Sequence	BD038394	Sequence	C 312	54	1.5	2386	8	BNA9608	Brassica
C 240	55	1.5	172	6	AX261854	Sequence	AX261854	Sequence	C 313	54	1.5	2436	5	BC080972	BC080972 Xenopus t
C 241	55	1.5	432	9	BC040830	Homo sapi	BC040830	Homo sapi	C 314	54	1.5	2455	10	BC061762	BC061762 Rattus no
C 242	55	1.5	604	6	BD072953	70 human	BD072953	70 human	C 315	54	1.5	2530	10	BC052848	BC052848 Mus muscu
C 243	55	1.5	809	6	BD260752	50 human	BD260752	50 human	C 316	54	1.5	2649	9	BC063539	BC063539 Homo sapi
C 244	55	1.5	974	6	CQ493762	Sequence	CQ493762	Sequence	C 317	54	1.5	3006	6	AX497163	AX497163 Sequence
C 245	55	1.5	1001	6	BD276420	143 Human	BD276420	143 Human	C 318	54	1.5	3214	6	I32738	I32738 Sequence 17
C 246	55	1.5	3069	9	BC010058	Homo sapi	BC010058	Homo sapi	C 319	54	1.5	3214	6	I38714	I38714 Sequence 17
C 247	55	1.5	3451	6	EI3998	Cyanidium c	EI3998	Cyanidium c	C 320	54	1.5	3273	9	BC030532	BC030532 Homo sapi
C 248	55	1.5	36942	9	AC093782	Homo sapi	AC093782	Homo sapi	C 321	54	1.5	3552	6	CQ412820	CQ412820 Sequence
C 249	55	1.5	38486	9	AC083880	Homo sapi	AC083880	Homo sapi	C 322	54	1.5	3552	6	CQ489581	CQ489581 Sequence
C 250	55	1.5	38852	9	AC006261	Homo sapi	AC006261	Homo sapi	C 323	54	1.5	3552	6	CQ495422	CQ495422 Sequence
C 251	55	1.5	68557	2	AC130386	Homo sapi	AC130386	Homo sapi	C 324	54	1.5	5962	5	BC070852	BC070852 Xenopus l
C 252	55	1.5	75698	9	AP000228	Homo sapi	AP000228	Homo sapi	C 325	54	1.5	67024	9	AP001494	AP001494 Homo sapi
C 253	55	1.5	80878	9	AC011480	Homo sapi	AC011480	Homo sapi	C 326	54	1.5	85538	9	AC127904	AC127904 Homo sapi
C 254	55	1.5	100000	9	AP000140	Homo sapi	AP000140	Homo sapi	C 327	54	1.5	119569	9	AC020929	AC020929 Homo sapi
C 255	55	1.5	123722	9	AC018515	Homo sapi	AC018515	Homo sapi	C 328	54	1.5	123101	9	HS108P13	HS108P13
C 256	55	1.5	132832	9	AC091934	Homo sapi	AC091934	Homo sapi	C 329	54	1.5	143045	9	AC008750	AC008750 Homo sapi
C 257	55	1.5	148290	9	AL359199	Human DNA	AL359199	Human DNA	C 330	54	1.5	164508	2	AC104130	AC104130 Homo sapi
C 258	55	1.5	150236	2	AC023392	Homo sapi	AC023392	Homo sapi	C 331	54	1.5	164508	2	AC021625	AC021625 Homo sapi
C 259	55	1.5	161014	9	AP000088	Homo sapi	AP000088	Homo sapi	C 332	54	1.5	172024	2	AC078971	AC078971 Homo sapi
C 260	55	1.5	168658	9	AC019278	Homo sapi	AC019278	Homo sapi	C 333	54	1.5	174695	2	AC149448	AC149448 Papio anu
C 261	55	1.5	169118	2	AC073313	Homo sapi	AC073313	Homo sapi	C 334	54	1.5	183946	2	AC009164	AC009164 Homo sapi
C 262	55	1.5	172274	9	AP000924	Homo sapi	AP000924	Homo sapi	C 335	54	1.5	184264	2	AC118233	AC118233 Mus muscu
C 263	55	1.5	172482	9	AC022309	Homo sapi	AC022309	Homo sapi	C 336	54	1.5	195993	2	AC134953	AC134953 Pan trogl
C 264	55	1.5	172985	2	AC087695	Homo sapi	AC087695	Homo sapi	C 337	54	1.5	212011	2	AC129932	AC129932 Mus muscu
C 265	55	1.5	174084	2	AC084395	Homo sapi	AC084395	Homo sapi	C 338	54	1.5	220173	9	AC012183	AC012183 Homo sapi
C 266	55	1.5	174311	9	AP002788	Homo sapi	AP002788	Homo sapi	C 339	53	1.5	58	6	AX381765	AX381765 Sequence
C 267	55	1.5	175645	9	AC073114	Homo sapi	AC073114	Homo sapi	C 340	53	1.5	60	6	AX381481	AX381481 Sequence
C 268	55	1.5	177163	9	AC100786	Homo sapi	AC100786	Homo sapi	C 341	53	1.5	69	6	E82858	E82858 Secretary p
C 269	55	1.5	178704	2	AC023180	Homo sapi	AC023180	Homo sapi	C 342	53	1.5	85	6	BD003061	BD003061 Polynucle
C 270	55	1.5	182557	2	AC091942	Homo sapi	AC091942	Homo sapi	C 343	53	1.5	90	6	AX381279	AX381279 Sequence
C 271	55	1.5	188992	9	AL157834	Human DNA	AL157834	Human DNA	C 344	53	1.5	125	6	AX494464	AX494464 Sequence
C 272	55	1.5	190394	9	AL157834	Human DNA	AL157834	Human DNA	C 345	53	1.5	127	9	IROEST143	IROEST143
C 273	55	1.5	190592	2	AC015806	Homo sapi	AC015806	Homo sapi	C 346	53	1.5	144	6	BD138840	BD138840 Secreted
C 274	55	1.5	198146	2	AC023499	Homo sapi	AC023499	Homo sapi	C 347	53	1.5	144	6	I89947	I89947 Sequence 26
C 275	55	1.5	198764	9	AC103809	Homo sapi	AC103809	Homo sapi	C 348	53	1.5	144	6	BD005387	BD005387 Secreted
C 276	55	1.5	202418	2	AC150815	Callithr	AC150815	Callithr	C 349	53	1.5	160	6	AX494504	AX494504 Sequence
C 277	55	1.5	203521	9	BS000205	Pan trogl	BS000205	Pan trogl	C 350	53	1.5	173	6	AX185626	AX185626 Sequence
C 278	55	1.5	340000	9	AP001694	Homo sapi	AP001694	Homo sapi	C 351	53	1.5	204	6	CQ487345	CQ487345 Sequence
C 279	54	1.5	93	6	CQ832576	Sequence	CQ832576	Sequence	C 352	53	1.5	211	6	CQ483120	CQ483120 Sequence
C 280	54	1.5	221	6	CQ527278	Sequence	CQ527278	Sequence	C 353	53	1.5	214	6	CQ670912	CQ670912 Sequence
C 281	54	1.5	351	6	AR506477	Sequence	AR506477	Sequence	C 354	53	1.5	219	6	CQ528993	CQ528993 Sequence
C 282	54	1.5	510	6	CQ411734	Sequence	CQ411734	Sequence	C 355	53	1.5	222	6	CQ411279	CQ411279 Sequence
C 283	54	1.5	625	8	AF049925	Petunia x	AF049925	Petunia x	C 356	53	1.5	225	6	CQ701286	CQ701286 Sequence
C 284	54	1.5	763	10	BC028541	Mus muscu	BC028541	Mus muscu	C 357	53	1.5	226	6	CQ473951	CQ473951 Sequence
C 285	54	1.5	796	6	AX364304	Sequence	AX364304	Sequence	C 358	53	1.5	234	6	CQ397739	CQ397739 Sequence
C 286	54	1.5	854	6	AX430945	Sequence	AX430945	Sequence	C 359	53	1.5	234	6	CQ404036	CQ404036 Sequence
C 287	54	1.5	873	8	BT009024	Triticum	BT009024	Triticum	C 360	53	1.5	235	6	CQ529081	CQ529081 Sequence
C 288	54	1.5	911	8	AF083749	Arabidops	AF083749	Arabidops	C 361	53	1.5	240	6	CQ405709	CQ405709 Sequence
C 289	54	1.5	970	9	BC035850	Homo sapi	BC035850	Homo sapi	C 362	53	1.5	241	6	CQ398756	CQ398756 Sequence
C 290	54	1.5	1118	8	AF305075	Nicotiana	AF305075	Nicotiana	C 363	53	1.5	248	6	CQ529028	CQ529028 Sequence
C 291	54	1.5	1150	3	AF332209	Caenorhab	AF332209	Caenorhab	C 364	53	1.5	264	6	CQ467407	CQ467407 Sequence
C 292	54	1.5	1194	6	AX105295	Sequence	AX105295	Sequence	C 365	53	1.5	269	6	CQ475616	CQ475616 Sequence
C 293	54	1.5	1418	10	AF361490	Rattus no	AF361490	Rattus no	C 366	53	1.5	275	6	AX381137	AX381137 Sequence
C 294	54	1.5	1532	9	BC053733	Homo sapi	BC053733	Homo sapi	C 367	53	1.5	281	6	CQ410312	CQ410312 Sequence
C 295	54	1.5	1640	10	BC062007	Rattus no	BC062007	Rattus no	C 368	53	1.5	281	6	CQ504127	CQ504127 Sequence
C 296	54	1.5	1723	6	BD223494	94 human	BD223494	94 human	C 369	53	1.5	283	6	CQ529455	CQ529455 Sequence
C 297	54	1.5	1723	6	AR243128	Sequence	AR243128	Sequence	C 370	53	1.5	289	6	CQ423504	CQ423504 Sequence
C 298	54	1.5	1821	9	BC004309	Sequence	BC004309	Sequence	C 371	53	1.5	293	6	CQ432641	CQ432641 Sequence
C 299	54	1.5	1821	9	BC003056	Homo sapi	BC003056	Homo sapi	C 372	53	1.5	296	6	CQ398869	CQ398869 Sequence
C 300	54	1.5	1931	6	CQ38265	Sequence	CQ38265	Sequence	C 373	53	1.5	296	6	CQ405149	CQ405149 Sequence
C 301	54	1.5	1931	6	BD131019	67 Human	BD131019	67 Human	C 374	53	1.5	300	6	AX185628	AX185628 Sequence
C 302	54	1.5	1932	6	CQ381819	Sequence	CQ381819	Sequence	C 375	53	1.5	317	6	CQ483299	CQ483299 Sequence
C 303	54	1.5	1932	6	BD130953	67 Human	BD130953	67 Human	C 376	53	1.5	318	6	CQ399318	CQ399318 Sequence
C 304	54	1.5	1953	10	BC034135	Mus muscu	BC034135	Mus muscu	C 377	53	1.5	318	6	CQ405595	CQ405595 Sequence
C 305	54	1.5	1985	9	BC006345	Homo sapi	BC006345	Homo sapi	C 378	53	1.5	323	6	CQ529148	CQ529148 Sequence
C 306	54	1.5	2030	10	BC051019	Mus muscu	BC051019	Mus muscu	C 379	53	1.5	328	6	CQ410507	CQ410507 Sequence
C 307	54	1.5	2073	9	HSW801468	Homo sapi	HSW801468	Homo sapi	C 380	53	1.5	332	6	CQ398523	CQ398523 Sequence
C 308	54	1.5	2093	5	BC074543	Xenopus t	BC074543	Xenopus t	C 381	53	1.5	332	6	CQ404810	CQ404810 Sequence
C 309	54	1.5	2240	5	BC066420	Danio rer	BC066420	Danio rer	C 382	53	1.5	336	6	CQ397671	CQ397671 Sequence
C 310	54	1.5	2261	10	BC043710	Mus muscu	BC043710	Mus muscu	C 383	53	1.5	336	6	CQ403968	CQ403968 Sequence
C 311	54	1.5	2369	6	AX280370	Sequence	AX280370	Sequence	C 384	53	1.5	337	6	CQ529025	CQ529025 Sequence

c 385	53	1.5	338	6	CQ517148	Sequence	CQ517148	Sequence	458	53	1.5	524	6	CQ528859	Sequence	CQ528859	Sequence	458	53	1.5	524	6	CQ528859	Sequence	CQ528859	Sequence
386	53	1.5	343	6	CQ529095	Sequence	CQ529095	Sequence	459	53	1.5	531	6	CQ394991	Sequence	CQ394991	Sequence	459	53	1.5	531	6	CQ394991	Sequence	CQ394991	Sequence
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391	53	1.5	351	6	CQ404123	Sequence	CQ404123	Sequence	464	53	1.5	539	6	CQ410791	Sequence	CQ410791	Sequence	464	53	1.5	539	6	CQ410791	Sequence	CQ410791	Sequence
c 392	53	1.5	352	6	CQ525050	Sequence	CQ525050	Sequence	c 465	53	1.5	553	8	AY080594	Arabidops	AY080594	Arabidops	c 465	53	1.5	553	8	AY080594	Arabidops	AY080594	Arabidops
393	53	1.5	352	6	CQ529009	Sequence	CQ529009	Sequence	466	53	1.5	554	6	CQ417692	Sequence	CQ417692	Sequence	466	53	1.5	554	6	CQ417692	Sequence	CQ417692	Sequence
394	53	1.5	358	6	CQ399231	Sequence	CQ399231	Sequence	467	53	1.5	567	6	CQ525234	Sequence	CQ525234	Sequence	467	53	1.5	567	6	CQ525234	Sequence	CQ525234	Sequence
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c 397	53	1.5	367	6	CQ523125	Sequence	CQ523125	Sequence	c 470	53	1.5	577	8	BT009563	Triticum	BT009563	Triticum	c 470	53	1.5	577	8	BT009563	Triticum	BT009563	Triticum
398	53	1.5	375	6	CQ411403	Sequence	CQ411403	Sequence	c 471	53	1.5	587	9	BC070308	Homo sapi	BC070308	Homo sapi	c 471	53	1.5	587	9	BC070308	Homo sapi	BC070308	Homo sapi
399	53	1.5	375	6	CQ513063	Sequence	CQ513063	Sequence	472	53	1.5	612	6	AX187052	Sequence	AX187052	Sequence	472	53	1.5	612	6	AX187052	Sequence	AX187052	Sequence
400	53	1.5	380	6	CQ410420	Sequence	CQ410420	Sequence	473	53	1.5	621	6	AX187054	Sequence	AX187054	Sequence	473	53	1.5	621	6	AX187054	Sequence	AX187054	Sequence
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402	53	1.5	383	6	CQ502211	Sequence	CQ502211	Sequence	475	53	1.5	638	6	CQ398462	Sequence	CQ398462	Sequence	475	53	1.5	638	6	CQ398462	Sequence	CQ398462	Sequence
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407	53	1.5	386	6	CQ525228	Sequence	CQ525228	Sequence	c 480	53	1.5	686	10	BC060302	Mus muscu	BC060302	Mus muscu	c 480	53	1.5	686	10	BC060302	Mus muscu	BC060302	Mus muscu
408	53	1.5	388	6	CQ410454	Sequence	CQ410454	Sequence	c 481	53	1.5	693	6	CQ422235	Sequence	CQ422235	Sequence	c 481	53	1.5	693	6	CQ422235	Sequence	CQ422235	Sequence
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417	53	1.5	406	6	CQ528922	Sequence	CQ528922	Sequence	490	53	1.5	755	6	CQ410683	Sequence	CQ410683	Sequence	490	53	1.5	755	6	CQ410683	Sequence	CQ410683	Sequence
418	53	1.5	407	6	CQ528868	Sequence	CQ528868	Sequence	491	53	1.5	764	6	AX187080	Sequence	AX187080	Sequence	491	53	1.5	764	6	AX187080	Sequence	AX187080	Sequence
419	53	1.5	410	6	CQ397607	Sequence	CQ397607	Sequence	492	53	1.5	796	8	AY114140	Apium gra	AY114140	Apium gra	492	53	1.5	796	8	AY114140	Apium gra	AY114140	Apium gra
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421	53	1.5	414	6	CQ410920	Sequence	CQ410920	Sequence	c 494	53	1.5	826	6	AR184158	Sequence	AR184158	Sequence	c 494	53	1.5	826	6	AR184158	Sequence	AR184158	Sequence
422	53	1.5	420	6	CQ524985	Sequence	CQ524985	Sequence	c 495	53	1.5	830	6	CQ482724	Sequence	CQ482724	Sequence	c 495	53	1.5	830	6	CQ482724	Sequence	CQ482724	Sequence
423	53	1.5	425	6	CQ506214	Sequence	CQ506214	Sequence	496	53	1.5	851	6	CQ427278	Sequence	CQ427278	Sequence	496	53	1.5	851	6	CQ427278	Sequence	CQ427278	Sequence
424	53	1.5	426	6	CQ507189	Sequence	CQ507189	Sequence	497	53	1.5	862	8	AF465822	Allium ce	AF465822	Allium ce	497	53	1.5	862	8	AF465822	Allium ce	AF465822	Allium ce
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426	53	1.5	428	6	AX286914	Sequence	AX286914	Sequence	c 499	53	1.5	892	6	BD269299	33 human	BD269299	33 human	c 499	53	1.5	892	6	BD269299	33 human	BD269299	33 human
427	53	1.5	433	6	CQ397727	Sequence	CQ397727	Sequence	c 500	53	1.5	933	10	BC048388	Mus muscu	BC048388	Mus muscu	c 500	53	1.5	933	10	BC048388	Mus muscu	BC048388	Mus muscu
428	53	1.5	433	6	CQ404024	Sequence	CQ404024	Sequence	c 501	53	1.5	951	10	BC039793	Mus muscu	BC039793	Mus muscu	c 501	53	1.5	951	10	BC039793	Mus muscu	BC039793	Mus muscu
429	53	1.5	433	6	CQ411349	Sequence	CQ411349	Sequence	c 502	53	1.5	951	10	BC060993	Mus muscu	BC060993	Mus muscu	c 502	53	1.5	951	10	BC060993	Mus muscu	BC060993	Mus muscu
430	53	1.5	434	6	CQ410846	Sequence	CQ410846	Sequence	c 503	53	1.5	961	14	MDU76034	Microplis	MDU76034	Microplis	c 503	53	1.5	961	14	MDU76034	Microplis	MDU76034	Microplis
431	53	1.5	436	6	CQ503829	Sequence	CQ503829	Sequence	c 504	53	1.5	1019	10	BC002004	Mus muscu	BC002004	Mus muscu	c 504	53	1.5	1019	10	BC002004	Mus muscu	BC002004	Mus muscu
432	53	1.5	436	6	CQ512635	Sequence	CQ512635	Sequence	c 505	53	1.5	1034	6	AR487878	Sequence	AR487878	Sequence	c 505	53	1.5	1034	6	AR487878	Sequence	AR487878	Sequence
433	53	1.5	440	6	CQ396156	Sequence	CQ396156	Sequence	c 506	53	1.5	1052	6	BD223087	98 human	BD223087	98 human	c 506	53	1.5	1052	6	BD223087	98 human	BD223087	98 human
434	53	1.5	440	6	CQ402481	Sequence	CQ402481	Sequence	c 507	53	1.5	1052	6	AR243785	Sequence	AR243785	Sequence	c 507	53	1.5	1052	6	AR243785	Sequence	AR243785	Sequence
435	53	1.5	443	6	CQ524562	Sequence	CQ524562	Sequence	c 508	53	1.5	1053	5	BC077790	Xenopus l	BC077790	Xenopus l	c 508	53	1.5	1053	5	BC077790	Xenopus l	BC077790	Xenopus l
436	53	1.5	445	6	CQ473555	Sequence	CQ473555	Sequence	c 509	53	1.5	1064	3	AK174286	Ciona int	AK174286	Ciona int	c 509	53	1.5	1064	3	AK174286	Ciona int	AK174286	Ciona int
437	53	1.5	457	6	CQ427379	Sequence	CQ427379	Sequence	c 510	53	1.5	1071	9	BC009727	Homo sapi	BC009727	Homo sapi	c 510	53	1.5	1071	9	BC009727	Homo sapi	BC009727	Homo sapi
c 438	53	1.5	457	6	CQ516772	Sequence	CQ516772	Sequence	c 511	53	1.5	1123	5	BC077523	Xenopus l	BC077523	Xenopus l	c 511	53	1.5	1123	5	BC0			

C 531	1.5	1301	8	BT009271	Triticum	C 604	53	1.5	1845	5	XLICYB	Z13966 Xenopus lae
C 532	1.5	1305	8	PCDIALDHA	Z19568 P.deltoides	C 605	53	1.5	1851	9	AK026744	AK026744 Homo sapi
C 533	1.5	1310	8	AF464902	Oryza sat	C 606	53	1.5	1862	10	BC060687	BC060687 Mus muscu
C 534	1.5	1310	10	BC019402	BC019402 Mus muscu	C 607	53	1.5	1866	8	AB042956	AB042956 Nicotiana
C 535	1.5	1320	8	AF061570	Arabidops	C 608	53	1.5	1910	9	HSM801106	AL117416 Homo sapi
C 536	1.5	1334	3	AV360135	Dictyoste	C 609	53	1.5	1921	10	BC005597	BC005597 Mus muscu
C 537	1.5	1355	6	AR527700	Sequence	C 610	53	1.5	1929	8	AB025714	AB025714 Nicotiana
C 538	1.5	1355	6	AX074159	Sequence	C 611	53	1.5	1941	5	BC077766	BC077766 Xenopus l
C 539	1.5	1376	6	BD194853	86 human	C 612	53	1.5	1951	5	BC078039	BC078039 Xenopus l
C 540	1.5	1376	6	CQ855181	Sequence	C 613	53	1.5	1975	5	BC067563	BC067563 Danio rer
C 541	1.5	1400	5	BC071084	Xenopus l	C 614	53	1.5	1977	6	BD192668	BD192668 123 human
C 542	1.5	1403	10	BC024509	Mus muscu	C 615	53	1.5	1977	6	AR184139	AR184139 Sequence
C 543	1.5	1407	3	AF344172	Ciona int	C 616	53	1.5	1988	10	BC029720	BC029720 Mus muscu
C 544	1.5	1407	10	BC013450	Mus muscu	C 617	53	1.5	1993	10	BC062202	BC062202 Mus muscu
C 545	1.5	1410	9	BC008364	Homo sapi	C 618	53	1.5	2009	3	AK116580	AK116580 Ciona int
C 546	1.5	1410	10	BC081336	Mus muscu	C 619	53	1.5	2075	9	HSM802983	AL713655 Homo sapi
C 547	1.5	1414	10	BC010336	Mus muscu	C 620	53	1.5	2083	5	BC077186	BC077186 Xenopus l
C 548	1.5	1443	10	BC061219	Mus muscu	C 621	53	1.5	2102	5	BC056790	BC056790 Danio rer
C 549	1.5	1445	6	AX052751	Sequence	C 622	53	1.5	2102	10	BC039217	BC039217 Mus muscu
C 550	1.5	1473	10	BC013520	Mus muscu	C 623	53	1.5	2103	6	BD223104	BD223104 98 human
C 551	1.5	1481	10	BC034714	Mus muscu	C 624	53	1.5	2103	6	AR243802	AR243802 Sequence
C 552	1.5	1494	5	BC063335	Xenopus t	C 625	53	1.5	2134	10	BC024712	BC024712 Mus muscu
C 553	1.5	1495	5	BC046652	Xenopus l	C 626	53	1.5	2155	9	BC015749	BC015749 Homo sapi
C 554	1.5	1505	9	BC015512	Homo sapi	C 627	53	1.5	2174	10	BC036173	BC036173 Mus muscu
C 555	1.5	1518	9	BC008591	Homo sapi	C 628	53	1.5	2175	5	AB056480	AB056480 Rana cate
C 556	1.5	1521	9	BC014584	Homo sapi	C 629	53	1.5	2181	10	BC026983	BC026983 Mus muscu
C 557	1.5	1526	5	BC084319	Xenopus l	C 630	53	1.5	2187	10	BC052181	BC052181 Mus muscu
C 558	1.5	1534	5	BC076027	Danio rer	C 631	53	1.5	2191	9	BC034703	BC034703 Homo sapi
C 559	1.5	1550	6	CQ795868	Sequence	C 632	53	1.5	2193	9	AB070198	AB070198 Macaca fa
C 560	1.5	1550	8	AF486650	Citrus x	C 633	53	1.5	2198	9	BC031550	BC031550 Homo sapi
C 561	1.5	1582	6	A77033	Sequence 10	C 634	53	1.5	2208	9	BC016137	BC016137 Homo sapi
C 562	1.5	1582	6	A77035	Sequence 12	C 635	53	1.5	2230	9	BC053996	BC053996 Homo sapi
C 563	1.5	1582	6	AR100218	Sequence	C 636	53	1.5	2329	5	BC074616	BC074616 Xenopus t
C 564	1.5	1582	6	AR100220	Sequence	C 637	53	1.5	2384	6	AX780522	AX780522 Sequence
C 565	1.5	1585	5	BC083224	Danio rer	C 638	53	1.5	2384	6	AX780523	AX780523 Sequence
C 566	1.5	1591	9	HSM801261	AF087943 Rattus no	C 639	53	1.5	2430	9	HSM805511	AL834423 Homo sapi
C 567	1.5	1602	9	AF111801	BC024516 Mus muscu	C 640	53	1.5	2444	8	AF401636	AF401636 Rehmannia
C 568	1.5	1602	10	BC024516	BC024516 Mus muscu	C 641	53	1.5	2444	10	BC051679	BC051679 Mus muscu
C 569	1.5	1603	10	BC024516	BC024516 Mus muscu	C 642	53	1.5	2463	10	BC005449	BC005449 Mus muscu
C 570	1.5	1605	8	BT009414	Triticum	C 643	53	1.5	2492	5	BC074549	BC074549 Xenopus t
C 571	1.5	1612	10	BC079028	Rattus no	C 644	53	1.5	2515	9	BC081769	BC081769 Rattus no
C 572	1.5	1615	5	BC044158	Danio rer	C 645	53	1.5	2516	9	BC020965	BC020965 Homo sapi
C 573	1.5	1616	9	BC013416	Homo sapi	C 646	53	1.5	2578	10	BC026526	BC026526 Mus muscu
C 574	1.5	1617	10	BC043453	Mus muscu	C 647	53	1.5	2609	10	BC034658	BC034658 Mus muscu
C 575	1.5	1621	9	HSM803093	AL713720 Homo sapi	C 648	53	1.5	2635	5	BC067384	BC067384 Danio rer
C 576	1.5	1623	9	BC030572	Homo sapi	C 649	53	1.5	2645	3	AV118446	AV118446 Drosophil
C 577	1.5	1632	5	BC045260	BC045260 Xenopus l	C 650	53	1.5	2678	9	HSM802267	AL137533 Homo sapi
C 578	1.5	1638	5	BC049298	Danio rer	C 651	53	1.5	2712	6	AX686742	AX686742 Sequence
C 579	1.5	1640	9	BC050738	BC050738 Homo sapi	C 652	53	1.5	2712	9	BC001199	AX780361 Sequence
C 580	1.5	1656	5	BC064161	Xenopus t	C 653	53	1.5	2712	9	BC001199	BC001199 Homo sapi
C 581	1.5	1656	5	BC068336	Danio rer	C 654	53	1.5	2722	10	BC075615	BC075615 Mus muscu
C 582	1.5	1665	3	AB025584	Dictyoste	C 655	53	1.5	2756	5	BC063896	BC063896 Xenopus t
C 583	1.5	1667	10	BC019215	BC019215 Mus muscu	C 656	53	1.5	2767	10	BC066791	BC066791 Mus muscu
C 584	1.5	1678	9	HSM802263	AL137530 Homo sapi	C 657	53	1.5	2780	5	BC056280	BC056280 Danio rer
C 585	1.5	1694	6	BD132536	BD132536 Secreted	C 658	53	1.5	2789	5	BC023021	BC023021 Homo sapi
C 586	1.5	1707	6	AR487851	Sequence	C 659	53	1.5	2819	5	AF267849	AF267849 Xenopus l
C 587	1.5	1707	10	BC026570	BC026570 Mus muscu	C 660	53	1.5	2838	6	AX249742	AX249742 Sequence
C 588	1.5	1719	10	BC056192	Mus muscu	C 661	53	1.5	2914	10	BC050274	BC050274 Mus muscu
C 589	1.5	1724	9	BC003101	Homo sapi	C 662	53	1.5	3016	10	BC083896	BC083896 Rattus no
C 590	1.5	1744	8	ATPYK10	X89413 Arabidopsis	C 663	53	1.5	3038	9	HSM806221	BX538031 Homo sapi
C 591	1.5	1760	9	BC035407	BC035407 Homo sapi	C 664	53	1.5	3285	9	AK130342	AK130342 Homo sapi
C 592	1.5	1779	9	BC068210	BC068210 Homo sapi	C 665	53	1.5	3353	9	HSM807301	BX647157 Homo sapi
C 593	1.5	1782	5	BC080059	BC080059 Xenopus l	C 666	53	1.5	3370	9	BC036689	BC036689 Homo sapi
C 594	1.5	1784	9	BC018906	BC018906 Homo sapi	C 667	53	1.5	3390	10	BC010727	BC010727 Mus muscu
C 595	1.5	1795	9	BC009439	BC009439 Homo sapi	C 668	53	1.5	3396	5	BC070774	BC070774 Xenopus l
C 596	1.5	1802	3	AK112634	AK112634 Ciona int	C 669	53	1.5	3440	9	BC013609	BC013609 Homo sapi
C 597	1.5	1806	6	BC045509	BC045509 Danio rer	C 670	53	1.5	3468	10	BC054379	BC054379 Mus muscu
C 598	1.5	1812	6	BD227271	BD227271 Secreted	C 671	53	1.5	3473	9	BC030601	BC030601 Homo sapi
C 599	1.5	1817	9	BC038370	BC038370 Homo sapi	C 672	53	1.5	3478	10	BC068301	BC068301 Mus muscu
C 600	1.5	1820	5	BC056518	BC056518 Danio rer	C 673	53	1.5	3501	6	AR528471	AR528471 Sequence
C 601	1.5	1827	6	AX556899	AX556899 Sequence	C 674	53	1.5	3501	6	AX463904	AX463904 Sequence
C 602	1.5	1838	9	BC039122	BC039122 Homo sapi	C 675	53	1.5	3581	6	AR034821	AR034821 Sequence
C 603	1.5	1840	3	DDU73686	U73686 Dictyostell	C 676	53	1.5	3581	6	EO7381	EO7381 cDNA encodi

C 677	53	1.5	3724	10	BC044902	BC044902 Mus muscu	C 750	53	1.5	191728	2	AL512269	AL512269 Homo sapi
C 678	53	1.5	3734	9	HS806342	BX538141 Homo sapi	751	53	1.5	193072	2	AC110986	AC110986 Rattus no
C 679	53	1.5	3815	9	BC025777	BC025777 Homo sapi	752	53	1.5	193894	2	AC114730	AC114730 Homo sapi
C 680	53	1.5	3859	10	MMU289242	AJ289242 Mus muscu	C 753	53	1.5	197817	2	AP001185	AP001185 Homo sapi
C 681	53	1.5	3922	9	HS804163	AL832852 Homo sapi	C 754	53	1.5	197915	2	BX927328	BX927328 Danio rer
C 682	53	1.5	4325	10	BC060196	BC060196 Mus muscu	755	53	1.5	197925	2	AC091308	AC091308 Mus muscu
C 683	53	1.5	4329	9	BC071579	BC071579 Homo sapi	756	53	1.5	198466	2	AC150006	AC150006 Pan trogl
C 684	53	1.5	4435	5	XLMTLZ	Z97214 Xenopus lae	C 757	53	1.5	200711	2	AC133960	AC133960 Homo sapi
C 685	53	1.5	4533	9	BC030221	BC030221 Homo sapi	758	53	1.5	201400	2	AL929539	AL929539 Homo sapi
C 686	53	1.5	4875	3	ABO09080	ABO09080 Dictyoste	C 759	53	1.5	203120	2	AC148499	AC148499 Callithri
C 687	53	1.5	6163	10	BC052150	BC052150 Mus muscu	C 760	53	1.5	205012	2	AC148500	AC148500 Callithri
C 688	53	1.5	6182	5	BC073527	BC073527 Dictyoste	761	53	1.5	209387	2	AC096448	AC096448 Rattus no
C 689	53	1.5	7801	3	AY160101	AY160101 Dictyoste	762	53	1.5	212104	9	AC012497	AC012497 Homo sapi
C 690	53	1.5	10008	9	HS807741	BX647595 Homo sapi	763	53	1.5	221265	2	AC106345	AC106345 Rattus no
C 691	53	1.5	21526	9	AP001618	AP001618 Homo sapi	764	53	1.5	221897	2	AC106320	AC106320 Rattus no
C 692	53	1.5	23499	2	AC149322	AC149322 Phakopsor	765	53	1.5	222685	2	AC140971	AC140971 Canis fam
C 693	53	1.5	30439	2	AC145658	AC145658 Homo sapi	766	53	1.5	223958	2	AC127401	AC127401 Rattus no
C 694	53	1.5	38692	3	AC116919	AC116919 Dictyoste	767	53	1.5	237615	2	AC138257	AC138257 Mus muscu
C 695	53	1.5	40116	6	AX573409	AX573409 Sequence	C 768	53	1.5	238604	2	AC115164	AC115164 Rattus no
C 696	53	1.5	40116	6	AX573409	AX573409 Sequence	769	53	1.5	252989	2	AC126984	AC126984 Rattus no
C 697	53	1.5	40611	3	AC116987	AX593386 Sequence	C 770	53	1.5	264232	2	AC151602	AC151602 Mus muscu
C 698	53	1.5	40661	8	BX424817	AX116987 Dictyoste	C 771	53	1.5	296096	2	AC110522	AC110522 Mus muscu
C 699	53	1.5	49999	9	AX015915	AX015915 Neurospor	772	53	1.5	331039	3	AC116979	AC116979 Dictyoste
C 700	53	1.5	54865	9	AC126124	AC126124 Homo sapi	773	53	1.5	336578	9	AP001745	AP001745 Homo sapi
C 701	53	1.5	64707	3	AC115607	AC115607 Dictyoste	C 774	53	1.5	342743	2	AC103119	AC103119 Rattus no
C 702	53	1.5	82139	3	AC115684	AC115684 Dictyoste	775	52	1.5	56	6	AX381739	AX381739 Sequence
C 703	53	1.5	84550	3	PFWAL1P2_3	Continuation (4 of	776	52	1.5	72	6	AX381405	AX381405 Sequence
C 704	53	1.5	85165	8	NC59H12	AL451018 Neurospor	777	52	1.5	193	6	CQ411913	CQ411913 Sequence
C 705	53	1.5	94636	2	BX897739	BX897739 Danio rer	778	52	1.5	226	6	AX184991	AX184991 Sequence
C 706	53	1.5	97790	2	AC101676_3	Continuation (4 of	C 779	52	1.5	258	6	AX423856	AX423856 Sequence
C 707	53	1.5	102370	9	HSJ976013	AL117354 Human DNA	C 780	52	1.5	258	6	AX984550	AX984550 Sequence
C 708	53	1.5	110000	2	AC140833_1	Continuation (2 of	C 781	52	1.5	258	6	BD119409	BD119409 EST and e
C 709	53	1.5	110000	3	AC116305_3	Continuation (4 of	C 782	52	1.5	267	6	CQ524749	CQ524749 Sequence
C 710	53	1.5	111882	3	AC115612	AC115612 Dictyoste	783	52	1.5	271	6	CQ423793	CQ423793 Sequence
C 711	53	1.5	119219	8	BX842631	BX842631 Neurospor	C 784	52	1.5	276	6	CQ526564	CQ526564 Sequence
C 712	53	1.5	120379	3	AC1073885	AC1073885 Homo sapi	C 785	52	1.5	276	6	AX426832	AX426832 Sequence
C 713	53	1.5	125958	3	AC115592	AC115592 Dictyoste	C 786	52	1.5	276	6	AX987526	AX987526 Sequence
C 714	53	1.5	132644	9	AC104801	AC104801 Homo sapi	C 787	52	1.5	282	6	BD122385	BD122385 EST and e
C 715	53	1.5	138403	9	BS000131	BS000131 Pan trogl	788	52	1.5	290	8	CNS01DKQ	AL116946 Botrytis
C 716	53	1.5	142916	9	AL928921	AL928921 Human DNA	789	52	1.5	294	6	CQ398035	CQ398035 Sequence
C 717	53	1.5	147201	9	AC053469	AC053469 Homo sapi	790	52	1.5	294	6	CQ398035	CQ398035 Sequence
C 718	53	1.5	151700	9	AC133528	AC133528 Homo sapi	791	52	1.5	294	6	CQ404327	CQ404327 Sequence
C 719	53	1.5	151759	2	AC149967	AC149967 Strongylo	C 792	52	1.5	294	6	CQ524533	CQ524533 Sequence
C 720	53	1.5	152665	2	AC027005	AC027005 Homo sapi	C 793	52	1.5	295	6	CQ488101	CQ488101 Sequence
C 721	53	1.5	153751	3	AC116551	AC116551 Dictyoste	C 794	52	1.5	303	6	CQ517890	CQ517890 Sequence
C 722	53	1.5	153807	2	AC015823	AC015823 Homo sapi	C 795	52	1.5	314	6	CQ472429	CQ472429 Sequence
C 723	53	1.5	156975	2	CR394534	CR394534 Danio rer	C 796	52	1.5	337	6	CQ523858	CQ523858 Sequence
C 724	53	1.5	158198	2	AC012013	AC012013 Homo sapi	C 797	52	1.5	358	6	CQ516500	CQ516500 Sequence
C 725	53	1.5	158408	2	BX927402	BX927402 Danio rer	C 798	52	1.5	373	6	CQ526143	CQ526143 Sequence
C 726	53	1.5	159234	2	AC108397	AC108397 Mus muscu	C 799	52	1.5	380	6	CQ517942	CQ517942 Sequence
C 727	53	1.5	160237	2	AC149093	AC149093 Pan trogl	800	52	1.5	384	6	AX185690	AX185690 Sequence
C 728	53	1.5	160390	2	AC068186	AC068186 Homo sapi	C 801	52	1.5	391	6	CQ515943	CQ515943 Sequence
C 729	53	1.5	162771	9	AC138781	AC138781 Homo sapi	C 802	52	1.5	394	6	CQ517396	CQ517396 Sequence
C 730	53	1.5	163494	2	AP002391	AP002391 Homo sapi	803	52	1.5	396	6	AR391219	AR391219 Sequence
C 731	53	1.5	163635	2	CR392027	CR392027 Danio rer	804	52	1.5	396	6	AR392924	AR392924 Sequence
C 732	53	1.5	163635	2	CR392027	CR392027 Danio rer	805	52	1.5	396	6	AR489654	AR489654 Sequence
C 733	53	1.5	165415	2	AC016663	AC016663 Homo sapi	806	52	1.5	396	6	AR493895	AR493895 Sequence
C 734	53	1.5	167082	2	AC021472	AC021472 Homo sapi	807	52	1.5	396	6	AX093224	AX093224 Sequence
C 735	53	1.5	167403	2	AC015686	AC015686 Homo sapi	808	52	1.5	399	6	AR085693	AR085693 Sequence
C 736	53	1.5	169032	2	AP0156431	AP0156431 Homo sapi	C 809	52	1.5	399	6	I18358	I18358 Sequence 13
C 737	53	1.5	169124	2	AP001375	AP001375 Homo sapi	C 810	52	1.5	399	6	I21345	I21345 Sequence 12
C 738	53	1.5	169932	2	AC141741	AC141741 Apis mell	811	52	1.5	399	6	I34395	I34395 Sequence 13
C 739	53	1.5	173169	9	AC068538	AC068538 Homo sapi	C 812	52	1.5	402	6	AX0334	AX0334 Sequence 13
C 740	53	1.5	173232	2	AC009830	AC009830 Homo sapi	813	52	1.5	404	6	CQ427146	CQ427146 Sequence
C 741	53	1.5	180736	2	AC023925	AC023925 Homo sapi	C 814	52	1.5	404	6	CQ517410	CQ517410 Sequence
C 742	53	1.5	182871	3	AC117176	AC117176 Dictyoste	C 815	52	1.5	419	9	BC079477	BC079477 Homo sapi
C 743	53	1.5	183689	2	AC146129	AC146129 Pan trogl	C 816	52	1.5	423	6	CQ669214	CQ669214 Sequence
C 744	53	1.5	185571	9	AC133781	AC133781 Homo sapi	C 817	52	1.5	425	3	AK174345	AK174345 Ciona int
C 745	53	1.5	185666	2	AC101747	AC101747 Mus muscu	C 818	52	1.5	429	6	CQ517247	CQ517247 Sequence
C 746	53	1.5	187549	2	CR405687	CR405687 Danio rer	C 819	52	1.5	435	8	CAR487043	AJ487043 Cicer ari
C 747	53	1.5	189072	2	AC113496	AC113496 Mus muscu	C 820	52	1.5	436	6	AX186794	AX186794 Sequence
C 748	53	1.5	189445	2	AC018739	AC018739 Homo sapi	C 821	52	1.5	441	6	CQ524625	CQ524625 Sequence
C 749	53	1.5	191154	2	AC132150	AC132150 Homo sapi	822	52	1.5	451	6	CQ467469	CQ467469 Sequence

C 823	823	52	1.5	467	6	CQ524824	Sequence	C 896	52	1.5	1174	6	CQ827970	Sequence
C 824	824	52	1.5	495	6	CQ409678	Sequence	C 897	52	1.5	1175	9	AB072787	Macaca fa
C 825	825	52	1.5	496	6	CQ525103	Sequence	C 898	52	1.5	1202	3	AY122189	Drosophil
C 826	826	52	1.5	501	5	BC077673	Xenopus t	C 899	52	1.5	1207	9	BC042078	Homo sapi
C 827	827	52	1.5	515	6	CQ399071	Sequence	C 900	52	1.5	1208	5	GSPMADPR	X82397 Gallus sp.
C 828	828	52	1.5	515	6	CQ405350	Sequence	C 901	52	1.5	1220	5	BC065349	Danio rer
C 829	829	52	1.5	534	6	CX284254	Sequence	C 902	52	1.5	1229	10	BC055401	Mus muscu
C 830	830	52	1.5	556	6	CQ508215	Sequence	C 903	52	1.5	1248	9	BC013747	Homo sapi
C 831	831	52	1.5	556	6	CQ508315	Sequence	C 904	52	1.5	1255	9	BC069211	Homo sapi
C 832	832	52	1.5	556	6	CQ510257	Sequence	C 905	52	1.5	1271	9	BC035309	Homo sapi
C 833	833	52	1.5	556	6	CQ511753	Sequence	C 906	52	1.5	1291	6	BD250012	Insect p5
C 834	834	52	1.5	560	3	AF107490	Pascioloa	C 907	52	1.5	1301	3	AK174651	Ciona int
C 835	835	52	1.5	571	10	BC035956	Mus muscu	C 908	52	1.5	1301	3	AK174651	Ciona int
C 836	836	52	1.5	572	9	BC032439	Homo sapi	C 909	52	1.5	1325	9	BC002365	Homo sapi
C 837	837	52	1.5	574	6	CQ525654	Sequence	C 910	52	1.5	1335	9	AF271350	Homo sapi
C 838	838	52	1.5	605	8	AF079185	Arabidops	C 911	52	1.5	1340	5	BC055268	Xenopus l
C 839	839	52	1.5	605	9	BC016300	Homo sapi	C 912	52	1.5	1340	9	AK024992	Homo sapi
C 840	840	52	1.5	612	6	AR506683	Sequence	C 913	52	1.5	1345	10	BC048718	Mus muscu
C 841	841	52	1.5	620	6	AR090422	Sequence	C 914	52	1.5	1353	3	AY070501	Drosophil
C 842	842	52	1.5	629	3	AY437139	Amblyomma	C 915	52	1.5	1370	8	BT009638	Triticum
C 843	843	52	1.5	663	10	BC058460	Rattus no	C 916	52	1.5	1380	5	BC078271	Danio rer
C 844	844	52	1.5	677	5	BC053818	Xenopus l	C 917	52	1.5	1400	5	BC076441	Danio rer
C 845	845	52	1.5	681	6	CQ487445	Sequence	C 918	52	1.5	1414	9	BC063670	Homo sapi
C 846	846	52	1.5	695	6	CQ467211	Sequence	C 919	52	1.5	1418	3	AK113899	Ciona int
C 847	847	52	1.5	739	3	AF466588	Aedes aeg	C 920	52	1.5	1426	10	BC078790	Rattus no
C 848	848	52	1.5	756	3	AK174008	Ciona int	C 921	52	1.5	1430	3	AK115508	Ciona int
C 849	849	52	1.5	759	8	AF002226	Nicotiana	C 922	52	1.5	1445	9	BC040875	Homo sapi
C 850	850	52	1.5	768	6	CQ415516	Sequence	C 923	52	1.5	1457	6	AX535066	Sequence
C 851	851	52	1.5	783	6	AX046873	Sequence	C 924	52	1.5	1480	9	BC030516	Homo sapi
C 852	852	52	1.5	814	6	CQ482030	Sequence	C 925	52	1.5	1494	6	CQ879142	Sequence
C 853	853	52	1.5	834	9	BC063494	Homo sapi	C 926	52	1.5	1497	5	BC067639	Danio rer
C 854	854	52	1.5	843	6	CQ769391	Sequence	C 927	52	1.5	1514	9	BC050367	Homo sapi
C 855	855	52	1.5	878	6	AX482482	Sequence	C 928	52	1.5	1517	10	BC083686	Rattus no
C 856	856	52	1.5	899	6	CQ432465	Sequence	C 929	52	1.5	1525	8	PSBSYN	X79904 Phalaenopsi
C 857	857	52	1.5	912	8	AB061251	Solanum t	C 930	52	1.5	1527	10	BC051428	Mus muscu
C 858	858	52	1.5	912	8	AB061251	Solanum t	C 931	52	1.5	1535	5	BC080491	Xenopus t
C 859	859	52	1.5	912	8	AB061251	Solanum t	C 932	52	1.5	1538	10	BC024943	Mus muscu
C 860	860	52	1.5	916	6	RPUG61144	U61144 Rhodnius pr	C 933	52	1.5	1547	9	BC071644	Homo sapi
C 861	861	52	1.5	916	6	E12747	U61144 Rhodnius pr	C 934	52	1.5	1553	3	BT003593	Drosophil
C 862	862	52	1.5	916	6	E17385	cDNA encodi	C 935	52	1.5	1566	9	BC073938	Catharant
C 863	863	52	1.5	951	6	BD021498	Novel gen	C 936	52	1.5	1567	9	HSM806640	Homo sapi
C 864	864	52	1.5	951	6	BD101436	Novel gen	C 937	52	1.5	1576	6	BD275146	Homo sapi
C 865	865	52	1.5	976	6	AX780228	Sequence	C 938	52	1.5	1579	10	BC078941	Rattus no
C 866	866	52	1.5	979	5	BC082389	Sequence	C 939	52	1.5	1589	10	BC014703	Mus muscu
C 867	867	52	1.5	989	8	CPCR7	Y08243 C. pteroides	C 940	52	1.5	1602	5	BC074563	Xenopus t
C 868	868	52	1.5	991	6	AR123139	Sequence	C 941	52	1.5	1606	9	BC065192	Homo sapi
C 869	869	52	1.5	991	6	AR124091	Sequence	C 942	52	1.5	1619	10	BC057862	Mus muscu
C 870	870	52	1.5	991	6	AX100360	Sequence	C 943	52	1.5	1620	5	BC068394	Danio rer
C 871	871	52	1.5	991	8	AF243368	Glycine m	C 944	52	1.5	1625	9	BC072433	Homo sapi
C 872	872	52	1.5	1010	5	BC065601	Danio rer	C 945	52	1.5	1634	9	HSM807708	Homo sapi
C 873	873	52	1.5	1013	6	A32826	Synthetic c	C 946	52	1.5	1648	10	BC063167	Rattus no
C 874	874	52	1.5	1013	6	I11571	I11571 Sequence 23	C 947	52	1.5	1661	8	AY299287	Arabidops
C 875	875	52	1.5	1013	6	I24003	Sequence 30	C 948	52	1.5	1665	5	BC077976	Xenopus l
C 876	876	52	1.5	1014	3	AY118285	AY118285 Drosophil	C 949	52	1.5	1673	6	AX772808	Sequence
C 877	877	52	1.5	1014	6	A30330	A30330 Artificial	C 950	52	1.5	1680	10	BC049920	Mus muscu
C 878	878	52	1.5	1015	6	A32827	A32827 Synthetic c	C 951	52	1.5	1708	3	BT006334	Drosophil
C 879	879	52	1.5	1016	6	A30331	A30331 Artificial	C 952	52	1.5	1716	9	AB060897	Macaca fa
C 880	880	52	1.5	1032	6	BD266697	BD266697 29 human	C 953	52	1.5	1719	5	BC063347	Xenopus t
C 881	881	52	1.5	1032	6	AR216196	Sequence	C 954	52	1.5	1737	3	AY084201	Drosophil
C 882	882	52	1.5	1049	3	AK174965	AK174965 Ciona int	C 955	52	1.5	1738	6	CQ768038	Sequence
C 883	883	52	1.5	1052	3	AK115940	AK115940 Ciona int	C 956	52	1.5	1738	6	AX538151	Sequence
C 884	884	52	1.5	1061	8	THIGPWR	Z11528 T. harzianum	C 957	52	1.5	1739	6	PCU42442	Sequence
C 885	885	52	1.5	1071	3	BT015310	BT015310 Drosophil	C 958	52	1.5	1743	6	CQ767534	Sequence
C 886	886	52	1.5	1095	5	BC061298	BC061298 Xenopus t	C 959	52	1.5	1743	6	AX454788	Sequence
C 887	887	52	1.5	1114	6	AR229215	Sequence	C 960	52	1.5	1743	6	AX470409	Sequence
C 888	888	52	1.5	1114	6	AR229215	Sequence	C 961	52	1.5	1743	6	AX491266	Sequence
C 889	889	52	1.5	1114	6	BD084191	BD084191 28 human	C 962	52	1.5	1743	6	AX538144	Sequence
C 890	890	52	1.5	1115	9	BC014240	BC014240 Homo sapi	C 963	52	1.5	1745	5	BC068326	Danio rer
C 891	891	52	1.5	1141	10	BC071255	BC071255 Mus muscu	C 964	52	1.5	1750	9	BC060667	Homo sapi
C 892	892	52	1.5	1162	8	AF275315	AF275315 Lotus jap	C 965	52	1.5	1769	9	BC084179	Xenopus t
C 893	893	52	1.5	1174	6	A92311	A92311 Sequence 1	C 966	52	1.5	1771	9	BC071744	Homo sapi
C 894	894	52	1.5	1174	6	AR075389	AR075389 Sequence	C 967	52	1.5	1772	10	BC058245	Mus muscu
C 895	895	52	1.5	1174	6	AR094310	AR094310 Sequence	C 968	52	1.5	1790	9	BC042674	Homo sapi

cl115	52	1.5	6200	6	AR349304	Sequence	1188	51	1.4	94	6	AX366494	Sequence
cl116	52	1.5	6200	6	AX353687	Sequence	1189	51	1.4	101	6	AX494448	Sequence
cl117	52	1.5	6200	6	AX490847	Sequence	1190	51	1.4	102	6	AX381427	Sequence
cl118	52	1.5	6889	10	BC053522	Mus muscu	cl1191	51	1.4	132	6	AX496057	Sequence
cl119	52	1.5	7084	9	HSB803370	Sequence	cl1192	51	1.4	143	6	AX255922	Sequence
cl120	52	1.5	8281	9	HSB801490	Sequence	cl1193	51	1.4	179	6	CQ525853	Sequence
cl121	52	1.5	6854	2	AC100175	Mus muscu	cl1194	51	1.4	188	6	CQ527214	Sequence
cl122	52	1.5	105682	3	AC116957_3	Continuation (4 of	cl1195	51	1.4	188	6	CQ525204	Sequence
cl123	52	1.5	110000	3	AC112124_2	Continuation (3 of	cl1196	51	1.4	195	6	CQ525204	Sequence
cl124	52	1.5	110000	3	AC116305_2	Continuation (3 of	cl1197	51	1.4	195	6	AX423817	Sequence
cl125	52	1.5	110000	3	AC116984_1	Continuation (2 of	cl1198	51	1.4	195	6	AX984511	Sequence
cl126	52	1.5	129517	2	AC016400	Continuation (2 of	cl1199	51	1.4	195	6	BD119370	EST and e
cl127	52	1.5	132254	3	AC116330	AC016400 Homo sapi	cl1200	51	1.4	196	6	CQ525476	Sequence
cl128	52	1.5	149677	9	AF004712	AC116330 Dictyoste	cl1201	51	1.4	198	6	CQ488001	Sequence
cl129	52	1.5	150789	9	HS2187	AP004712 Homo sapi	cl1202	51	1.4	199	6	CQ526519	Sequence
cl130	52	1.5	150864	9	AC096588	AC033375 Human DNA	cl1203	51	1.4	200	6	CQ525905	Sequence
cl131	52	1.5	152336	9	AP004714	AC096588 Homo sapi	cl1204	51	1.4	201	6	CQ506341	Sequence
cl132	52	1.5	153751	3	AC116551	AP004714 Homo sapi	cl1205	51	1.4	202	6	CQ703652	Sequence
cl133	52	1.5	154375	2	AC145837	AC116551 Dictyoste	cl1206	51	1.4	203	6	CQ703652	Sequence
cl134	52	1.5	158420	9	AL732326	AC145837 Pan trogl	cl1207	51	1.4	210	6	CQ395202	Sequence
cl135	52	1.5	158591	9	AL139277	AL732326 Human DNA	cl1208	51	1.4	210	6	CQ401542	Sequence
cl136	52	1.5	158595	10	AC133487	AL139277 Human DNA	cl1209	51	1.4	210	6	CQ525162	Sequence
cl137	52	1.5	159238	9	AC093575	AC133487 Mus muscu	cl1210	51	1.4	212	6	CQ525883	Sequence
cl138	52	1.5	159472	2	AC023780	AC093575 Homo sapi	cl1211	51	1.4	212	6	CQ677317	Sequence
cl139	52	1.5	163958	2	AC019303	AC023780 Homo sapi	cl1212	51	1.4	215	6	CQ526670	Sequence
cl140	52	1.5	166025	2	AC036200	AC019303 Homo sapi	cl1213	51	1.4	215	6	AX423824	Sequence
cl141	52	1.5	166048	2	AC133471	AC036200 Homo sapi	cl1214	51	1.4	215	6	AX984518	Sequence
cl142	52	1.5	168169	2	AC145953	AC133471 Homo sapi	cl1215	51	1.4	215	6	BD119377	EST and e
cl143	52	1.5	168169	2	AC145953	AC145953 Pan trogl	cl1216	51	1.4	222	6	CQ525084	Sequence
cl144	52	1.5	171939	2	AC021855	AC145953 Pan trogl	cl1217	51	1.4	223	6	CQ523534	Sequence
cl145	52	1.5	173527	10	AC140193	AC021855 Homo sapi	cl1218	51	1.4	229	6	CQ525160	Sequence
cl146	52	1.5	173614	2	AC147388	AC140193 Mus muscu	cl1219	51	1.4	230	6	CQ523457	Sequence
cl147	52	1.5	174608	2	BR890570	AC147388 Pan trogl	cl1220	51	1.4	230	6	CQ526466	Sequence
cl148	52	1.5	179918	2	CR792451	BR890570 Danio rer	cl1221	51	1.4	234	6	CQ525561	Sequence
cl149	52	1.5	181792	2	CR388184	CR792451 Danio rer	cl1222	51	1.4	239	6	CQ520526	Sequence
cl150	52	1.5	182870	3	AC116960	CR388184 Danio rer	cl1223	51	1.4	244	6	CQ669081	Sequence
cl151	52	1.5	183982	2	AC009825	AC116960 Dictyoste	cl1224	51	1.4	255	6	CQ521197	Sequence
cl152	52	1.5	184332	2	AC141745	AC009825 Homo sapi	cl1225	51	1.4	255	6	AX211073	Sequence
cl153	52	1.5	185559	2	AC019166	AC141745 Apis mell	cl1226	51	1.4	261	6	CQ524994	Sequence
cl154	52	1.5	185634	2	AC119930	AC019166 Homo sapi	cl1227	51	1.4	265	6	CQ525645	Sequence
cl155	52	1.5	188873	2	AC019223	AC119930 Mus muscu	cl1228	51	1.4	266	6	CQ475720	Sequence
cl156	52	1.5	189071	9	AC067902	AC019223 Homo sapi	cl1229	51	1.4	267	6	CQ526755	Sequence
cl157	52	1.5	190185	9	AC026464	AC067902 Homo sapi	cl1230	51	1.4	267	6	AX338096	Sequence
cl158	52	1.5	192337	2	CR762383	AC026464 Homo sapi	cl1231	51	1.4	279	6	AX418723	Sequence
cl159	52	1.5	193919	2	AC115047	CR762383 Danio rer	cl1232	51	1.4	279	6	AX979417	Sequence
cl160	52	1.5	197843	2	AC024373	AC115047 Mus muscu	cl1233	51	1.4	279	6	BD114276	EST and e
cl161	52	1.5	198146	2	AC023499	AC024373 Homo sapi	cl1234	51	1.4	285	6	CQ486689	Sequence
cl162	52	1.5	198146	2	AC023499	AC023499 Homo sapi	cl1235	51	1.4	292	6	CQ517287	Sequence
cl163	52	1.5	208341	9	AC107933	AL928914 Mouse DNA	cl1236	51	1.4	299	6	AX418714	Sequence
cl164	52	1.5	210414	10	AC116773	AC107933 Homo sapi	cl1237	51	1.4	299	6	AX979408	Sequence
cl165	52	1.5	213308	2	AC079164	AC116773 Mus muscu	cl1238	51	1.4	301	6	BD114267	EST and e
cl166	52	1.5	214056	10	AC118011	AC079164 Mus muscu	cl1239	51	1.4	304	6	CQ516894	Sequence
cl167	52	1.5	215228	2	AC099586	AC118011 Mus muscu	cl1240	51	1.4	306	6	CQ512954	Sequence
cl168	52	1.5	219138	2	AC136690	AC099586 Mus muscu	cl1241	51	1.4	307	11	G73825	Sequence
cl169	52	1.5	221951	10	AC122857	AC136690 Mus muscu	cl1242	51	1.4	309	6	CQ525525	Sequence
cl170	52	1.5	225024	2	CR394539	AC122857 Mus muscu	cl1243	51	1.4	311	3	AF159977	Sequence
cl171	52	1.5	226099	10	AC145557	CR394539 Danio rer	cl1244	51	1.4	312	6	CQ528973	Sequence
cl172	52	1.5	234985	2	AC139570	AC145557 Mus muscu	cl1245	51	1.4	315	3	BCA270225	Sequence
cl173	52	1.5	241725	3	AC117075	AC139570 Mus muscu	cl1246	51	1.4	316	6	CQ408965	Sequence
cl174	52	1.5	254733	3	AC117075	AC109724 Rattus no	cl1247	51	1.4	317	6	CQ528915	Sequence
cl175	52	1.5	256879	3	AC116982	AC117075 Dictyoste	cl1248	51	1.4	321	6	CQ502741	Sequence
cl176	52	1.5	265444	3	AC116956	AC116982 Dictyoste	cl1249	51	1.4	321	6	CQ511598	Sequence
cl177	52	1.5	276496	2	AC091135	AC116956 Dictyoste	cl1250	51	1.4	321	6	CQ524273	Sequence
cl178	52	1.5	317666	2	AC094275	AC091135 Rattus no	cl1251	51	1.4	327	6	CQ519687	Sequence
cl179	52	1.5	333321	3	AC116986	AC094275 Rattus no	cl1252	51	1.4	327	6	CQ523365	Sequence
cl180	52	1.5	333321	3	AC116986	AC116986 Dictyoste	cl1253	51	1.4	327	6	AX424644	Sequence
cl181	51	1.4	94	6	AX381752	BD264876 Compositi	cl1254	51	1.4	327	6	AX985338	Sequence
cl182	51	1.4	94	6	AR238279	BD264876 Compositi	cl1255	51	1.4	327	6	BD120197	EST and e
cl183	51	1.4	94	6	AR257820	AR238279 Sequence	cl1256	51	1.4	328	10	BC051203	Sequence
cl184	51	1.4	94	6	AR257820	AR257820 Sequence	cl1257	51	1.4	329	6	CQ518231	Sequence
cl185	51	1.4	94	6	AR283866	AR257820 Sequence	cl1258	51	1.4	332	6	CQ482015	Sequence
cl186	51	1.4	94	6	AR443540	AR283866 Sequence	cl1259	51	1.4	332	6	CQ517520	Sequence
cl187	51	1.4	94	6	AR478618	AR443540 Sequence	cl1260	51	1.4	332	6	CQ523998	Sequence

c1261	51	1.4	335	6	CQ524296	CQ524296 Sequence	c1334	51	1.4	481	6	CQ522448	Sequence
c1262	51	1.4	335	6	AX284648	Sequence	c1335	51	1.4	481	6	CQ524400	Sequence
c1263	51	1.4	341	6	AX24638	Sequence	c1336	51	1.4	481	6	CQ525538	Sequence
c1264	51	1.4	341	6	AX985332	Sequence	c1337	51	1.4	486	6	CQ406735	Sequence
c1265	51	1.4	341	6	BD120191	Sequence	c1338	51	1.4	487	6	CQ526794	Sequence
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c1332	51	1.4	478	6	CQ526461	Sequence	c1405	51	1.4	617	8	AF323605	AF323605 Manihot e
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C1414	AX381975 Sequence	51	1.4	660	6	AX381975
C1415	BC034329 Mus muscu	51	1.4	666	10	BC034329
C1416	BC074190 Xenopus l	51	1.4	668	5	BC074190
C1417	BC059905 Mus muscu	51	1.4	670	10	BC059905
C1418	BC059112 Rattus no	51	1.4	675	10	BC059112
C1419	BD192651 123 human	51	1.4	685	6	BD192651
C1420	AX184122 Sequence	51	1.4	685	6	AX184122
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C1425	AX987051 Sequence	51	1.4	711	6	AX987051
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C1427	BD020426 Novel gen	51	1.4	726	6	BD020426
C1428	BD100364 Novel gen	51	1.4	726	6	BD100364
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C1431	AY095188 Drosophill	51	1.4	743	3	AY095188
C1432	CQ432369 Sequence	51	1.4	743	6	CQ432369
C1433	BC046646 Homo sapi	51	1.4	751	9	BC046646
C1434	AK174753 Clona int	51	1.4	752	3	AK174753
C1435	BD018741 Novel gen	51	1.4	754	6	BD018741
C1436	BD098679 Novel gen	51	1.4	754	6	BD098679
C1437	BC043579 Homo sapi	51	1.4	754	9	BC043579
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C1439	BD019227 Novel gen	51	1.4	761	6	BD019227
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C1441	AR432941 Sequence	51	1.4	763	6	AR432941
C1442	BC065793 Mus muscu	51	1.4	771	10	BC065793
C1443	BC030674 Mus muscu	51	1.4	774	10	BC030674
C1444	BD019338 Novel gen	51	1.4	781	6	BD019338
C1445	BD099276 Novel gen	51	1.4	781	6	BD099276
C1446	BC061900 Homo sapi	51	1.4	789	9	BC061900
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C1451	BC075785 Danio rer	51	1.4	836	5	BC075785
C1452	AX575537 Sequence	51	1.4	841	6	AX575537
C1453	BC027507 Mus muscu	51	1.4	842	10	BC027507
C1454	X57848 B.napus cru	51	1.4	848	8	BNCR04RNA
C1455	BD018434 Novel gen	51	1.4	849	6	BD018434
C1456	BD098372 Novel gen	51	1.4	849	6	BD098372
C1457	AY119449 Drosophill	51	1.4	853	9	AY119449
C1458	AF049923 Petunia x	51	1.4	868	8	AF049923
C1459	BC049711 Mus muscu	51	1.4	868	10	BC049711
C1460	AY369135 Anopheles	51	1.4	871	3	AY369135
C1461	BC049733 Mus muscu	51	1.4	881	10	BC049733
C1462	X94979 B.oileracea	51	1.4	882	8	BOPC34
C1463	BD074358 50 human	51	1.4	886	6	BD074358
C1464	AY267688 Bigelowie	51	1.4	892	3	AY267688
C1465	AX512900 Sequence	51	1.4	893	6	AX512900
C1466	BC039684 Homo sapi	51	1.4	897	9	BC

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LOCUS
DEFINITION Homo sapiens clone DNAS9218 CDAN1 (UNQ664) mRNA linear PRI 03-OCT-2003
ACCESSION AY358467
VERSION AY358467.1 GI:37182057
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3580)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,K., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 3580)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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100.0%; Score 3580; DB 9; Length 3580;
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passed the following selection criteria: Hexamer frequency ORF analysis.

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Location/Qualifiers

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ORIGIN

Query Match 42.8%; Score 1534; DB 9; Length 3212;
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Matches 1534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7

BC066640

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

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AUTHORS

TITLE

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AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

BC066640 4350 bp mRNA linear PRI 30-MAR-2004
Homo sapiens congenital dyserythropoietic anemia, type I, mRNA
(cDNA clone MGC:71365 IMAGE:6577335), complete cds.

BC066640
Homo sapiens (human)
MGC.

BC066640.1 GI:45219716
Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4350)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, M., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

2 (bases 1 to 4350)
Straussberg, R.
Direct Submission
Submitted (01-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc mgc@hgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/L1NL at: <http://image.llnl.gov>
Series: IRL Plate: 50 Row: O Column: 8
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passed the following selection criteria: GenomeScan gene
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FEATURES

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Location/Qualifiers

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ORIGIN

Query Match

33.9%; Score 1214; DB 9; Length 4350;

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RESULT 8

BC052568

LOCUS

DEFINITION

Homo sapiens congenital dyserythropoietic anemia, type I, mRNA

ACCESSION

BC052568

VERSION

BC052568.1

KEYWORDS

GI:30851636

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE

22388257

PUBMED

12477932

REFERENCE

AUTHORS

Strausberg, R.

TITLE

Direct Submission

JOURNAL

Submitted (16-MAY-2003)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
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Clone distribution: MGC clone distribution information can be found
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 Series: IRAL Plate: 47 Row: O Column: 19
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FEATURES

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DEFINITION         Homo sapiens mRNA; cDNA DKFZp434G2127 (from clone DKFZp434G2127).
ACCESSION          AL133019
VERSION            AL133019.1  GI:6453499
KEYWORDS
SOURCE
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE           1 (bases 1 to 2145)
AUTHORS            Bloecher,H., Boescher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
                    Wiemann,S.
TITLE              Direct Submission
JOURNAL            Submitted (15-NOV-1999) MIPS, Am Klopferspitz 18a, D-82152
                    Martinsried, GERMANY
COMMENT            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                    Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
                    sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                    Braunschweig/Germany) within the cDNA sequencing consortium of the
                    German Genome Project.
                    This clone (DKFZp434G2127) is available at the RZPD in Berlin.
                    Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                    Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                    information about the clone and the sequencing project is available
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DEFINITION AC016400
ACCESSION AC016400
VERSION AC016400.1 GI:6468793
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ben-Asher, E., Avidan, N., Olender, T., Lancet, D., Salmon, L. and
Tamary, H.
Sequencing of human chromosome 15 D15S488 region
TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 129517)
AUTHORS Ben-Asher, E., Avidan, N., Olender, T., Lancet, D., Salmon, L. and
Tamary, H.
Direct Submission
Submitted (26-NOV-1999) Dept. of Molecular Genetics, Weizmann
Institute of Science, P.O.Box 26, Rehovot 76100, Israel
center: The Weizmann Institute, Crown Genome Center Web site:
http://bioinfo.weizmann.ac.il/genome_center/sequencing.html
Contact: lgbenash@weizmann.weizmann.ac.il ----- Summary
Statistics Sequencing vector: PUC18 Chemistry: Big Dye
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terminators.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 6441 8285: contig of 1845 bp in length
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* 8286 9535: contig of 1250 bp in length
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* 18052 31986: contig of 13935 bp in length
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DEFINITION sequence.
ACCESSION AC090510
VERSION AC090510.4 GI:18249987
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 148295)
AUTHORS Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
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TITLE
JOURNAL
REFERENCE
AUTHORS
Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
2 (bases 1 to 148295)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A.,
Nesbitt,R., Traicoff,R. and Hood,L.
Direct Submission
Submitted (27-FEB-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
3 (bases 1 to 148295)
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
Direct Submission
Submitted (19-JAN-2002) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
On Jan 19, 2002 this sequence version replaced gi:17436948.
----- Genome Center
Center: Multimegabase Sequencing Center
Center code: UMWSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leserow@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Note: data from AC018362 [Drafting center UMWSC] ans AC068727
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DEFINITION Human chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL136332
VERSION AL136332.5 GI:14572584
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 209157)
AUTHOR Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
Unpublished
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2 (bases 1 to 209157)
Genoscope.
Direct Submission
Submitted (22-MAY-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 27, 2001 this sequence version replaced gi:12657317.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
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The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-188113 (AC-AL132987)
Downstream BAC (overlapping the SP6 end) : R-828K24 -----
Finishing boundaries
FINISHED SEGMENT STARTS AT BASE 34450
FINISHED SEGMENT ENDS AT BASE 103340
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Assembly program: Phrap; version 2.0
Quality coverage: 6.39x in Q20 bases; sum-of-contigs
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Range : bases
0 : 35
1 - 9 : 69
10 - 19 : 442
20 - 29 : 1059
30 - 39 : 3289
40 - 49 : 12373
50 - 59 : 16399
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80 - 89 : 53955
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QY 3379 CACAGGAAGTGGGTCTCCGCAACACAGGCGAGGGCGGGCTCCCGCGCGCGCGCC 3434
|
|
|
Db 1975 CACAGGAAGTGGGTCTCCGCAACACAGGCGAGGGCGGGCTCCCGCGCGCGCGCC 1920
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|
|
RESULT 15
CQ851120/c 3589 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 1589 from Patent EP1447413.
ACCESSION CQ851120
VERSION CQ851120.1 GI:51509332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
TITLE Full-length human cDNA
JOURNAL Patent: EP 1447413-A 1589 18-AUG-2004;
Research Association for Biotechnology (JP)
FEATURES
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1..3589
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ORIGIN

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Query Match 20.3%; Score 725; DB 6; Length 3589;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2659 AAATTCTCCACACAGATGGCTCTCGAATCTGCCACAGCTCTGGGGCGGTCTCCGTAGG 2718
|
|
|
Db 3573 AAATTCTCCACACAGATGGCTCTCGAATCTGCCACAGCTCTGGGGCGGTCTCTCTAGG 3514
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Search completed: March 29, 2005, 04:09:36
Job time : 14865 secs

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Run on: March 28, 2005, 21:04:22 ; Search time 1702 Seconds
(without alignments)
12451.630 Million cell updates/sec

Title: US-10-015-388A-53
Perfect score: 3580
Sequence: 1 gacccggtccctccggtcctg.....cacgaacagccggtgcgcct 3580
Scoring table: OLGOW-NUC

Searched: Gapop 60.0 , Gapext 60.0
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : N_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAC58112	standard; cDNA; 3580 BP.				
DE	Human PRO1295	nucleotide sequence SEQ ID NO:28.				
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 3;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 2						
ID	AAA37037	standard; cDNA; 3580 BP.				
DE	Human PRO1295 (UNQ664)	cDNA sequence SEQ ID NO:53.				
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 3;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 3						
ID	AAF54239	standard; DNA; 3580 BP.				
DE	DNA encoding protein of the invention #16.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 4;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 4						
ID	ACD68276	standard; cDNA; 3580 BP.				
DE	Novel human secreted and transmembrane protein PRO1295.					
PN	US2003073130-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 9;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 5						
ID	ACH04378	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003044841-A1.					
PD	06-MAR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 9;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 6						
ID	ADB50343	standard; cDNA; 3580 BP.				

ID	ACD67922	standard; cDNA; 3580 BP.				
DE	Novel human secreted and transmembrane protein PRO1295	cDNA.				
PN	US2003073129-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 9;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 7						
ID	ADC17922	standard; cDNA; 3580 BP.				
DE	Human PRO polynucleotide #16.					
PN	US2003064925-A1.					
PD	03-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 8						
ID	ADD70568	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US200309625-A1.					
PD	29-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 9						
ID	ADD39645	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003083462-A1.					
PD	01-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 10						
ID	ADD70091	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003054406-A1.					
PD	20-MAR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 11						
ID	ADD38212	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003096955-A1.					
PD	22-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 12						
ID	ADD39168	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003096954-A1.					
PD	22-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 13						
ID	ADD38691	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003092061-A1.					
PD	15-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 14						
ID	ADD40122	standard; cDNA; 3580 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO1295.					
PN	US2003082627-A1.					
PD	01-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3580;	DB 10;	Length 3580;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 15						
ID	ADB50343	standard; cDNA; 3580 BP.				

DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 16
 ID ADE19955 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 17
 ID ADE49866 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 18
 ID ADE21424 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 19
 ID ADF29849 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 20
 ID ADF5742 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 21
 ID ADH99246 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 10; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 22
 ID ADE96426 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 23
 ID ADF25737 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 24
 ID ADF24636 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.

PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 25
 ID ADF29372 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 26
 ID ADE96903 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 27
 ID ADH02941 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 28
 ID ADH03895 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 29
 ID ADH03418 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 30
 ID ADH04372 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 31
 ID ADH61373 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 32
 ID ADL94572 standard; cDNA; 3580 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1295.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3580; DB 12; Length 3580;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 33
 ID ADO05609 standard; DNA; 4725 BP.
 DE Human erythrocyte differentiation factor, Codanin-1 encoding DNA.
 PN WO2004035535-A2.

PD 29-APR-2004.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
 Query Match
 Best Local Similarity 42.3%; Score 1515; DB 12; Length 4725;
 RESULT 34
 ID AA199229 standard; DNA; 4137 BP.
 DE Human excretory related polynucleotide SEQ ID NO 993.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 29.5%; Score 1056; DB 4; Length 4137;
 RESULT 35
 ID AA163579 standard; DNA; 4137 BP.
 DE Human kidney related polynucleotide SEQ ID NO 894.
 PN WO200155323-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 29.5%; Score 1056; DB 5; Length 4137;
 RESULT 36
 ID ADM44207 standard; cDNA; 2240 BP.
 DE Novel human arginine-rich protein cDNA #571.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Query Match
 Best Local Similarity 27.8%; Score 995; DB 12; Length 2240;
 RESULT 37
 ID AB211689 standard; cDNA; 1833 BP.
 DE Human polynucleotide SEQ ID NO 571.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 26.3%; Score 941; DB 6; Length 1833;
 RESULT 38
 ID AAK89946 standard; DNA; 32187 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3522.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 24.3%; Score 871; DB 4; Length 32187;
 RESULT 39
 ID ADP22979 standard; cDNA; 2793 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:73.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 20.3%; Score 725; DB 13; Length 2793;
 RESULT 40
 ID ADP22979 standard; cDNA; 3589 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1589.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match
 Best Local Similarity 20.3%; Score 725; DB 13; Length 3589;
 RESULT 41
 ID AA252877 standard; cDNA; 802 BP.
 DE Human prostate tumor cDNA library derived EST fragment #20.
 PN DE19820190-A1.
 PD 04-NOV-1999.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Query Match
 Best Local Similarity 16.7%; Score 598; DB 2; Length 802;
 RESULT 42
 ID AAF66762 standard; cDNA; 413 BP.
 DE Novel human polynucleotide, SEQ ID NO: 2518.
 PN WO200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 9.8%; Score 350; DB 5; Length 413;
 RESULT 43
 ID ADF80502 standard; DNA; 357 BP.
 DE Leukaemia-related DNA sequence #1058.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAPE/) HAFERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match
 Best Local Similarity 8.8%; Score 314; DB 10; Length 357;
 RESULT 44
 ID AAH99000 standard; cDNA; 403 BP.
 DE Human EST-derived coding sequence SEQ ID NO: 857.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 8.3%; Score 296; DB 4; Length 403;
 RESULT 45
 ID ACH42160 standard; cDNA; 464 BP.
 DE Human foetal brain cDNA #3527.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match
 Best Local Similarity 7.7%; Score 274; DB 9; Length 464;
 RESULT 46
 ID AB211935 standard; cDNA; 2223 BP.
 DE Human polynucleotide SEQ ID NO 817.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 5.6%; Score 201; DB 6; Length 2223;
 RESULT 47
 ID ADM44453 standard; cDNA; 2223 BP.
 DE Novel human arginine-rich protein cDNA #817.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRMA/) DRMANAC R T.
 Query Match
 Best Local Similarity 5.6%; Score 201; DB 12; Length 2223;
 RESULT 48
 ID ABN97391 standard; DNA; 177 BP.
 DE Gene #3889 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match
 Best Local Similarity 4.8%; Score 173; DB 6; Length 177;
 RESULT 49
 ID AA198743 standard; cDNA; 441 BP.
 DE Human excretory related polynucleotide SEQ ID NO 187.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 4.2%; Score 152; DB 4; Length 441;
 RESULT 50
 ID AAF66762 standard; cDNA; 413 BP.

Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Score 60; DB 5; Length 1408;

RESULT 59
ID ABT10750 standard; cDNA; 1746 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 884.
ID WO2002592711-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Score 59; DB 6; Length 1746;

RESULT 60
ID ADL15034 standard; DNA; 1746 BP.
DE Human uterus clone DKFZp586B211 DNA for cancer treatment.
ID WO2003088268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Score 59; DB 10; Length 1746;

RESULT 61
ID ADN04609 standard; cDNA; 1746 BP.
DE Antipeptidic cDNA sequence #513.
ID WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Score 59; DB 12; Length 1746;

RESULT 62
ID ADP55055 standard; cDNA; 1746 BP.
DE Human PRO cDNA sequence SEQ ID NO:1031.
ID WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Score 59; DB 13; Length 1746;

RESULT 63
ID ADP24618 standard; cDNA; 1746 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1796.
ID WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Score 59; DB 13; Length 1746;

RESULT 64
ID ABEK71347 standard; cDNA; 2695 BP.
DE Human nucleic acid management-associated cDNA from clone DKFZp586B211.
ID WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Score 59; DB 5; Length 2695;

RESULT 65
ID ADT95789 standard; cDNA; 81 BP.
DE Colon cancer associated human cDNA sequence #1308.
ID US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIAX CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Score 58; DB 11; Length 81;

RESULT 66
ID ADT95235 standard; cDNA; 81 BP.
DE Colon cancer associated human cDNA sequence #754.
ID US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIAX CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Score 58; DB 11; Length 81;

RESULT 67
ID ADQ92140 standard; DNA; 81 BP.
DE Human autoantigen DNA fragment MPMGP800121571.
ID WO2004058972-A1.
PD 15-JUL-2004.
PA (THIE/) THIESSEN H.
PA (LORE/) LORENZ P.

Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 81;
RESULT 68
ID ADT95070 standard; cDNA; 89 BP.
DE Colon cancer associated human cDNA sequence #589.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 89;
RESULT 69
ID ADT95330 standard; cDNA; 92 BP.
DE Colon cancer associated human cDNA sequence #849.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 92;
RESULT 70
ID ABX55117 standard; cDNA; 93 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5046.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 93;
RESULT 71
ID ADD35066 standard; DNA; 95 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2846.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 95;
RESULT 72
ID ADT94820 standard; cDNA; 97 BP.
DE Colon cancer associated human cDNA sequence #339.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 97;
RESULT 73
ID ABX60796 standard; DNA; 102 BP.
DE Arabidopsis thaliana polynucleotide #142.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 102;
RESULT 74
ID ABX61529 standard; DNA; 103 BP.
DE Arabidopsis thaliana polynucleotide #875.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 103;
RESULT 75
ID ABX61191 standard; DNA; 103 BP.
DE Arabidopsis thaliana polynucleotide #537.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 103;
RESULT 76
ID ADT95788 standard; cDNA; 103 BP.
DE Colon cancer associated human cDNA sequence #1307.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 103;
RESULT 77
ID ABX61368 standard; DNA; 104 BP.
DE Arabidopsis thaliana polynucleotide #714.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 104;
RESULT 78
ID ADT94949 standard; cDNA; 104 BP.
DE Colon cancer associated human cDNA sequence #468.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 104;
RESULT 79
ID ABX60741 standard; DNA; 105 BP.
DE Arabidopsis thaliana polynucleotide #87.
PN US2002142319-A1.
PD 03-OCT-2002.

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PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 105;
RESULT 80
ID ADD35198 standard; DNA; 106 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2978.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEW-) UNIV EMORY.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 106;
RESULT 81
ID ABX61169 standard; DNA; 109 BP.
DE Arabidopsis thaliana polynucleotide #515.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 109;
RESULT 82
ID ABX61450 standard; DNA; 109 BP.
DE Arabidopsis thaliana polynucleotide #796.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 109;
RESULT 83
ID ABX42131 standard; cDNA; 111 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7296.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 100.0%; Score 58; DB 8; Length 111;
RESULT 84
ID ABX61125 standard; DNA; 112 BP.
DE Arabidopsis thaliana polynucleotide #471.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 112;
RESULT 85
ID ADT94947 standard; cDNA; 112 BP.
DE Colon cancer associated human cDNA sequence #466.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Score 58; DB 11; Length 112;
RESULT 86
ID ABX61189 standard; DNA; 113 BP.
DE Arabidopsis thaliana polynucleotide #535.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 113;
RESULT 87
ID ABX61401 standard; DNA; 114 BP.
DE Arabidopsis thaliana polynucleotide #747.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 113;
RESULT 88
ID ADT95198 standard; cDNA; 114 BP.
DE Colon cancer associated human cDNA sequence #717.
PN US2003087818-A1.

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PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 114;
Pred. No. 1.6e-06;
RESULT 89
ID ABX60912 standard; DNA; 115 BP.
DE Arabidopsis thaliana polynucleotide #258.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 115;
Pred. No. 1.6e-06;
RESULT 90
ID ABX61120 standard; DNA; 116 BP.
DE Arabidopsis thaliana polynucleotide #466.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 116;
Pred. No. 1.6e-06;
RESULT 91
ID ADT95242 standard; cDNA; 116 BP.
DE Colon cancer associated human cDNA sequence #761.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 116;
Pred. No. 1.6e-06;
RESULT 92
ID ADT95224 standard; cDNA; 117 BP.
DE Colon cancer associated human cDNA sequence #743.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 117;
Pred. No. 1.6e-06;
RESULT 93
ID ABX61196 standard; DNA; 118 BP.
DE Arabidopsis thaliana polynucleotide #542.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.

PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 118;
Pred. No. 1.6e-06;
RESULT 94
ID ADT95578 standard; cDNA; 118 BP.
DE Colon cancer associated human cDNA sequence #1097.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 118;
Pred. No. 1.6e-06;
RESULT 95
ID ABX35904 standard; cDNA; 119 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1069.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TRON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 119;
Pred. No. 1.6e-06;
RESULT 96
ID ADT95794 standard; cDNA; 119 BP.
DE Colon cancer associated human cDNA sequence #1313.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 119;
Pred. No. 1.6e-06;
RESULT 97
ID ABX60705 standard; DNA; 121 BP.
DE Arabidopsis thaliana polynucleotide #51.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 121;
Pred. No. 1.6e-06;
RESULT 98
ID ADT95271 standard; cDNA; 121 BP.
DE Colon cancer associated human cDNA sequence #790.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 121;
Pred. No. 1.6e-06;
RESULT 99
ID ADT94786 standard; cDNA; 122 BP.
DE Colon cancer associated human cDNA sequence #305.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 122;
Pred. No. 1.6e-06;
RESULT 100
ID ADT95288 standard; cDNA; 122 BP.
DE Colon cancer associated human cDNA sequence #807.

PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 101
ID ADT95241 standard; cDNA; 123 BP.
DE Colon cancer associated human cDNA sequence #760.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 102
ID ABX0896 standard; DNA; 124 BP.
DE Arabidopsis thaliana polynucleotide #242.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORG/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 1.6%; Score 58; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 103
ID ADT95479 standard; cDNA; 126 BP.
DE Colon cancer associated human cDNA sequence #998.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 104
ID ABX61459 standard; DNA; 128 BP.
DE Arabidopsis thaliana polynucleotide #805.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORG/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 1.6%; Score 58; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 105
ID ADT95260 standard; cDNA; 133 BP.
DE Colon cancer associated human cDNA sequence #779.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 106
ID ADT95694 standard; cDNA; 135 BP.
DE Colon cancer associated human cDNA sequence #1213.
PN US2003087818-A1.

PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
RESULT 107
ID ABX42392 standard; cDNA; 136 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7557.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 108
ID ADT95450 standard; cDNA; 141 BP.
DE Colon cancer associated human cDNA sequence #969.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 109
ID ADT95577 standard; cDNA; 145 BP.
DE Colon cancer associated human cDNA sequence #1096.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 110
ID ADT95485 standard; cDNA; 145 BP.
DE Colon cancer associated human cDNA sequence #1004.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 11; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 111
ID ABX41830 standard; cDNA; 152 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6995.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 112
ID AAI84674 standard; cDNA; 165 BP.
DE Human polynucleotide SEQ ID NO 4734.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 58; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
RESULT 113
ID ABX35959 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1124.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
RESULT 114
ID ABX36136 standard; cDNA; 181 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1301.
PN US2002137139-A1.


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PD 26-SEP-2002...
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 181;
RESULT 115
ID ABX61443 standard; DNA; 186 BP.
DE Arabidopsis thaliana polynucleotide #789.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL//) GORLACH J.
PA (ANY//) AN Y.
PA (HAMI//) HAMILTON C M.
PA (PRIC//) PRICE J L.
PA (HARG//) HARGISS T R.
PA (YUY//) YU Y.
PA (RAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 186;
RESULT 116
ID ABX60862 standard; DNA; 196 BP.
DE Arabidopsis thaliana polynucleotide #208.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL//) GORLACH J.
PA (ANY//) AN Y.
PA (HAMI//) HAMILTON C M.
PA (PRIC//) PRICE J L.
PA (HARG//) HARGISS T R.
PA (YUY//) YU Y.
PA (RAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 196;
RESULT 117
ID ABX49827 standard; cDNA; 203 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14992.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 203;
RESULT 118
ID ABX38577 standard; cDNA; 203 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3742.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 203;
RESULT 119
ID ABX38781 standard; cDNA; 207 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3946.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 207;
RESULT 120
ID ABX41435 standard; cDNA; 208 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6600.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 208;
RESULT 121
ID ABX39781 standard; cDNA; 219 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4946.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 219;
RESULT 122
ID ABX49357 standard; cDNA; 220 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14522.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 220;
RESULT 123
ID ABX35502 standard; cDNA; 223 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #667.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 223;
RESULT 124
ID ABX45169 standard; cDNA; 228 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10334.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 228;
RESULT 125
ID ABX47018 standard; cDNA; 236 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12183.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 236;

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RESULT 126
ID ABX48174 standard; cDNA; 239 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13339.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 239;
Pred. No. 1.3e-06;
RESULT 127
ID ABX47809 standard; cDNA; 241 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12974.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 241;
Pred. No. 1.3e-06;
RESULT 128
ID ABX38052 standard; cDNA; 242 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3217.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 242;
Pred. No. 1.3e-06;
RESULT 129
ID ABX35484 standard; cDNA; 272 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #649.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 272;
Pred. No. 1.3e-06;
RESULT 130
ID ABX37131 standard; cDNA; 277 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2296.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 277;
Pred. No. 1.2e-06;
RESULT 131
ID ABX46910 standard; cDNA; 283 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12075.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 283;
Pred. No. 1.2e-06;
RESULT 132
ID ABX48177 standard; cDNA; 286 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13342.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 312;
Pred. No. 1.2e-06;
RESULT 133
ID ABX41150 standard; cDNA; 312 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6315.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 312;
Pred. No. 1.2e-06;
RESULT 134
ID ABX37883 standard; cDNA; 296 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3048.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 296;
Pred. No. 1.2e-06;
RESULT 135
ID ABX61005 standard; DNA; 301 BP.
DE Arabidopsis thaliana polynucleotide #351.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL//) GORLACH J.
PA (ANYV//) AN Y.
PA (HAMI//) HAMILTON C M.
PA (PRIC//) PRICE J L.
PA (HARG//) HARGISS T R.
PA (YUYU//) YU Y.
PA (RAME//) RAMEAKA J G.
PA (PAGE//) PAGE A.
PA (MATH//) MATHW A V.
PA (LEDF//) LEDFORD B L.
PA (WOES//) WOESSNER J P.
PA (HAAS//) HAAS W D.
PA (GARC//) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 301;
Pred. No. 1.2e-06;
RESULT 136
ID ABX87211 standard; cDNA; 310 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10189.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI//) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 310;
Pred. No. 1.2e-06;
RESULT 137
ID ABX41150 standard; cDNA; 312 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6315.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 312;
Pred. No. 1.2e-06;
RESULT 138
ID ABX37743 standard; cDNA; 316 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2908.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT//) BYATT J C.
PA (MATH//) MATHIALAGAN N.
PA (TAON//) TAO N.
PA (WARR//) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 312;
Pred. No. 1.2e-06;
```

PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 139
 ID ABX43454 standard; cDNA; 325 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #8619.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 140
 ID ADQ03196 standard; DNA; 330 BP.
 DE Arabidopsis homeobox transcription factor seqid 42.
 PN US2004123339-A1.
 PD 24-JUN-2004.
 PA (CONN//) CONNER T W.
 PA (HECK//) HECK G R.
 PA (LIUJ//) LIU J.
 Query Match 1.6%; Score 58; DB 12; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 141
 ID ABX41811 standard; cDNA; 337 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #6976.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 142
 ID ABX46565 standard; cDNA; 350 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #11730.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 143
 ID ABX49433 standard; cDNA; 358 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #14598.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 358;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 144
 ID ACN88453 standard; DNA; 358 BP.
 DE Breast cancer related marker, seq id 9603.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 11; Length 358;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 RESULT 145
 ID ABQ85687 standard; DNA; 359 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 557.
 PN US2002062014-A1.
 PD 23-MAY-2002.
 PA (GORL//) GORLACH J.
 PA (ANYI//) AN Y.
 PA (HAMI//) HAMILTON C M.

PA (PRIC//) PRICE J L.
 PA (RAIN//) RAINES T M.
 PA (YUYV//) YU Y.
 PA (RAME//) RAMEAKA J G.
 PA (PAGE//) PAGE A.
 PA (MATH//) MATHIEW A V.
 PA (LEDF//) LEDFORD B L.
 PA (WOES//) WOESSNER J P.
 PA (HAAS//) HAAS W D.
 PA (GARC//) GARCIA C A.
 PA (KRIC//) KRICKER M.
 PA (SLAT//) SLATER T.
 PA (DAVI//) DAVIS K R.
 PA (ALLE//) ALLEN K.
 PA (HOFF//) HOFFMAN N.
 PA (HURB//) HURBAN P.
 Query Match 1.6%; Score 58; DB 6; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 RESULT 146
 ID ABX41004 standard; cDNA; 370 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #6169.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 RESULT 147
 ID ABX38044 standard; cDNA; 382 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3209.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.
 PA (TAON//) TAO N.
 PA (WARR//) WARREN W C.
 Query Match 1.6%; Score 58; DB 8; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 RESULT 148
 ID ABQ85229 standard; DNA; 385 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 99.
 PN US2002062014-A1.
 PD 23-MAY-2002.
 PA (GORL//) GORLACH J.
 PA (ANYV//) AN Y.
 PA (HAMI//) HAMILTON C M.
 PA (PRIC//) PRICE J L.
 PA (RAIN//) RAINES T M.
 PA (YUYV//) YU Y.
 PA (RAME//) RAMEAKA J G.
 PA (PAGE//) PAGE A.
 PA (MATH//) MATHIEW A V.
 PA (LEDF//) LEDFORD B L.
 PA (WOES//) WOESSNER J P.
 PA (HAAS//) HAAS W D.
 PA (GARC//) GARCIA C A.
 PA (KRIC//) KRICKER M.
 PA (SLAT//) SLATER T.
 PA (DAVI//) DAVIS K R.
 PA (ALLE//) ALLEN K.
 PA (HOFF//) HOFFMAN N.
 PA (HURB//) HURBAN P.
 Query Match 1.6%; Score 58; DB 6; Length 385;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 RESULT 149
 ID ABX47838 standard; cDNA; 392 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #13003.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT//) BYATT J C.
 PA (MATH//) MATHIALAGAN N.

PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 1.6%; Score 58; DB 8; Length 392;
Query Match 100.0%; Pred. No. 1.1e-06;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 150
ID AAS44810 standard; DNA; 394 BP.
DE Human contig polynucleotide sequence #63.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 58; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 151
ID ABX42549 standard; cDNA; 394 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7714.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 152
ID ABX53255 standard; cDNA; 401 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3184.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 153
ID ABX42327 standard; cDNA; 410 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7492.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 154
ID ABX39273 standard; cDNA; 410 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4438.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 155
ID ABX43996 standard; cDNA; 414 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9161.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 156
ID ABX41704 standard; cDNA; 415 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6869.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C. 1.6%; Score 58; DB 8; Length 415;
Query Match 100.0%; Pred. No. 1.1e-06;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 157
ID ABX39702 standard; cDNA; 418 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4867.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 158
ID ABX47983 standard; cDNA; 420 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13148.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 159
ID ABX40752 standard; cDNA; 432 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5917.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 58; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 160
ID AAI93088 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 13148.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 58; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 161
ID ABL94042 standard; cDNA; 445 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027807 SEQ ID NO:807.
PN US2002023280-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 1.6%; Score 58; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 162

ID ABX39235 standard; cDNA; 446 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3400.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 8; Length 446;
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 11; Length 617;
 RESULT 163
 ID ABX44495 standard; cDNA; 453 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3660.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 8; Length 453;
 PD 31-JAN-2002.
 PA (DOWC) DOW CHEM CO.
 PA (REDD) REDDY S A.
 PA (LARR/) LARRINUA M I.
 PA (RUEG/) RUEGGER M.
 PA (WEGL/) WEGLARZ T.
 PA (BLAK/) BLAKESLEE B.
 PA (ORIE/) ORIEDO V B J.
 PA (SAVI/) SAVICKAS J P.
 PA (MCCR/) MCCREY A D.
 PA (MILL/) MILLER A B.
 PA (POGU/) POGUE P G.
 PA (DELL/) DELLA-CIOPPA R G.
 PA (WOLF/) WOLFE M G.
 PA (ZHEN/) ZHENG W.
 PA (GACH/) GACHOTTE D.
 PA (GROS/) GROSLEY R.
 PA (PELL/) PELL R.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 6; Length 554;
 PD 06-MAY-1999.
 PA (PLAC) MAX PLANCK GBS FOERDERUNG WISSENSCHAFTEN.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 6; Length 568;
 RESULT 166
 ID AAX61373 standard; cDNA; 589 BP.
 DE DNA encoding a human secreted protein.
 PN WO9922243-A1.
 PD 06-MAY-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 2; Length 589;
 RESULT 167
 ID ACN87190 standard; DNA; 592 BP.
 DE Breast cancer related marker, seq id 8340.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 11; Length 592;
 RESULT 168
 ID AAC81083 standard; cDNA; 594 BP.
 DE Human secreted protein cDNA sequence #36.
 PN WO200063230-A2.
 PD 26-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 3; Length 594;
 RESULT 169
 ID ACN87667 standard; DNA; 617 BP.
 DE Breast cancer related marker, seq id 8817.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 11; Length 617;
 RESULT 170
 ID ACN81732 standard; DNA; 631 BP.
 DE Breast cancer related marker, seq id 2882.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 11; Length 631;
 RESULT 171
 ID AAH33423 standard; cDNA; 637 BP.
 DE Human colon cancer antigen encoding cDNA seq ID NO:479.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 4; Length 637;
 RESULT 172
 ID ABQ66000 standard; DNA; 646 BP.
 DE Arabidopsis thaliana polynucleotide seq ID NO 577.
 PN US2002059663-A1.
 PD 16-MAY-2002.
 PA (GORL/) GORLACH J.
 PA (ANYI/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYV/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOBES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 6; Length 646;
 RESULT 173
 ID AAC87363 standard; cDNA; 703 BP.
 DE Human developmentally-regulated hippocampus EST, SEQ ID NO:6.
 PN WO200070036-A2.
 PD 23-NOV-2000.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 4; Length 703;
 RESULT 174
 ID ABL89582 standard; cDNA; 722 BP.
 DE Human polynucleotide seq ID NO 144.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 58; DB 6; Length 722;
 RESULT 175
 ID ABL87202 standard; cDNA; 735 BP.
 DE Human ovarian cancer related cDNA clone seq ID NO:10180.

PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 58; DB 6; Length 735;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
RESULT 176
ID AAF18114 standard; DNA; 786 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 133.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 1.6%; Score 58; DB 3; Length 786;
Best Local Similarity 100.0%; Pred. No. 9e-07;
RESULT 177
ID AAC59594 standard; cDNA; 820 BP.
DE Human secreted protein gene 29 SEQ ID NO:39.
PN WO200056883-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 820;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
RESULT 178
ID ABN98845 standard; DNA; 856 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOPE/) HOFFMAN N.
PA (HURE/) HUREAN P.
Query Match 1.6%; Score 58; DB 6; Length 856;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
RESULT 179
ID ADJ57936 standard; cDNA; 863 BP.
DE Rat NARC 14A cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 12; Length 863;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
RESULT 180
ID ACC48070 standard; cDNA; 905 BP.
DE Nucleotide sequence of cDNA pPC86-Clone 28R.
PN WO2003000273-A1.
PD 03-JAN-2003.
PA (AUTO-) AUTOGEN RES PTY LTD.
Query Match 1.6%; Score 58; DB 10; Length 905;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
RESULT 181
ID ADI42584 standard; DNA; 923 BP.
DE Plant transcription factor polynucleotide #673.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.

PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 1.6%; Score 58; DB 12; Length 923;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
RESULT 182
ID ADO02885 standard; cDNA; 923 BP.
DE Soybean orthologue of Thalecress transcription factor, cDNA #154.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 1.6%; Score 58; DB 12; Length 923;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
RESULT 183
ID AAS04268 standard; cDNA; 932 BP.
DE Murine secreted protein TANGO 269 cDNA sequence.
PN WO200130831-A1.
PD 03-MAY-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 4; Length 932;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
RESULT 184
ID AAD07722 standard; cDNA; 938 BP.
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 5; Length 938;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
RESULT 185
ID AAF98707 standard; DNA; 950 BP.
DE Human ovarian cancer cell expressed sequence 10807.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 950;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
RESULT 186
ID AAD07796 standard; cDNA; 1023 BP.
DE Mouse fibroblast growth factor (zFGF5) cDNA.
PN WO200139788-A2.
PD 07-JUN-2001.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 1.6%; Score 58; DB 4; Length 1023;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 187
ID ADF17709 standard; cDNA; 1023 BP.
DE cDNA encoding mouse fibroblast growth factor zFGF5.

PN US2003152568-A1.
PD 14-AUG-2003.
PA (WEST/) WEST J W.
Query Match 1.6%; Score 58; DB 10; Length 1023;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 188
ID AAD64162 standard; cDNA; 1023 BP.
DE Mouse zFGF5 cDNA.
PN US2003199443-A1.
PD 23-OCT-2003.
PA (DEIS/) DEISHER T A.
PA (CONK/) CONKLIN D C.
Query Match 1.6%; Score 58; DB 10; Length 1023;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 189
ID AAC93426 standard; cDNA; 1030 BP.
DE Human secreted protein gene 5 SEQ ID NO:15.
PN WO2000616235-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 1.6%; Score 58; DB 3; Length 1030;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 190
ID AAA26373 standard; cDNA; 1048 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1048;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 191
ID ADL71434 standard; cDNA; 1048 BP.
DE Novel human secreted protein cDNA seqid 38.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSU G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.6%; Score 58; DB 12; Length 1048;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
RESULT 192
ID AA210645 standard; cDNA; 1057 BP.
DE cDNA encoding a human secreted protein.
PN WO9943693-A1.
PD 02-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 2; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 193
ID ADA39739 standard; cDNA; 1057 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 194
ID ACC50402 standard; cDNA; 1057 BP.
DE Human secreted protein coding sequence, SEQ ID 69.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 195
ID AB271222 standard; cDNA; 1057 BP.
DE Human secreted protein-encoding gene 33 cDNA clone HDPFP29, SEQ ID NO:43.

PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 8; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 196
ID ADC73455 standard; DNA; 1057 BP.
DE Human secreted protein-related DNA - SEQ ID 88.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1057;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 197
ID AAX85048 standard; DNA; 1064 BP.
DE Human secreted protein gene No. 116.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 2; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 198
ID ACD18972 standard; cDNA; 1064 BP.
DE Novel human secreted protein cDNA #114.
PN US2003028003-A1.
PD 06-FEB-2003.
PA (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJJ/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAPL/) LAPLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
Query Match 1.6%; Score 58; DB 8; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 199
ID ADC73543 standard; DNA; 1064 BP.
DE Human secreted protein-related DNA - SEQ ID 176.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 200
ID ADD37606 standard; cDNA; 1064 BP.
DE Human secreted protein encoding sequence #88.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 201
ID ADA56073 standard; DNA; 1064 BP.
DE Gene encoding human secreted protein #252.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 202
ID ADG78365 standard; cDNA; 1064 BP.
DE Human secreted protein cDNA #116.
PN US2003211472-A1.
PD 13-NOV-2003.

PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJU/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAF/) LAFLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
Query Match 1.6%; Score 58; DB 12; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 203
ID ADN60654 standard; cDNA; 1064 BP.
DE Human secreted polynucleotide #114.
PN US2004038277-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 12; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 204
ID ABT31935 standard; DNA; 1070 BP.
DE Human breast cancer / ovarian cancer related coding sequence #42.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 1070;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 205
ID AAS28837 standard; cDNA; 1083 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 83.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 206
ID AAS28771 standard; cDNA; 1083 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 17.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 207
ID ABA06707 standard; cDNA; 1083 BP.
DE Human cDNA SEQ ID NO: 373.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 208
ID ABV4044 standard; cDNA; 1083 BP.
DE Human polynucleotide SEQ ID NO 373.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 58; DB 6; Length 1083;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 209
ID ADB31562 standard; cDNA; 1083 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 83.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1172;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 210
ID ADB31496 standard; cDNA; 1083 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 17.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 10; Length 1083;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 211
ID ADO62876 standard; DNA; 1091 BP.
DE Transcription factor G3055 orthologous sequence, SEQ ID 1343.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 1.6%; Score 58; DB 12; Length 1091;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
RESULT 212
ID AAC59409 standard; cDNA; 1126 BP.
DE Human secreted protein cDNA #18.
PN WO200056765-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1126;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
RESULT 213
ID AAC98004 standard; cDNA; 1140 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:14.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1140;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
RESULT 214
ID AAC81030 standard; cDNA; 1149 BP.
DE Human secreted protein cDNA sequence #3.
PN WO200063230-A2.
PD 26-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 8e-07;
RESULT 215
ID ABQ54664 standard; cDNA; 1156 BP.
DE Human ovarian antigen HVVCF30 cDNA, SEQ ID NO:544.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 6; Length 1156;
Best Local Similarity 100.0%; Pred. No. 8e-07;
RESULT 216
ID AAF98699 standard; DNA; 1164 BP.
DE Human ovarian cancer cell expressed sequence 10799.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 1164;
Best Local Similarity 100.0%; Pred. No. 8e-07;
RESULT 217
ID AAC98117 standard; cDNA; 1172 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:127.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1172;
Best Local Similarity 100.0%; Pred. No. 8e-07;
RESULT 218
ID AAH33220 standard; cDNA; 1172 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:276.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1172;

Best Local Similarity 100.0%; Pred. No. 8e-07;
RESULT 219
ID AAC83102 standard; DNA; 1204 BP.
DE DNA encoding a protein involved in the cell cycle SEQ ID 5.
PN WO200065040-A2.
PD 02-NOV-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.6%; Score 58; DB 3; Length 1204;
Best Local Similarity 100.0%; Pred. No. 7.9e-07;
RESULT 220
ID AAD35593 standard; cDNA; 1257 BP.
DE Human ZSIG89 cDNA #2.
PN US2002042095-A1.
PD 11-APR-2002.
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
PA (NELS/) NELSON A J.
Query Match 1.6%; Score 58; DB 6; Length 1257;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
RESULT 221
ID AAF98696 standard; DNA; 1314 BP.
DE Human ovarian cancer cell expressed sequence 10796.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 1314;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 222
ID ADR63284 standard; cDNA; 1325 BP.
DE Cotton cDNA sequence, SEQ ID 4065.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 1.6%; Score 58; DB 13; Length 1325;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 223
ID AAZ06261 standard; DNA; 1329 BP.
DE Human secreted protein gene.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 2; Length 1329;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 224
ID AAD16502 standard; DNA; 1331 BP.
DE Human ABC transporter-encoding gene 1 cDNA clone HTFOB57, SEQ ID NO:11.
PN WO200155208-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 1331;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 225
ID ADA27251 standard; cDNA; 1331 BP.
DE cDNA encoding human ABC transport receptor #1.
PN US2003049652-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 9; Length 1331;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 226
ID ADAL2854 standard; cDNA; 1331 BP.
DE Human ABC transporter-related cDNA HTFOB57 #1.
PN US2002161208-A1.
PD 31-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 58; DB 10; Length 1331;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 227
ID ABL90076 standard; cDNA; 1334 BP.

DE Human polynucleotide SEQ ID NO 638.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 6; Length 1334;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
RESULT 228
ID AAA26399 standard; cDNA; 1361 BP.
DE Human secreted protein gene 54 SEQ ID NO:64.
PN WO20000698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
RESULT 229
ID ADL71460 standard; cDNA; 1361 BP.
DE Novel human secreted protein cDNA seqid 64.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSUOLIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.6%; Score 58; DB 12; Length 1361;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
RESULT 230
ID AAA26453 standard; cDNA; 1375 BP.
DE Human secreted protein gene 56 SEQ ID NO:118.
PN WO20000698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1375;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
RESULT 231
ID ADL71516 standard; cDNA; 1375 BP.
DE Novel human secreted protein cDNA seqid 120.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSUOLIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.6%; Score 58; DB 12; Length 1375;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
RESULT 232
ID AAA26401 standard; cDNA; 1376 BP.
DE Human secreted protein gene 56 SEQ ID NO:66.
PN WO20000698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 1376;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
RESULT 233
ID ADL71462 standard; cDNA; 1376 BP.
DE Novel human secreted protein cDNA seqid 66.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSUOLIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.

Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 1376;
RESULT 234
ID AAC59295 standard; cDNA; 1388 BP.
DE Human secreted protein cDNA #19.
PN WO200056753-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 1388;
RESULT 235
ID AAC79804 standard; cDNA; 1390 BP.
DE Human secreted protein gene 6 SEQ ID NO:16.
PN WO200058336-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 1390;
RESULT 236
ID AAX58673 standard; cDNA; 1411 BP.
DE Rat organic cation transporter OCT-3 cDNA.
PN WO9924810-A1.
PD 20-MAY-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 2; Length 1411;
RESULT 237
ID ABL90182 standard; cDNA; 1459 BP.
DE Human polynucleotide SEQ ID NO 744.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 1459;
RESULT 238
ID ADF81719 standard; DNA; 1480 BP.
DE Leukaemia-related DNA sequence #2275.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE-) HAERLACH T.
PA (SCHO-) SCHOCH C.
PA (KERN-) KERN W.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 1480;
RESULT 239
ID ADF81720 standard; DNA; 1480 BP.
DE Leukaemia-related DNA sequence #2276.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE-) HAERLACH T.
PA (SCHO-) SCHOCH C.
PA (KERN-) KERN W.
Query Match
Best Local Similarity 1.6%; Score 58; DB 10; Length 1480;
RESULT 240
ID ADM47744 standard; DNA; 1494 BP.
DE Polynucleotide sequence #162 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE-) EDGERTON M D.
PA (CHOM-) CHOMET P S.
PA (LACC-) LACCETTI L B.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 1494;
RESULT 241
ID AAX24921 standard; cDNA; 1549 BP.
DE Guman ras carboxy-terminal processing protein cDNA.
PN WO9914343-A1.
PD 25-MAR-1999.

PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 2; Length 1549;
RESULT 242
ID ABQ54972 standard; cDNA; 1551 BP.
DE Human ovarian antigen HNOAH83 cDNA, SEQ ID NO:852.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 1551;
RESULT 243
ID ADI42788 standard; DNA; 1574 BP.
DE Plant transcription factor polynucleotide #798.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAK-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 1574;
RESULT 244
ID ADJ57939 standard; cDNA; 1596 BP.
DE Rat NARC 19 cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 1596;
RESULT 245
ID AAF97902 standard; cDNA; 1618 BP.
DE Human secreted protein cDNA, SEQ ID NO: 29.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 1618;
RESULT 246
ID ADI42377 standard; DNA; 1637 BP.
DE Plant transcription factor polynucleotide #512.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAK-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match
Best Local Similarity 1.6%; Score 58; DB 13; Length 1637;
RESULT 247
ID AAV81394 standard; DNA; 1733 BP.

DE Human tumour antigen zsig15 coding sequence.
 PN WO9850552-A1.
 PD 12-NOV-1998.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 1.6%; Score 58; DB 2; Length 1733;
 Best Local Similarity 100.0%; Pred. No. 7.1e-07;
 RESULT 248
 ID AAD17173 standard; cDNA; 1779 BP.
 DE Human ion channel-31d6 (ion31d6) cDNA.
 PN WO200168849-A2.
 PD 20-SEP-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 1.6%; Score 58; DB 4; Length 1779;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 249
 ID ACD01559 standard; cDNA; 1779 BP.
 DE cDNA clone Ion31c4 encoding human ion channel.
 PN WO2003023014-A2.
 PD 20-MAR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 1.6%; Score 58; DB 8; Length 1779;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 250
 ID ADE29300 standard; cDNA; 1779 BP.
 DE Novel human ion channel ion-31d6 cDNA.
 PN US2003190714-A1.
 PD 09-OCT-2003.
 PA (ROBE) ROBERTS S L.
 PA (BENJ) BENJAMIN C W.
 PA (KARN) KARNOVSKY A M.
 PA (RUBL) RUBLE C L.
 PA (LINS) LINSKE-O'CONNELL L I.
 PA (WANG) WANG.
 PA (LIUD) LIU D.
 Query Match 1.6%; Score 58; DB 10; Length 1779;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 251
 ID AA200802 standard; cDNA; 1810 BP.
 DE Human secreted protein cDNA encoding gene 1.
 PN WO9940100-A1.
 PD 12-AUG-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 58; DB 2; Length 1810;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 252
 ID AAF98705 standard; DNA; 1815 BP.
 DE Human ovarian cancer cell expressed sequence 10805.
 PN WO200118542-A2.
 PD 15-MAR-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.6%; Score 58; DB 5; Length 1815;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 253
 ID AA294198 standard; cDNA; 1834 BP.
 DE Membrane-bound herpesvirus entry mediator-2 (mhVEM2) cDNA.
 PN WO200014230-A1.
 PD 16-MAR-2000.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 1.6%; Score 58; DB 3; Length 1834;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 254
 ID ABX90577 standard; cDNA; 1834 BP.
 DE Human membrane-bound Herpesvirus Entry Mediator-2 (mhVEM-2) cDNA.
 PN US2002132297-A1.
 PD 19-SEP-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 10; Length 1834;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 RESULT 255
 ID AB190541 standard; cDNA; 1857 BP.
 DE Human polynucleotide SEQ ID NO 1103.
 PN WO200190304-A2.
 PD 29-NOV-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 58; DB 6; Length 1857;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 256
 ID ACD01569 standard; DNA; 1865 BP.
 DE DNA clone 5HT-3C encoding human ion channel.
 PN WO2003023014-A2.
 PD 20-MAR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 1.6%; Score 58; DB 8; Length 1865;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 257
 ID ADI42386 standard; DNA; 1885 BP.
 DE Plant transcription factor polynucleotide #521.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER) SHERMAN B K.
 PA (RIEC) RIECHMANN J L.
 PA (JIAN) JIANG C.
 PA (HEAR) HEARD J E.
 PA (HAAR) HAAKE V.
 PA (CREE) CREELMAN R A.
 PA (RATC) RATCLIFFE O.
 PA (ADAM) ADAM L J.
 PA (REUB) REUBER T L.
 PA (KEDD) KEDDIE J.
 PA (BROU) BROUN P E.
 PA (PILG) PILGRIM M L.
 PA (DUBE) DUBELL A N.
 PA (PINE) PINEDA O.
 PA (YUGG) YU G.
 Query Match 1.6%; Score 58; DB 12; Length 1885;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 258
 ID ABA96106 standard; cDNA; 1902 BP.
 DE Human mut dGTPase 26493 cDNA.
 PN WO200190374-A2.
 PD 29-NOV-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 6; Length 1902;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 259
 ID ADM47642 standard; DNA; 1920 BP.
 DE Polynucleotide sequence #60 useful in producing transgenic plants.
 PN US2003233670-A1.
 PD 18-DEC-2003.
 PA (EDGE) EDGERTON M D.
 PA (CHOM) CHOMET P S.
 PA (LACC) LACCETTI L B.
 Query Match 1.6%; Score 58; DB 12; Length 1920;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 260
 ID AAF24994 standard; DNA; 1928 BP.
 DE Nucleotide sequence of an inositol polyphosphate phosphatase.
 PN WO200104147-A2.
 PD 18-JAN-2001.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 58; DB 4; Length 1928;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 RESULT 261
 ID AAC83106 standard; DNA; 1980 BP.
 DE DNA encoding a protein involved in the cell cycle SEQ ID 21.
 PN WO200065040-A2.
 PD 02-NOV-2000.
 PA (PTON) PIONEER HI-BRED INT INC.
 Query Match 1.6%; Score 58; DB 3; Length 1980;
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 RESULT 262
 ID AAF21635 standard; DNA; 2022 BP.
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 22.
 PN WO200055173-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2022;
RESULT 263
ID AAC84241 standard; cDNA; 2029 BP.
DE Human secreted protein encoding cDNA.
PN WO200070059-A2.
PD 23-NOV-2000.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2029;
RESULT 264
ID AA339965 standard; cDNA; 2030 BP.
DE Murine TANGO 185 cDNA.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2030;
RESULT 265
ID AAC55227 standard; cDNA; 2031 BP.
DE Human secreted protein gene 8 SEQ ID NO:48.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2031;
RESULT 266
ID AAC55226 standard; cDNA; 2031 BP.
DE Human secreted protein gene 8 SEQ ID NO:47.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2031;
RESULT 267
ID AAD06011 standard; DNA; 2034 BP.
DE Human neuronal apoptosis regulated candidate (NARC) 10C DNA.
PN WO20011007-A2.
PD 03-MAY-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2034;
RESULT 268
ID ABS56722 standard; cDNA; 2034 BP.
DE Human NARC10 cDNA.
PN WO200281516-A2.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 8; Length 2034;
RESULT 269
ID ADJ57918 standard; cDNA; 2034 BP.
DE Human NARC 10C cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 2034;
RESULT 270
ID ABS53034 standard; DNA; 2038 BP.
DE Arabidopsis thaliana squalene epoxidase polynucleotide #4.
PN WO200261072-A2.
PD 08-AUG-2002.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 2038;
RESULT 271
ID AAH33367 standard; cDNA; 2073 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:423.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2073;
RESULT 272
ID AAC99923 standard; cDNA; 2076 BP.
DE Human secreted protein gene 106 SEQ ID NO:116.
PN WO200070042-A1.
PD 23-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2076;
RESULT 273
ID AAC84404 standard; cDNA; 2093 BP.
DE Mouse TANGO 206 variant 1 cDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;
RESULT 274
ID AAC84406 standard; cDNA; 2093 BP.
DE Mouse TANGO 206 variant 3 cDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;
RESULT 275
ID AAC84405 standard; cDNA; 2093 BP.
DE Mouse TANGO 206 variant 2 cDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;
RESULT 276
ID AAC84387 standard; cDNA; 2093 BP.
DE Mouse TANGO 206 polypeptide encoding cDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2093;
RESULT 277
ID AAC81061 standard; cDNA; 2110 BP.
DE Human secreted protein cDNA sequence #34.
PN WO200063230-A2.
PD 26-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2110;
RESULT 278
ID ABA06584 standard; cDNA; 2140 BP.
DE Human cDNA SEQ ID NO: 250.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2140;
RESULT 279
ID ABV83921 standard; cDNA; 2140 BP.
DE Human polynucleotide SEQ ID NO 250.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 2140;
RESULT 280
ID AAF98703 standard; DNA; 2156 BP.
DE Human ovarian cancer cell expressed sequence 10803.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match
Best Local Similarity 1.6%; Score 58; DB 5; Length 2156;
RESULT 281
ID AAF98708 standard; DNA; 2159 BP.
DE Human ovarian cancer cell expressed sequence 10808.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 5; Length 2159;
RESULT 282
ID AA252286 standard; cDNA; 2202 BP.
DE Maize replication protein A large subunit homologue-2 (ZmRPALSH2) cDNA.
PN WO200015816-A2.
PD 23-MAR-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2202;
RESULT 283
ID AAV04680 standard; cDNA; 2205 BP.
DE Human presenilin interacting protein gene mutTM1-TM2.
PN WO9801549-A2.
PD 15-JAN-1998.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
PA (HSCR-) HSC RES & DEV LP.
Query Match
Best Local Similarity 1.6%; Score 58; DB 2; Length 2205;
RESULT 284
ID ADL45474 standard; DNA; 2236 BP.
DE Human ovarian cancer DNA marker #19364.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 5; Length 2236;
RESULT 285
ID ACN92442 standard; DNA; 2241 BP.
DE Breast cancer related marker, seq id 13592.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 11; Length 2241;
RESULT 286
ID ABV22595 standard; cDNA; 2242 BP.
DE Human prostate expression marker cDNA 22586.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 5; Length 2242;
RESULT 287
ID ABV28416 standard; cDNA; 2242 BP.
DE Human prostate expression marker cDNA 28407.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 5; Length 2242;
RESULT 288
ID ADI43025 standard; DNA; 2252 BP.
DE Plant transcription factor polynucleotide #976.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAK-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.

PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 2252;
RESULT 289
ID ADO03163 standard; cDNA; 2252 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #167.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN-) ZHANG J.
PA (FROM-) FROMM M E.
PA (HEAR-) HEARD J E.
PA (RIEC-) RIECHMANN J L.
PA (ADAM-) ADAM L J.
PA (BROU-) BROUN P E.
PA (PINE-) PINEDA O.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J S.
PA (YUGG-) YU G.
PA (JIAN-) JIANG C.
PA (SAMA-) SAWAHA R S.
PA (PILG-) PILGRIM M L.
PA (CREE-) CREELMAN R A.
PA (DUBE-) DUBELL A N.
PA (RATC-) RATCLIFFE O.
PA (KUMI-) KUMIMOTO R.
PA (SHER-) SHERMAN B K.
Query Match
Best Local Similarity 1.6%; Score 58; DB 12; Length 2252;
RESULT 290
ID AAC84274 standard; cDNA; 2257 BP.
DE Signal transduction protein encoding cDNA.
PN WO200070059-A2.
PD 23-NOV-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 4; Length 2257;
RESULT 291
ID AAC74401 standard; cDNA; 2259 BP.
DE Human secreted protein gene 6 SEQ ID NO:16.
PN WO200058496-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2259;
RESULT 292
ID ABQ54591 standard; cDNA; 2266 BP.
DE Human ovarian antigen HVVBR10 cDNA, SEQ ID NO:471.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 6; Length 2266;
RESULT 293
ID ADAL1585 standard; DNA; 2274 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 113.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 58; DB 9; Length 2274;
RESULT 294
ID AAF22390 standard; cDNA; 2287 BP.
DE Human secreted protein gene 18 SEQ ID NO:28.
PN WO200061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE-) ROSEN C A.
Query Match
Best Local Similarity 1.6%; Score 58; DB 3; Length 2287;

Best Local Similarity 100.0%; Pred. No. 6.5e-07;
RESULT 295
ID ABK43731 standard; cDNA; 2292 BP.
DE DNA encoding novel central nervous system protein #311.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 2292;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
RESULT 296
ID AD154118 standard; cDNA; 2292 BP.
DE cDNA encoding novel human protein seq id 321.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 58; DB 12; Length 2292;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
RESULT 297
ID ABQ54938 standard; cDNA; 2294 BP.
DE Human ovarian antigen HOPKL18 cDNA, SEQ ID NO:818.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 6; Length 2294;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
RESULT 298
ID AAD33824 standard; cDNA; 2339 BP.
DE Human secreted protein-encoding gene 13 cDNA clone HNTBN41, SEQ ID NO:23.
PN WO200224719-A1.
PD 28-MAR-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 6; Length 2339;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
RESULT 299
ID AAH34945 standard; cDNA; 2357 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2027.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 2357;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
RESULT 300
ID ADMA47733 standard; DNA; 2419 BP.
DE Polynucleotide sequence #151 useful in producing transgenic plants.
PN US2003333670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 1.6%; Score 58; DB 12; Length 2419;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
RESULT 301
ID ABV21274 standard; cDNA; 2591 BP.
DE Human prostate expression marker cDNA 21265.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 2591;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
RESULT 302
ID ABV27093 standard; cDNA; 2591 BP.
DE Human prostate expression marker cDNA 27084.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 2591;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
RESULT 303
ID AAF98706 standard; DNA; 2614 BP.
DE Human ovarian cancer cell expressed sequence 10806.
PN WO200118542-A2.

PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 5; Length 2614;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 304
ID AAD43556 standard; cDNA; 2713 BP.
DE Human CD2000 cDNA.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 305
ID AAD43566 standard; DNA; 2713 BP.
DE Human CD2000 DNA #3.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 306
ID AAD43565 standard; DNA; 2713 BP.
DE Human CD2000 DNA #2.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 307
ID AAD43564 standard; DNA; 2713 BP.
DE Human CD2000 DNA #1.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 308
ID AAD43567 standard; DNA; 2713 BP.
DE Human CD2000 DNA #4.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 309
ID AAG63369 standard; cDNA; 2713 BP.
DE Human CD2000 cDNA #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 310
ID AAD63378 standard; cDNA; 2713 BP.
DE Human CD2000 cDNA #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 311
ID AAD63379 standard; cDNA; 2713 BP.
DE Human CD2000 cDNA #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 2713;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
RESULT 312
ID AAD63376 standard; cDNA; 2713 BP.
DE Human CD2000 cDNA #2.
PN US2003180888-A1.
PD 25-SEP-2003.

PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 10; Length 2713;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 313
 ID AAD63377 standard; cDNA; 2713 BP.
 DE Human CD2000 cDNA #3.
 PN US2003180888-A1.
 PD 25-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 10; Length 2713;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 314
 ID AAC68661 standard; cDNA; 2719 BP.
 DE Human APO4 cDNA.
 PN US6140098-A.
 PD 31-OCT-2000.
 PA (SCHE) SCHERING CORP.
 Query Match 1.6%; Score 58; DB 4; Length 2719;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 315
 ID ADJ63968 standard; DNA; 2719 BP.
 DE DNA sequence encoding human APO4 protease.
 PN US6638507-B1.
 PD 28-OCT-2003.
 PA (SCHE) SCHERING CORP.
 Query Match 1.6%; Score 58; DB 10; Length 2719;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 316
 ID AAD06007 standard; DNA; 2738 BP.
 DE Human neuronal apoptosis regulated candidate (NARC) 9B DNA.
 PN WO200131007-A2.
 PD 03-MAY-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 4; Length 2738;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 317
 ID ADJ57931 standard; cDNA; 2738 BP.
 DE Human NARC 9 cDNA.
 PN US2004009553-A1.
 PD 15-JAN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 12; Length 2738;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 RESULT 318
 ID ABT31931 standard; DNA; 2778 BP.
 DE Human breast cancer / ovarian cancer related coding sequence #38.
 PN WO200300012-A2.
 PD 03-JAN-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 10; Length 2778;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 RESULT 319
 ID AAD17208 standard; cDNA; 2875 BP.
 DE Human carnitine acyltransferase, 26886 cDNA.
 PN WO200166759-A2.
 PD 13-SEP-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 4; Length 2875;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 RESULT 320
 ID AAF45127 standard; cDNA; 2964 BP.
 DE Human TANGO 273 cDNA.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 5; Length 2964;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 RESULT 321
 ID ABX94104 standard; cDNA; 2964 BP.
 DE cDNA encoding human TANGO 273.
 PN US2002182675-A1.
 PD 05-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.

Query Match 1.6%; Score 58; DB 8; Length 2964;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 RESULT 322
 ID ADM42009 standard; cDNA; 2964 BP.
 DE Human TANGO 273 cDNA.
 PN US2003170821-A1.
 PD 11-SEP-2003.
 PA (MCCA) MCCARTHY S A.
 PA (FRAS) FRASER C C.
 PA (SHAR) SHARP J D.
 PA (BARN) BARNES T M.
 PA (KIRS) KIRST S J.
 PA (MYER) MYERS P S.
 PA (WRIG) WRIGHTON N.
 PA (GOOD) GOODEARL A D J.
 PA (HOLT) HOLTZMAN D A.
 PA (KHOD) KHODADOUST M.
 Query Match 1.6%; Score 58; DB 11; Length 2964;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 RESULT 323
 ID ADO98245 standard; cDNA; 2964 BP.
 DE Human polynucleotide #7.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 12; Length 2964;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 RESULT 324
 ID AAC80579 standard; cDNA; 3021 BP.
 DE Human secreted protein gene 49 SEQ ID NO:59.
 PN WO200058467-A1.
 PD 05-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 58; DB 3; Length 3021;
 Best Local Similarity 100.0%; Pred. No. 6e-07;
 RESULT 325
 ID ABZ24009 standard; cDNA; 3102 BP.
 DE Mouse adipose abundant protein (AAP) encoding cDNA.
 PN WO200296355-A2.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 58; DB 8; Length 3102;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 RESULT 326
 ID ABZ24027 standard; cDNA; 3102 BP.
 DE Mouse adipose abundant protein (AAP) encoding cDNA.
 PN WO200297036-A2.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 58; DB 8; Length 3102;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 RESULT 327
 ID AAF15989 standard; cDNA; 3118 BP.
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:424.
 PN WO200055174-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE) ROSEN C A.
 Query Match 1.6%; Score 58; DB 3; Length 3118;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 RESULT 328
 ID AAF27781 standard; cDNA; 3169 BP.
 DE Human MANGO 003 coding sequence SEQ ID NO: 4.
 PN WO200100673-A1.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 58; DB 4; Length 3169;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 RESULT 329
 ID AAZ36812 standard; DNA; 3196 BP.
 DE DNA encoding a brain-derived signalling factor polypeptide.
 PN WO9961463-A1.
 PD 02-DEC-1999.

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 1.6%; Score 58; DB 3; Length 3196;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
RESULT 330
ID ABS63368 standard; cDNA; 3196 BP.
DE Mouse brain-derived signalling factor (BDSF-1) DNA sequence #1.
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUWW/) GU W.
Query Match 1.6%; Score 58; DB 6; Length 3196;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
RESULT 331
ID ADR45578 standard; cDNA; 3196 BP.
DE Mouse cDNA encoding brain-derived signalling factor, BDSF-1, #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 13; Length 3196;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
RESULT 332
ID AAF22384 standard; cDNA; 3268 BP.
DE Human secreted protein gene 12 SEQ ID NO:22.
PN WO200061629-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 1.6%; Score 58; DB 3; Length 3268;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
RESULT 333
ID AAQ80228 standard; DNA; 3344 BP.
DE Rat NDF clone 22 DNA.
PN WO9428133-A1.
PD 08-DEC-1994.
PA (AMGE-) AMGEN INC.
Query Match 1.6%; Score 58; DB 2; Length 3344;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
RESULT 334
ID AAC55197 standard; cDNA; 3354 BP.
DE Human secreted protein gene 8 SEQ ID NO:18.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 3; Length 3354;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
RESULT 335
ID ABK43741 standard; cDNA; 3747 BP.
DE DNA encoding novel central nervous system protein #321.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 3747;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
RESULT 336
ID ADI54128 standard; cDNA; 3747 BP.
DE cDNA encoding novel human protein seq id 331.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 58; DB 12; Length 3747;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
RESULT 337
ID AAD08362 standard; cDNA; 3953 BP.
DE Human secreted protein-encoding gene 18 cDNA clone HJMBB20, SEQ ID NO:28.
PN WO200077022-A1.

PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 3953;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
RESULT 338
ID AAF32707 standard; cDNA; 3953 BP.
DE Human secreted protein gene 9 SEQ ID NO:19.
PN WO200077255-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 58; DB 4; Length 3953;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
RESULT 339
ID AAH73308 standard; cDNA; 3974 BP.
DE Human cervical cancer marker nucleic acid 4582.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.6%; Score 58; DB 4; Length 3974;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
RESULT 340
ID AAD56522 standard; DNA; 4897 BP.
DE Human KIAA1382, 17921 DNA.
PN WO20003039341-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 8; Length 4897;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
RESULT 341
ID ABZ70664 standard; cDNA; 5109 BP.
DE Human phospholipid transporter 67108 cDNA.
PN EP1266907-A1.
PD 18-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 5109;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
RESULT 342
ID ADC29731 standard; cDNA; 5502 BP.
DE cDNA encoding human aminopeptidase 55304.
PN US2002151696-A1.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 58; DB 10; Length 5502;
Best Local Similarity 100.0%; Pred. No. 5e-07;
RESULT 343
ID ADT95109 standard; cDNA; 87 BP.
DE Colon cancer associated human cDNA sequence #628.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 57; DB 11; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
RESULT 344
ID ADT94951 standard; cDNA; 108 BP.
DE Colon cancer associated human cDNA sequence #470.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 57; DB 11; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
RESULT 345
ID AAH33326 standard; cDNA; 131 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:382.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
RESULT 346
ID AAS29047 standard; cDNA; 155 BP.
DE cDNA encoding for human DNA-binding protein #18.
PN WO200155162-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
RESULT 347
ID ABS68187 standard; cDNA; 155 BP.
DE cDNA encoding human DNA-binding protein #18.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 57; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
RESULT 348
ID ADC25181 standard; cDNA; 155 BP.
DE Human cDNA from extracellular matrix gene 18.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 10; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
RESULT 349
ID ABX49026 standard; cDNA; 179 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #14191.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 57; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 350
ID ABZ08680 standard; cDNA; 226 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8671.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 1.6%; Score 57; DB 6; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 351
ID AAS29084 standard; cDNA; 237 BP.
DE cDNA encoding for human DNA-binding protein #55.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 352
ID ABS68224 standard; cDNA; 237 BP.
DE cDNA encoding human DNA-binding protein #55.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 57; DB 6; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 353
ID ADC25218 standard; cDNA; 237 BP.
DE Human cDNA from extracellular matrix gene 55.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 354
ID AAH33643 standard; cDNA; 303 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:699.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 57; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;
RESULT 355
ID ABX37863 standard; cDNA; 369 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3028.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.6%; Score 57; DB 8; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
RESULT 356
ID AA190395 standard; cDNA; 410 BP.
DE Human polynucleotide SEQ ID NO 10455.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 57; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
RESULT 357
ID ABX62372 standard; DNA; 415 BP.
DE Arabidopsis thaliana expressed sequence related polynucleotide #487.
PN US2002040490-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WORS/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 1.6%; Score 57; DB 8; Length 415;
Best Local Similarity 100.0%; Pred. No. 2e-06;
RESULT 358
ID ABX60904 standard; DNA; 417 BP.
DE Arabidopsis thaliana polynucleotide #250.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WORS/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 1.6%; Score 57; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 2e-06;
RESULT 359
ID ABL93801 standard; cDNA; 455 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027566 SEQ ID NO:566.
PN US2002023280-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.

PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYI/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 6; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 RESULT 360
 ID ABX60882 standard; DNA; 457 BP.
 DE Arabidopsis thaliana polynucleotide #228.
 PN US2002142319-A1.
 PD 03-OCT-2002.
 PA (GORL/) GORLACH J.
 PA (ANYI/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (HARG/) HARGISS T R.
 PA (YUYI/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 10; Length 457;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 RESULT 361
 ID ADK11877 standard; DNA; 495 BP.
 DE Breast cancer differentially expressed gene product #283.
 PN WO2003057926-A1.
 PD 17-JUL-2003.
 PA (CHIR/) CHIRON CORP.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 10; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 RESULT 362
 ID AAF16171 standard; cDNA; 738 BP.
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:606.
 PN WO200055174-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 3; Length 738;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 RESULT 363
 ID AAS41669 standard; cDNA; 819 BP.
 DE cDNA encoding novel human enzyme polypeptide #885.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 4; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 RESULT 364
 ID AAF26575 standard; DNA; 893 BP.
 DE DNA encoding human secreted protein #29.
 PN WO200076531-A1.
 PD 21-DEC-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 4; Length 893;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 RESULT 365
 ID AAS40950 standard; cDNA; 900 BP.
 DE cDNA encoding novel human enzyme polypeptide #166.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 4; Length 900;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 RESULT 366
 ID AD142854 standard; DNA; 1023 BP.
 DE Plant transcription factor polynucleotide #848.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PIIG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 12; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 RESULT 367
 ID ADO3052 standard; cDNA; 1023 BP.
 DE Soybean orthologue of Thalecress transcription factor, cDNA #214.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMARA R S.
 PA (PIIG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KIMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 12; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 RESULT 368
 ID AAC99079 standard; cDNA; 1046 BP.
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:307.
 PN WO200055320-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 3; Length 1046;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 RESULT 369
 ID AAC60044 standard; cDNA; 1108 BP.
 DE Human secreted protein gene 20 SEQ ID NO:30.
 PN WO200056766-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 1.6%; Score 57; DB 3; Length 1108;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 RESULT 370
 ID ABK43573 standard; cDNA; 1162 BP.
 DE DNA encoding novel central nervous system protein #153.

PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 4; Length 1162;
Pred. No. 1.5e-06;
RESULT 371
ID ADI53960 standard; cDNA; 1162 BP.
DE cDNA encoding novel human protein seq id 163.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.6%; Score 57; DB 12; Length 1162;
Pred. No. 1.5e-06;
RESULT 372
ID AAH34600 standard; cDNA; 1194 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1682.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 4; Length 1194;
Pred. No. 1.5e-06;
RESULT 373
ID AAF91866 standard; cDNA; 1198 BP.
DE Human secreted protein-encoding gene 9 cDNA clone HOEK12, SEQ ID NO:19.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 4; Length 1198;
Pred. No. 1.5e-06;
RESULT 374
ID AAA09025 standard; DNA; 1315 BP.
DE Human CSATP-1 coding sequence.
PN WO200018890-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 3; Length 1315;
Pred. No. 1.4e-06;
RESULT 375
ID AAC59772 standard; cDNA; 1464 BP.
DE Human secreted protein gene 35 SEQ ID NO:45.
PN WO200056751-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 3; Length 1464;
Pred. No. 1.4e-06;
RESULT 376
ID AA206222 standard; DNA; 1621 BP.
DE Human secreted protein gene No. 4.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 2; Length 1621;
Pred. No. 1.3e-06;
RESULT 377
ID AAC59400 standard; cDNA; 1734 BP.
DE Human secreted protein cDNA #9.
PN WO200056765-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 3; Length 1734;
Pred. No. 1.3e-06;
RESULT 378
ID AAC68120 standard; cDNA; 2000 BP.
DE Human secreted protein cDNA sequence #40.
PN WO200058335-A1.
PD 05-OCT-2000.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 1.6%; Score 57; DB 3; Length 2000;
Pred. No. 1.3e-06;
RESULT 379

ID AB273487 standard; cDNA; 2000 BP.
DE Secreted protein-encoding gene 207 cDNA clone HMUAE26, SEQ ID NO:217.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 8; Length 2000;
Pred. No. 1.3e-06;
RESULT 380
ID ADA98032 standard; cDNA; 2000 BP.
DE Human secreted protein cDNA sequence #136.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 8; Length 2000;
Pred. No. 1.3e-06;
RESULT 381
ID AB267096 standard; cDNA; 2000 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 216.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 10; Length 2000;
Pred. No. 1.3e-06;
RESULT 382
ID AAC84351 standard; DNA; 2235 BP.
DE Corn clone CPR951 FL cDNA sequence.
PN WO200070069-A1.
PD 23-NOV-2000.
PA (MONS-) MONSANTO CO.
Query Match
Best Local Similarity 1.6%; Score 57; DB 4; Length 2235;
Pred. No. 1.2e-06;
RESULT 383
ID AAD13360 standard; cDNA; 2346 BP.
DE Human secreted protein-encoding gene 16 cDNA clone HCUHQ40, SEQ ID NO:26.
PN WO200154708-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 4; Length 2346;
Pred. No. 1.2e-06;
RESULT 384
ID ABA93749 standard; cDNA; 2389 BP.
DE Human testis derived cDNA clone tes3_15n14.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match
Best Local Similarity 1.6%; Score 57; DB 6; Length 2389;
Pred. No. 1.2e-06;
RESULT 385
ID AAL60541 standard; cDNA; 2564 BP.
DE Human organelle-associated protein (ORGA)-1 cDNA.
PN WO2003044171-A2.
PD 30-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 9; Length 2564;
Pred. No. 1.2e-06;
RESULT 386
ID AA200842 standard; cDNA; 2581 BP.
DE Human secreted protein cDNA encoding gene 41.
PN WO9940100-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 2; Length 2581;
Pred. No. 1.2e-06;
RESULT 387
ID AA210676 standard; cDNA; 2584 BP.
DE cDNA encoding a human secreted protein.
PN WO9943693-A1.
PD 02-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 57; DB 2; Length 2584;
Pred. No. 1.2e-06;
RESULT 388
ID AD116404 standard; DNA; 2720 BP.

DE Human protein modification and maintenance molecule (PMM) gene #37.
PN WO2003100016-A2.
PD 04-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 1.6%; Score 57; DB 12; Length 2720;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 389
ID ADG15081 standard; cDNA; 2748 BP.
DE Human SECP-53 cDNA.
PN WO2003087300-A2.
PD 23-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 1.6%; Score 57; DB 10; Length 2748;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 390
ID ABX71352 standard; cDNA; 2853 BP.
DE Intracellular trafficking-associated cDNA from clone DKFZphtes3_17n18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 1.6%; Score 57; DB 5; Length 2853;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 391
ID AAI58066 standard; cDNA; 3160 BP.
DE Human polynucleotide SEQ ID NO 269.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 57; DB 4; Length 3160;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
RESULT 392
ID ABK54751 standard; cDNA; 72 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 221.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
RESULT 393
ID ABK55072 standard; cDNA; 73 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 542.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 73;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
RESULT 394
ID ABK54792 standard; cDNA; 74 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 262.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
RESULT 395
ID ABK54924 standard; cDNA; 74 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 394.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
RESULT 396
ID ACN54476 standard; cDNA; 74 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-K6-D12, SEQ:9257.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.6%; Score 56; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;

RESULT 397
ID ABK54665 standard; cDNA; 77 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 135.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
RESULT 398
ID ABK54736 standard; cDNA; 79 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 206.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
RESULT 399
ID ABK55279 standard; cDNA; 81 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 749.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 400
ID ABK54750 standard; cDNA; 82 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 220.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 401
ID ABK54808 standard; cDNA; 82 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 278.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 402
ID ABK54687 standard; cDNA; 90 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 157.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
RESULT 403
ID ABK54776 standard; cDNA; 95 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 246.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 404
ID ABK54958 standard; cDNA; 100 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 428.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
RESULT 405
ID ADT95353 standard; cDNA; 105 BP.
DE Colon cancer associated human cDNA sequence #872.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 56; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
RESULT 406

ID ABX54764 standard; cDNA; 113 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4693.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
RESULT 407
ID ABA82937 standard; DNA; 115 BP.
DE Human protective DNA sequence CNI-00749 fragment #36.
PN WO200176457-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
RESULT 408
ID AAS63020 standard; cDNA; 116 BP.
DE Cell death protective sequence CNI-00725, ORF #11.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
RESULT 409
ID ABK55292 standard; cDNA; 117 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 762.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
RESULT 410
ID ADT95697 standard; cDNA; 128 BP.
DE Colon cancer associated human cDNA sequence #1216.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 56; DB 11; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
RESULT 411
ID AAS63092 standard; cDNA; 139 BP.
DE Cell death protective sequence CNI-00728, ORF #24.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 139;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
RESULT 412
ID AAS63142 standard; cDNA; 152 BP.
DE Cell death protective sequence CNI-00732, ORF #8.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 413
ID ABK54692 standard; cDNA; 154 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 152.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 414
ID AAS41371 standard; cDNA; 159 BP.
DE cDNA encoding novel human enzyme polypeptide #587.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 4; Length 159;

Best Local Similarity 100.0%; Pred. No. 5.1e-06;
RESULT 415
ID ABA82875 standard; DNA; 160 BP.
DE Human protective DNA sequence CNI-00746 fragment #40.
PN WO200176457-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 160;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
RESULT 416
ID ABX45893 standard; cDNA; 160 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11058.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
RESULT 417
ID ABK54773 standard; cDNA; 161 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 243.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 161;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
RESULT 418
ID ABX42996 standard; cDNA; 286 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8161.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
RESULT 419
ID ABX46068 standard; cDNA; 408 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11233.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 408;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
RESULT 420
ID ABX48319 standard; cDNA; 424 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13484.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
RESULT 421
ID ABX60806 standard; DNA; 437 BP.
DE Arabidopsis thaliana polynucleotide #152.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.

PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match
Best Local Similarity 1.6%; Score 56; DB 10; Length 437;
Result 422
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
ID ABV55622 standard; cDNA; 485 BP.
DE Human prostate expression marker cDNA 55613.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 5; Length 485;
Result 423
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
ID AAX30156 standard; DNA; 487 BP.
DE Human secreted protein gene 12.
PN WO9910363-A1.
PD 04-MAR-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 2; Length 487;
Result 424
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
ID ACN50766 standard; cDNA; 554 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-001-Q1-N6-C8, SEQ:5547.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.6%; Score 56; DB 13; Length 554;
Result 425
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
ID ACN60732 standard; cDNA; 587 BP.
DE Cotton gymnoecium tissue EST Clone ID: LIB3829-027-Q6-K6-B6, SEQ:15513.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.6%; Score 56; DB 13; Length 587;
Result 426
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
ID AB258160 standard; cDNA; 639 BP.
DE Human neurotrophin cDNA.
PN WO2003005033-A2.
PD 16-JAN-2003.
PA (GENE-) GENEPROT INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 8; Length 639;
Result 427
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
ID AAD37774 standard; DNA; 767 BP.
DE Extended sequence for mouse IMX5_07.
PN WO200231116-A2.
PD 18-APR-2002.
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 767;
Result 428
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
ID AAX37387 standard; cDNA; 824 BP.
DE Human secreted protein cDNA fragment containing gene 19.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 2; Length 824;
Result 429
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
ID ACC48069 standard; cDNA; 907 BP.
DE Nucleotide sequence of cDNA pPC86-Clone 27R.

PN WO2003000273-A1.
PD 03-JAN-2003.
PA (AUTO-) AUTOGEN RES PTY LTD.
Query Match
Best Local Similarity 1.6%; Score 56; DB 10; Length 907;
Result 430
Best Local Similarity 100.0%; Pred. No. 3e-06;
ID AAS63009 standard; cDNA; 920 BP.
DE Cell death protective sequence CNI-00725.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 920;
Result 431
Best Local Similarity 100.0%; Pred. No. 3e-06;
ID AAZ98037 standard; cDNA; 931 BP.
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:31.
PN WO200004140-A1.
PD 27-JAN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 3; Length 931;
Result 432
Best Local Similarity 100.0%; Pred. No. 3e-06;
ID AAD11650 standard; cDNA; 931 BP.
DE Human secreted protein-encoding gene 21 cDNA clone HBAFA02, SEQ ID NO:31.
PN WO200151504-A1.
PD 19-JUL-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 4; Length 931;
Result 433
Best Local Similarity 100.0%; Pred. No. 3e-06;
ID ABK69746 standard; cDNA; 931 BP.
DE Human secreted protein gene 21.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 2; Length 980;
Result 435
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
ID AAS63134 standard; cDNA; 1046 BP.
DE Cell death protective sequence CNI-00732.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 6; Length 1046;
Result 436
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
ID AAC80536 standard; cDNA; 1058 BP.
DE Human secreted protein gene 6 SEQ ID NO:16.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 3; Length 1058;
Result 437
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
ID ADC20162 standard; DNA; 1058 BP.
DE Human secreted protein coding sequence #101.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 56; DB 10; Length 1058;
Result 438
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
ID ABT16807 standard; DNA; 1058 BP.
DE Human secreted protein gene sequence - SEQ ID NO 56.
PN WO200277188-A2.

PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1058;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
RESULT 439
ID ABZ67044 standard; cDNA; 1058 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 164.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1058;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
RESULT 440
ID ADC78224 standard; cDNA; 1088 BP.
DE Human secreted protein encoding cDNA SEQ ID NO:31.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1088;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
RESULT 441
ID AAF97917 standard; cDNA; 1138 BP.
DE Human secreted protein cDNA, SEQ ID NO: 44.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1138;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
RESULT 442
ID ADG79383 standard; cDNA; 1233 BP.
DE Human secreted protein cDNA of the invention SEQ ID NO:189.
PN WO200268639-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1233;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 443
ID AAX04382 standard; DNA; 1261 BP.
DE Human secreted protein gene 72 clone HCFNN01.
PN WO9856804-A1.
PD 17-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 2; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 444
ID ADA39705 standard; cDNA; 1261 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 445
ID ACC50381 standard; cDNA; 1361 BP.
DE Human secreted protein coding sequence, SEQ ID 48.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 446
ID ADA55899 standard; DNA; 1261 BP.
DE Gene encoding human secreted protein #78.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 447
ID AAS63048 standard; cDNA; 1293 BP.
DE Cell death protective sequence CNI-00727.
PN WO200176532-A2.
PD 18-OCT-2001.

PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match 1.6%; Score 56; DB 6; Length 1293;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 448
ID ABA82876 standard; DNA; 1350 BP.
DE Human protective DNA sequence CNI-00747.
PN WO200176457-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match 1.6%; Score 56; DB 6; Length 1350;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 449
ID AAO8379 standard; cDNA; 1351 BP.
DE Human secreted protein-encoding gene 35 cDNA clone HMVDU15, SEQ ID NO:45.
PN WO200077022-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1351;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 450
ID ABZ73488 standard; cDNA; 1351 BP.
DE Secreted protein-encoding gene 208 cDNA clone HMVDU15, SEQ ID NO:218.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1351;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 451
ID ABZ67097 standard; cDNA; 1351 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 217.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1351;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 452
ID AAX51714 standard; DNA; 1361 BP.
DE DNA encoding a human secreted protein.
PN WO9911293-A1.
PD 11-MAR-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 453
ID ABQ92566 standard; cDNA; 1361 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 24.
PN WO200257420-A2.
PD 25-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 454
ID ACC50395 standard; cDNA; 1361 BP.
DE Human secreted protein coding sequence, SEQ ID 62.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1361;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
RESULT 455
ID AAC69101 standard; DNA; 1362 BP.
DE Human secreted protein gene 18 clone HKAFH74.
PN WO200055371-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1362;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 456
ID AAX51727 standard; DNA; 1367 BP.
DE DNA encoding a human secreted protein.
PN WO9911293-A1.
PD 11-MAR-1999.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 56; DB 2; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 457
ID ABQ92579 standard; cDNA; 1367 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 37.
PN WO200257420-A2.
PD 25-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1367;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 458
ID AAD06008 standard; DNA; 1407 BP.
DE Human neuronal apoptosis regulated candidate (NARC) 8B DNA.
PN WO200131007-A2.
PD 03-MAY-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 56; DB 4; Length 1407;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 459
ID ADJ57919 standard; cDNA; 1407 BP.
DE Human NARC 8B cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.6%; Score 56; DB 12; Length 1407;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 460
ID ADA39727 standard; cDNA; 1421 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1421;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 461
ID AB271218 standard; cDNA; 1421 BP.
DE Human secreted protein-encoding gene 29 cDNA clone HDHEB60, SEQ ID NO:39.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1421;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 462
ID ADC73447 standard; DNA; 1421 BP.
DE Human secreted protein-related DNA - SEQ ID 80.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1421;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 463
ID ADD37560 standard; cDNA; 1421 BP.
DE Human secreted protein encoding sequence #42.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1421;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 464
ID ADA55918 standard; DNA; 1421 BP.
DE Gene encoding human secreted protein #97.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1421;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 465
ID AAS63068 standard; cDNA; 1466 BP.
DE Cell death protective sequence CNI-00728.
PN WO200176532-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match 1.6%; Score 56; DB 6; Length 1466;

Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 466
ID AAF18174 standard; DNA; 1524 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 193.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 467
ID AAC79956 standard; cDNA; 1526 BP.
DE Human secreted protein encoding cDNA for gene 9.
PN WO200058357-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1526;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 468
ID ABL89665 standard; cDNA; 1526 BP.
DE Human polynucleotide SEQ ID NO 227.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1526;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 469
ID AAC78187 standard; cDNA; 1574 BP.
DE Human cancer associated gene sequence SEQ ID NO:581.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1574;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 470
ID AAF32743 standard; cDNA; 1574 BP.
DE Human secreted protein gene 45 SEQ ID NO:55.
PN WO200077255-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1574;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 471
ID AAQ80218 standard; DNA; 1651 BP.
DE Human NDF-alpha2b clone 17 DNA.
PN WO9428133-A1.
PD 08-DEC-1994.
PA (AMGE-) AMGEN INC.
Query Match 1.6%; Score 56; DB 2; Length 1651;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 472
ID AAC77740 standard; cDNA; 1657 BP.
DE Human cancer associated gene sequence SEQ ID NO:134.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1657;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 473
ID AAD05081 standard; cDNA; 1666 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HDPCJ43, SEQ ID NO:39.
PN WO200134768-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1666;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 474
ID AAC98134 standard; cDNA; 1694 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:144.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1694;

Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 475
ID AA298108 standard; cDNA; 1722 BP.
DE Human secreted protein encoding nucleotide sequence SEQ ID NO:102.
PN WO200004140-A1.
PD 27-JAN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 476
ID AAD11721 standard; cDNA; 1722 BP.
DE Human secreted protein-encoding gene 71 cDNA clone HDP0Z56, SEQID NO:102.
PN WO200151504-A1.
PD 19-JUL-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 477
ID ABK69818 standard; cDNA; 1722 BP.
DE Human secreted protein gene 71 #2.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 478
ID ADA40305 standard; cDNA; 1722 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 479
ID ACC50714 standard; cDNA; 1722 BP.
DE Human secreted protein coding sequence, SEQ ID 381.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 8; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 480
ID ADA56466 standard; DNA; 1722 BP.
DE Gene encoding human secreted protein #118.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 481
ID ADM19675 standard; cDNA; 1724 BP.
DE Novel human channel/transporter gene #237 clone 2.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 5; Length 1724;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 482
ID ABL90677 standard; cDNA; 1724 BP.
DE Human polynucleotide SEQ ID NO 1239.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1724;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
RESULT 483
ID ADD19236 standard; cDNA; 1745 BP.
DE Human cDNA from secreted protein gene 53.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1745;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;

RESULT 484
ID AAZ65347 standard; DNA; 1779 BP.
DE Human secreted protein gene 18.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 3; Length 1779;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 485
ID ADE11737 standard; cDNA; 1779 BP.
DE Human secreted polypeptide cDNA #99.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAF/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 1.6%; Score 56; DB 10; Length 1779;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 486
ID ADC78218 standard; cDNA; 1803 BP.
DE Human secreted protein encoding cDNA SEQ ID NO:25.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 10; Length 1803;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 487
ID AAH84170 standard; cDNA; 1825 BP.
DE Human cell death protective cDNA clone CNI-00714, SEQ:75.
PN WO200145638-A2.
PD 28-JUN-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match 1.6%; Score 56; DB 4; Length 1825;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 488
ID AAD07854 standard; cDNA; 1892 BP.
DE Human secreted protein-encoding gene 7 cDNA clone HDPDI45, SEQ ID NO:56.
PN WO200132675-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 4; Length 1892;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 489
ID ABL90762 standard; cDNA; 1892 BP.
DE Human polynucleotide SEQ ID NO 1324.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 56; DB 6; Length 1892;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 490
ID ABA82901 standard; DNA; 1895 BP.
DE Human protective DNA sequence CNI-00749.
PN WO200176457-A2.
PD 18-OCT-2001.
PA (COGE-) COGENT NEUROSCIENCE INC.
Query Match 1.6%; Score 56; DB 6; Length 1895;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
RESULT 491
ID ABL90655 standard; cDNA; 1977 BP.

ID ABX43725 standard; CDNA; 257 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #8890.
PN US2002137139-A1.

PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 55; DB 8; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
RESULT 509
ID ABX61239 standard; DNA; 277 BP.
DE Arabidopsis thaliana polynucleotide #585.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 1.5%; Score 55; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
RESULT 510
ID ABX47848 standard; cDNA; 321 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13013.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 55; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
RESULT 511
ID ABX37780 standard; cDNA; 355 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2945.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 55; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
RESULT 512
ID ABQ85688 standard; DNA; 359 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 558.
PN US2002062014-A1.
PD 23-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T W.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.

Query Match 1.5%; Score 55; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
RESULT 513
ID AAI63504 standard; cDNA; 381 BP.
DE Human polynucleotide SEQ ID NO 3564.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 55; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
RESULT 514
ID ACH21043 standard; cDNA; 381 BP.
DE Human adult liver cDNA #655.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 1.5%; Score 55; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
RESULT 515
ID AAI67804 standard; cDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 7864.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 55; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 516
ID AAG35447 standard; cDNA; 439 BP.
DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID NO 332.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 7e-06;
RESULT 517
ID AD845526 standard; cDNA; 439 BP.
DE Human cardiovascular system related polynucleotide #322.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 10; Length 439;
Best Local Similarity 100.0%; Pred. No. 7e-06;
RESULT 518
ID ADJ06944 standard; DNA; 439 BP.
DE Human cardiovascular system associated gene SeqID332.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 13; Length 439;
Best Local Similarity 100.0%; Pred. No. 7e-06;
RESULT 519
ID AAK63678 standard; cDNA; 466 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8738.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
RESULT 520
ID ACN58190 standard; cDNA; 564 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-008-Q6-K6-D6, SEQ:12971.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 55; DB 13; Length 564;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;

RESULT 521
ID ACN53521 standard; cDNA; 568 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-G2, SEQ:8302.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 55; DB 13; Length 568;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
RESULT 522
ID ACN63058 standard; cDNA; 579 BP.
DE Cotton carpel wall/septum EST Clone ID: LIB3831-002-Q1-N6-E12, SEQ:17839.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 55; DB 13; Length 579;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
RESULT 523
ID ACN51185 standard; cDNA; 603 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B6, SEQ:5966.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 55; DB 13; Length 603;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 524
ID AAX37373 standard; cDNA; 604 BP.
DE Human secreted protein cDNA fragment containing gene 5.
FN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 525
ID AAC79824 standard; cDNA; 809 BP.
DE Human secreted protein gene 26 SEQ ID NO:36.
FN WO200058336-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 3; Length 809;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
RESULT 526
ID AAX30363 standard; DNA; 832 BP.
DE DNA encoding a human secreted protein.
FN WO9907891-A1.
PD 18-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 2; Length 832;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
RESULT 527
ID ADB47735 standard; cDNA; 832 BP.
DE Novel human secreted protein cDNA #8.
FN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNEN R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.

PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match 1.5%; Score 55; DB 10; Length 832;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
RESULT 528
ID ADJ55290 standard; cDNA; 832 BP.
DE Novel human secreted protein cDNA #8.
FN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 12; Length 832;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
RESULT 529
ID ABV25640 standard; cDNA; 974 BP.
DE Human prostate expression marker cDNA 25631.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 55; DB 5; Length 974;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
RESULT 530
ID AAC99900 standard; cDNA; 1001 BP.
DE Human secreted protein gene 83 SEQ ID NO:93.
FN WO200070042-A1.
PD 23-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 3; Length 1001;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
RESULT 531
ID ABL90679 standard; cDNA; 1129 BP.
DE Human polynucleotide SEQ ID NO 1241.
FN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 6; Length 1129;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 532
ID ACC50489 standard; cDNA; 1142 BP.
DE Human secreted protein coding sequence, SEQ ID 156.
FN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 8; Length 1142;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 533
ID ABZ71271 standard; cDNA; 1142 BP.
DE Human secreted protein-encoding gene 82 cDNA clone HKB1E57, SEQ ID NO:92.
FN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 8; Length 1142;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 534
ID ADB91177 standard; cDNA; 1142 BP.
DE Human secreted protein cDNA #SEQ ID 123.
FN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 9; Length 1142;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 535
ID ADC73553 standard; DNA; 1142 BP.
DE Human secreted protein-related DNA - SEQ ID 186.
FN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 10; Length 1142;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
RESULT 536
ID ABQ55006 standard; cDNA; 1259 BP.
DE Human ovarian antigen HFIVR61 cDNA, SEQ ID NO:886.
FN WO200200677-A1.
PD 03-JAN-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 6; Length 1259;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
RESULT 537
ID AAA64408 standard; cDNA; 1473 BP.
DE DNA encoding a human TANGO 223 polypeptide.
PN WO200050442-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 3; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
RESULT 538
ID AAA64425 standard; cDNA; 1473 BP.
DE DNA encoding a human TANGO 223 variant polypeptide.
PN WO200050442-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 3; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
RESULT 539
ID AAA64424 standard; cDNA; 1473 BP.
DE DNA encoding a human TANGO 223 variant polypeptide.
PN WO200050442-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 3; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
RESULT 540
ID AAA64426 standard; cDNA; 1473 BP.
DE DNA encoding a human TANGO 223 variant polypeptide.
PN WO200050442-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 3; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
RESULT 541
ID AAF16012 standard; cDNA; 1539 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:447.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 1.5%; Score 55; DB 3; Length 1539;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
RESULT 542
ID ADQ22078 standard; DNA; 2197 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4898.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.5%; Score 55; DB 12; Length 2197;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
RESULT 543
ID AAQ80216 standard; DNA; 2335 BP.
DE Human prionDF-alpha2b DNA.
PN WO9428133-A1.
PD 08-DEC-1994.
PA (ANGE-) AMGEN INC.
Query Match 1.5%; Score 55; DB 2; Length 2335;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
RESULT 544
ID ABQ54916 standard; cDNA; 2438 BP.
DE Human ovarian antigen HNBV053 cDNA, SEQ ID NO:796.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 6; Length 2438;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
RESULT 545
ID AAX22123 standard; DNA; 2888 BP.
DE Human secreted protein gene 13 clone HUFAC36.
PN WO9901020-A2.
PD 14-JAN-1999.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 2; Length 2888;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 546
ID AAP29447 standard; cDNA; 2895 BP.
DE Human INTERCEPT 217 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 4; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 547
ID ACB66756 standard; cDNA; 2895 BP.
DE Secreted polypeptide-related cDNA #40.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 1.5%; Score 55; DB 8; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 548
ID ADB90805 standard; cDNA; 2895 BP.
DE Human cDNA encoding INTERCEPT 217.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 9; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 549
ID ADF71539 standard; cDNA; 2895 BP.
DE Human INTERCEPT 217 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 10; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 550
ID ADQ10277 standard; cDNA; 2895 BP.
DE Human polynucleotide #47.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 55; DB 12; Length 2895;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 551
ID ABQ55051 standard; cDNA; 3036 BP.
DE Human ovarian antigen HOCQ58 cDNA, SEQ ID NO:931.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 6; Length 3036;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 552
ID ACC50399 standard; cDNA; 3037 BP.
DE Human secreted protein coding sequence, SEQ ID 66.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 55; DB 8; Length 3037;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
RESULT 553
ID AB271220 standard; cDNA; 3037 BP.
DE Human secreted protein-encoding gene 31 cDNA clone HDPCL63, SEQ ID NO:41.
PN WO200276488-A1.

PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 55; DB 8; Length 3037;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 RESULT 554
 ID ADB91113 standard; cDNA; 3037 BP.
 DE Human secreted protein cDNA #SEQ ID 59.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 55; DB 9; Length 3037;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 RESULT 555
 ID ADC73450 standard; DNA; 3037 BP.
 DE Human secreted protein-related DNA - SEQ ID 83.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 55; DB 10; Length 3037;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 RESULT 556
 ID AAV02308 standard; cDNA; 3451 BP.
 DE Cell membrane proton-ATPase encoding cDNA.
 PN JP09252786-A.
 PD 30-SEP-1997.
 PA (ORY) ORIENTAL YEAST CO LTD.
 Query Match 1.5%; Score 55; DB 2; Length 3451;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 RESULT 557
 ID ADO08304 standard; cDNA; 6021 BP.
 DE Human NOVX polynucleotide #26.
 PN US2004018594-A1.
 PD 29-JAN-2004.
 PA (ALSC/) ALSOBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CASW/) CASMAN S J.
 PA (CHAP/) CHAPOVAL A.
 PA (EDIN/) EDINGER S R.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (GUNT/) GUNTHER E.
 PA (GUOX/) GUO X S.
 PA (KEKU/) KEKUDA R.
 PA (LEPL/) LEFLEY D M.
 PA (LILL/) LI L.
 PA (LIUX/) LIU X.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLER C E.
 PA (MILL/) MILLET I.
 PA (PADL/) PADIGARU M.
 PA (PATI/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (RIEG/) RIEGER D K.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (SPYT/) SPYTEK K A.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZERR/) ZERRHUSEN B D.
 Query Match 1.5%; Score 55; DB 12; Length 6021;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 RESULT 558
 ID ACA10136 standard; cDNA; 6033 BP.
 DE Human NOVX polynucleotide #26.
 PN WO200290504-A2.
 PD 14-NOV-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 1.5%; Score 55; DB 8; Length 6023;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 RESULT 559

ID AAK82933 standard; DNA; 14063 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37745.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 55; DB 4; Length 14063;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 RESULT 560
 ID AAK82934 standard; DNA; 14063 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37746.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 55; DB 4; Length 14063;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 RESULT 561
 ID ADT95066 standard; cDNA; 66 BP.
 DE Colon cancer associated human cDNA sequence #585.
 PN US2003087818-A1.
 PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 54; DB 11; Length 66;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 RESULT 562
 ID ADQ92259 standard; DNA; 93 BP.
 DE Human autoantigen DNA fragment MPWGP800P12530.
 PN WO2004058972-A1.
 PD 15-JUL-2004.
 PA (THIE/) THIESEN H.
 PA (LORE/) LORENZ P.
 Query Match 1.5%; Score 54; DB 12; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 RESULT 563
 ID ACN47721 standard; cDNA; 180 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-014-Q1-K6-E9, SEQ:2502.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 54; DB 13; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 RESULT 564
 ID ABX40273 standard; cDNA; 203 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #5438.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 54; DB 8; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 RESULT 565
 ID ABV59126 standard; cDNA; 221 BP.
 DE Human prostate expression marker cDNA 59117.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 54; DB 5; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 566
 ID ACN60904 standard; cDNA; 226 BP.
 DE Cotton gyroecium tissue EST Clone ID: LIB3829-029-Q6-K6-E8, SEQ:15685.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 54; DB 13; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;

RESULT 567

ID ABQ85662 standard; DNA; 360 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 532.
 PN US2002062014-A1.
 PD 23-MAY-2002.

PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.

Query Match 1.5%; Score 54; DB 6; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

RESULT 568

ID AAT84939 standard; cDNA; 375 BP.
 DE Human prostate protein HPA34 3' cDNA.
 PN WO9733909-A2.
 PD 18-SEP-1997.

PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 54; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

RESULT 569

ID AAX35869 standard; cDNA; 375 BP.
 DE cDNA encoding a prostate tumour cell polypeptide.
 PN WO9918210-A2.
 PD 15-APR-1999.

PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 54; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

RESULT 570

ID ABX61502 standard; DNA; 385 BP.
 DE Arabidopsis thaliana polynucleotide #848.
 PN US2002142319-A1.
 PD 03-OCT-2002.

PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (HARG/) HARGISS T R.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.

Query Match 1.5%; Score 54; DB 10; Length 385;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

RESULT 571

ID AAI82053 standard; cDNA; 399 BP.
 DE Human polynucleotide SEQ ID NO 2113.
 PN WO200164835-A2.
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 54; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 572

ID ACN54899 standard; cDNA; 407 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-K6-A1, SEQ:9680.

PN US2004123340-A1.
 PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.

Query Match 1.5%; Score 54; DB 13; Length 407;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 573

ID ABX43804 standard; cDNA; 410 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #8969.
 PN US2002137139-A1.
 PD 26-SEP-2002.

PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.

Query Match 1.5%; Score 54; DB 8; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 574

ID ACH19512 standard; cDNA; 417 BP.
 DE Human adult lung cDNA #515.
 PN US2003073623-A1.
 PD 17-APR-2003.

PA (DRNA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.

Query Match 1.5%; Score 54; DB 9; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 575

ID AAI86360 standard; cDNA; 418 BP.
 DE Human polynucleotide SEQ ID NO 6420.
 PN WO200164835-A2.
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 54; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 576

ID AAI87426 standard; cDNA; 423 BP.
 DE Human polynucleotide SEQ ID NO 7486.
 PN WO200164835-A2.
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 54; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 577

ID ABX61471 standard; DNA; 426 BP.
 DE Arabidopsis thaliana polynucleotide #817.
 PN US2002142319-A1.
 PD 03-OCT-2002.

PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (HARG/) HARGISS T R.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.

Query Match 1.5%; Score 54; DB 10; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 578

ID AAI88622 standard; cDNA; 438 BP.
 DE Human polynucleotide SEQ ID NO 8682.
 PN WO200164835-A2.
 PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 1.5%; Score 54; DB 4; Length 438;
RESULT 579
ID ACH24608 standard; cDNA; 484 BP.
DE Human adult ovary cDNA #2988.
PD 17-APR-2003.
PA (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.
PA (DICK//) DICKSON M C.
PA (JONE//) JONES L W.
Query Match
Best Local Similarity 1.5%; Score 54; DB 9; Length 484;
RESULT 580
ID ADR65444 standard; cDNA; 487 BP.
DE Cotton cDNA sequence, SEQ ID 6225.
PD US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA//) KOVALIC D K.
PA (ZHOU//) ZHOU Y.
PA (CAOY//) CAO Y.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 487;
RESULT 581
ID ACN53958 standard; cDNA; 487 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-K6-E3, SEQ:8739.
PD US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 487;
RESULT 582
ID ADL44915 standard; DNA; 510 BP.
DE Human ovarian cancer DNA marker #18805.
PD WO200170979-A2.
PD 27-SEP-2001.
PA (MILL//) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 5; Length 510;
RESULT 583
ID ACN52870 standard; cDNA; 514 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H11, SEQ:7651.
PD US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 514;
RESULT 584
ID AAX88727 standard; cDNA; 550 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 1043.
PD WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 4; Length 550;
RESULT 585
ID AAS31761 standard; cDNA; 550 BP.
DE Human liver associated cDNA polynucleotide #81.
PD WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 5; Length 550;
RESULT 586
ID ABN90116 standard; cDNA; 550 BP.
DE Human liver antigen HLDOM43 cDNA, SEQ ID NO:91.
FN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE//) ROSEN C A.
PA (RUBE//) RUBEN S M.
PA (BARA//) BARASH S C.
Query Match
Best Local Similarity 1.5%; Score 54; DB 6; Length 550;
RESULT 587
ID ADJ14883 standard; DNA; 550 BP.
DE Human liver-related contig DNA - SEQ ID 91.
PD US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 11; Length 550;
RESULT 588
ID ACN53260 standard; cDNA; 588 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-G11, SEQ:8041.
PD US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK//) DEIKMAN J.
PA (FENG//) FENG P C C.
PA (FINC//) FINCHER K L.
PA (ZIEG//) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 588;
RESULT 589
ID AAC78236 standard; cDNA; 638 BP.
DE Human cancer associated gene sequence SEQ ID NO:630.
PD WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 54; DB 3; Length 638;
RESULT 590
ID ADR61268 standard; cDNA; 752 BP.
DE Cotton cDNA sequence, SEQ ID 2049.
PD US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA//) KOVALIC D K.
PA (ZHOU//) ZHOU Y.
PA (CAOY//) CAO Y.
Query Match
Best Local Similarity 1.5%; Score 54; DB 13; Length 752;
RESULT 591
ID ABK30897 standard; cDNA; 796 BP.
DE Plant dwarfing/stunting related cDNA seq ID 311.
PD WO200208410-A2.
PD 31-JAN-2002.
PA (DOWC//) DOW CHEM CO.
PA (REDD//) REDDY S A.
PA (LARR//) LARRINUA M I.
PA (RUEG//) RUEGGER M.
PA (WEGE//) WEGELARZ T.
PA (BLAK//) BLAKESLEE B.
PA (ORIE//) ORIEDO V B J.
PA (SAVI//) SAVICKAS J P.
PA (MCCR//) MCCREARY A D.
PA (MILL//) MILLER A B.
PA (POGU//) POGUE P G.
PA (DELL//) DELLA-CIOPPA R G.
PA (WOLF//) WOLFE M G.
PA (ZHEN//) ZHENG W.
PA (GACH//) GACHOTTE D.
PA (GROS//) GROSLEY R.
PA (PELL//) PELL R.
Query Match
Best Local Similarity 1.5%; Score 54; DB 6; Length 796;
RESULT 592
ID AAX61366 standard; cDNA; 848 BP.
DE DNA encoding a human secreted protein.
PD WO9922243-A1.
PD 06-MAY-1999.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
RESULT 593
ID ACN87504 standard; DNA; 848 BP.
DE Breast cancer related marker, seq id 8654.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 54; DB 11; Length 848;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
RESULT 594
ID ABO303020 standard; DNA; 854 BP.
DE Human breast specific coding sequence SEQ ID NO: 25.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 54; DB 6; Length 854;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
RESULT 595
ID ABO54536 standard; cDNA; 883 BP.
DE Human ovarian antigen HCABR46 cDNA, SEQ ID NO:416.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 6; Length 883;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
RESULT 596
ID AAO05641 standard; cDNA; 923 BP.
DE Human secreted protein-encoding gene 18 cDNA clone HDTFE17, SEQ ID NO:73.
PN WO200134627-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 4; Length 923;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 597
ID AAO08435 standard; cDNA; 923 BP.
DE Human secreted protein-encoding gene 4 cDNA clone HCRPV17, SEQ ID NO:42.
PN WO200134643-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 8; Length 923;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 598
ID ADA40320 standard; cDNA; 923 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 8; Length 923;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 599
ID ADC73842 standard; DNA; 923 BP.
DE Human secreted protein-related DNA - SEQ ID 475.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 923;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 600
ID ADA56482 standard; DNA; 923 BP.
DE Gene encoding human secreted protein #136.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 923;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 601
ID ADR63577 standard; cDNA; 973 BP.
DE Cotton cDNA sequence, SEQ ID 4358.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.
Query Match 1.5%; Score 54; DB 13; Length 973;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 602
ID AAC98033 standard; cDNA; 1060 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:43.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 3; Length 1060;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
RESULT 603
ID ADD19241 standard; cDNA; 1142 BP.
DE Human cDNA from secreted protein gene 58.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1142;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
RESULT 604
ID AAS02224 standard; cDNA; 1194 BP.
DE Corn Wuschel (WUS) cDNA from clone p0083_cidev71r #2.
PN WO200123575-A2.
PD 05-APR-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 54; DB 4; Length 1194;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
RESULT 605
ID ACC00758 standard; cDNA; 1269 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:265.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 54; DB 8; Length 1269;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
RESULT 606
ID ADC23630 standard; cDNA; 1269 BP.
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 135).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 54; DB 10; Length 1369;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
RESULT 607
ID AAF33131 standard; cDNA; 1343 BP.
DE Human secreted protein gene 37 SEQ ID NO:47.
PN WO200077256-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 4; Length 1343;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
RESULT 608
ID AA297106 standard; cDNA; 1723 BP.
DE Human secreted protein gene 88 cDNA clone HNTSW57, SEQ ID NO:98.
PN WO9966041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 3; Length 1723;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
RESULT 609
ID ACH66735 standard; cDNA; 1723 BP.
DE Novel human secreted protein #88 cDNA.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 9; Length 1723;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
RESULT 610
ID ABO54940 standard; cDNA; 1847 BP.
DE Human ovarian antigen HTXKD84 cDNA, SEQ ID NO:820.

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PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 6; Length 1847;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
RESULT 611
ID ADA5928 standard; cDNA; 1931 BP.
DE Human secreted protein cDNA # 2 encoding gene 2.
PN WO9938881-A1.
PD 05-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 2; Length 1931;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 612
ID ADA40295 standard; cDNA; 1931 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 8; Length 1931;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 613
ID ADC73812 standard; DNA; 1931 BP.
DE Human secreted protein-related DNA - SEQ ID 445.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1931;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 614
ID ADD37730 standard; cDNA; 1931 BP.
DE Human secreted protein encoding sequence #212.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1931;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 615
ID ADA56463 standard; DNA; 1931 BP.
DE Gene encoding human secreted protein #107.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1931;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 616
ID AAZ00411 standard; cDNA; 1932 BP.
DE Human secreted protein cDNA encoding gene 2.
PN WO9938881-A1.
PD 05-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 2; Length 1932;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 617
ID ADA39736 standard; cDNA; 1932 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 8; Length 1932;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 618
ID ADC73452 standard; DNA; 1932 BP.
DE Human secreted protein-related DNA - SEQ ID 85.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1932;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 619
ID ADD37565 standard; cDNA; 1932 BP.
DE Human secreted protein encoding sequence #47.
PN WO200290526-A2.

PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1932;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 620
ID ADA5928 standard; DNA; 1932 BP.
DE Gene encoding human secreted protein #107.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 10; Length 1932;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
RESULT 621
ID AAF81813 standard; cDNA; 2150 BP.
DE Human secreted protein gene 18 SEQ ID NO:37.
PN WO200112775-A2.
PD 22-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 4; Length 2150;
Best Local Similarity 100.0%; Pred. No. 8e-06;
RESULT 622
ID AAT70845 standard; cDNA; 2369 BP.
DE Human heparanase II cDNA clone 338524_c102.
PN WO200177341-A2.
PD 18-OCT-2001.
PA (JANC ) JANSSEN PHARM NV.
Query Match 1.5%; Score 54; DB 6; Length 2369;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
RESULT 623
ID AAC77957 standard; cDNA; 2756 BP.
DE Human cancer associated gene sequence SEQ ID NO:351.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 54; DB 3; Length 2756;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
RESULT 624
ID AAT62360 standard; cDNA; 3214 BP.
DE Human origin of replication complex ORC1 gene.
PN WO9640977-A1.
PD 19-DEC-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 1.5%; Score 54; DB 2; Length 3214;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
RESULT 625
ID AAT73287 standard; cDNA; 3214 BP.
DE Human origin of replication complex protein 1 gene.
PN US5614618-A.
PD 25-MAR-1997.
PA (REGC ) UNIV CALIFORNIA.
Query Match 1.5%; Score 54; DB 2; Length 3214;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
RESULT 626
ID ABV21457 standard; cDNA; 3552 BP.
DE Human prostate expression marker cDNA 21448.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 54; DB 5; Length 3552;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
RESULT 627
ID ABV27275 standard; cDNA; 3552 BP.
DE Human prostate expression marker cDNA 27266.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 54; DB 5; Length 3552;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
RESULT 628
ID ADL46001 standard; DNA; 3552 BP.
DE Human ovarian cancer DNA marker #19891.
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PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 54; DB 5; Length 3552;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 RESULT 629
 ID ACN90329 standard; DNA; 3552 BP.
 DE Breast cancer related marker, seq id 11479.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.5%; Score 54; DB 11; Length 3552;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 RESULT 630
 ID ABL39412 standard; DNA; 29222 BP.
 DE Human electron-transfer flavoprotein, beta polypeptide (ETFB) gene.
 PN WO200202580-A2.
 PD 10-JAN-2002.
 PA (GENA-) GENAISSANCE PHARM INC.
 Query Match 1.5%; Score 54; DB 6; Length 29222;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 RESULT 631
 ID ABK5233 standard; cDNA; 58 BP.
 DE Human colon cancer-associated cDNA, SEQ ID No 703.
 PN WO200212280-A2.
 PD 14-FEB-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 632
 ID ABK54949 standard; cDNA; 60 BP.
 DE Human colon cancer-associated cDNA, SEQ ID No 419.
 PN WO200212280-A2.
 PD 14-FEB-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 6; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 633
 ID AAV02148 standard; cDNA; 69 BP.
 DE Human secreted protein AK296 3' portion including the polyA tail.
 PN WO9739123-A2.
 PD 23-OCT-1997.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;
 RESULT 634
 ID AAT88081 standard; cDNA; 69 BP.
 DE 3' portion of cDNA clone encoding secreted protein AK296.
 PN WO9739122-A2.
 PD 23-OCT-1997.
 PA (MURO-) MURO PHARM INC.
 Query Match 1.5%; Score 53; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;
 RESULT 635
 ID ADT95589 standard; cDNA; 74 BP.
 DE Colon cancer associated human cDNA sequence #1108.
 PN US2003087818-A1.
 PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 11; Length 74;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 RESULT 636
 ID AAV05720 standard; cDNA; 85 BP.
 DE Nucleotide sequence of the 3' portion from clone AZ302_1.
 PN WO9746683-A2.
 PD 11-DEC-1997.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 RESULT 637
 ID ABK54747 standard; cDNA; 90 BP.
 DE Human colon cancer-associated cDNA, SEQ ID No 217.
 PN WO200212280-A2.

PD 14-FEB-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 6; Length 90;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 RESULT 638
 ID ADT94809 standard; cDNA; 90 BP.
 DE Colon cancer associated human cDNA sequence #328.
 PN US2003087818-A1.
 PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 11; Length 90;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 RESULT 639
 ID AAT91300 standard; cDNA; 99 BP.
 DE Human M97-2 secreted protein cDNA 3' end.
 PN WO9740151-A2.
 PD 30-OCT-1997.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 RESULT 640
 ID AAV00420 standard; cDNA; 101 BP.
 DE 3' fragment of clone M97_2.
 PN WO9740069-A2.
 PD 30-OCT-1997.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 RESULT 641
 ID ADT96268 standard; cDNA; 107 BP.
 DE Colon cancer associated human cDNA sequence #1775.
 PN US2003087818-A1.
 PD 08-MAY-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.5%; Score 53; DB 11; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 RESULT 642
 ID ABQ94578 standard; DNA; 125 BP.
 DE Tumour suppression-related oligonucleotide #229.
 PN FR2819824-A1.
 PD 26-JUL-2002.
 PA (MOLE-) MOLECULAR ENGINES LAB SA.
 Query Match 1.5%; Score 53; DB 6; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 RESULT 643
 ID AAV21239 standard; cDNA; 144 BP.
 DE Homo sapiens clone H698_3 3' end.
 PN WO9807859-A2.
 PD 26-FEB-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 RESULT 644
 ID AAX77331 standard; DNA; 144 BP.
 DE Human secreted protein encoding DNA (clone H698-3) 3' portion.
 PN WO9926973-A1.
 PD 03-JUN-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 RESULT 645
 ID ADC38850 standard; cDNA; 144 BP.
 DE Human cDNA encoding a secreted protein #97 additional sequence.
 PN US2002193567-A1.
 PD 19-DEC-2002.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 10; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 RESULT 646
 ID ABQ94618 standard; DNA; 160 BP.
 DE Tumour suppression-related oligonucleotide #269.
 PN FR2819824-A1.
 PD 26-JUL-2002.

PA (MOLE-) MOLECULAR ENGINES LAB SA.
Query Match standard; cDNA; 170 BP.
Best Local Similarity 1.5%; Score 53; DB 6; Length 160;
Pred. No. 3.3e-05;
RESULT 647
ID AAH70047 standard; cDNA; 170 BP.
DE Human cervical cancer marker nucleic acid 1321.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 170;
Pred. No. 3.3e-05;
RESULT 648
ID ABX53070 standard; cDNA; 175 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2999.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 175;
Pred. No. 3.2e-05;
RESULT 649
ID AB055367 standard; cDNA; 197 BP.
DE Human ovarian antigen HNAE01 cDNA, SEQ ID NO:1247.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 197;
Pred. No. 3.1e-05;
RESULT 650
ID ABX43949 standard; cDNA; 202 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9114.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 202;
Pred. No. 3.1e-05;
RESULT 651
ID ABV19221 standard; cDNA; 204 BP.
DE Human prostate expression marker cDNA 19212.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 204;
Pred. No. 3.1e-05;
RESULT 652
ID ABV14996 standard; cDNA; 211 BP.
DE Human prostate expression marker cDNA 14987.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 211;
Pred. No. 3e-05;
RESULT 653
ID ABV60841 standard; cDNA; 219 BP.
DE Human prostate expression marker cDNA 60832.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 219;
Pred. No. 3e-05;
RESULT 654
ID ADL44460 standard; cDNA; 222 BP.
DE Human ovarian cancer DNA marker #18350.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 222;
Pred. No. 3e-05;
RESULT 655
ID ABV05827 standard; cDNA; 226 BP.
DE Human prostate expression marker cDNA 5818.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 226;
Pred. No. 3e-05;
RESULT 656
ID AD172068 standard; cDNA; 234 BP.
DE Human ovarian cancer DNA marker #4810.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 234;
Pred. No. 2.9e-05;
RESULT 657
ID ADL37217 standard; cDNA; 234 BP.
DE Human ovarian cancer DNA marker #11107.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 234;
Pred. No. 2.9e-05;
RESULT 658
ID ARV60929 standard; cDNA; 235 BP.
DE Human prostate expression marker cDNA 60920.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 235;
Pred. No. 2.9e-05;
RESULT 659
ID ADL38890 standard; cDNA; 240 BP.
DE Human ovarian cancer DNA marker #12780.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 240;
Pred. No. 2.9e-05;
RESULT 660
ID AD173085 standard; cDNA; 241 BP.
DE Human ovarian cancer DNA marker #5827.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 241;
Pred. No. 2.9e-05;
RESULT 661
ID ABV60876 standard; cDNA; 248 BP.
DE Human prostate expression marker cDNA 60867.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 248;
Pred. No. 2.9e-05;
RESULT 662
ID ABL87207 standard; cDNA; 264 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10185.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 264;
Pred. No. 2.8e-05;
RESULT 663
ID ABV07492 standard; cDNA; 269 BP.
DE Human prostate expression marker cDNA 7483.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 269;
Pred. No. 2.8e-05;
RESULT 664

ID ABK54605 standard; cDNA; 275 BP.
DE Human colon cancer-associated cDNA, SEQ ID No 75.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 665
ID ABV35976 standard; cDNA; 281 BP.
DE Human prostate expression marker cDNA 35967.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 666
ID ADL43493 standard; cDNA; 281 BP.
DE Human ovarian cancer DNA marker #17383.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 667
ID ABV61303 standard; cDNA; 283 BP.
DE Human prostate expression marker cDNA 61294.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 668
ID AAL16073 standard; cDNA; 289 BP.
DE Human breast cancer expressed polynucleotide 8530.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 669
ID AAL25205 standard; cDNA; 293 BP.
DE Human breast cancer expressed polynucleotide 17662.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
RESULT 670
ID AAS29052 standard; cDNA; 295 BP.
DE cDNA encoding for human DNA-binding protein #23.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 5; Length 295;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 671
ID ABS68192 standard; cDNA; 295 BP.
DE cDNA encoding human DNA-binding protein #23.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.5%; Score 53; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 672
ID ADC25186 standard; cDNA; 295 BP.
DE Human cDNA from extracellular matrix gene 23.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 295;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;

RESULT 673
ID ADL38330 standard; cDNA; 296 BP.
DE Human ovarian cancer DNA marker #12220.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 674
ID ADI73198 standard; cDNA; 296 BP.
DE Human ovarian cancer DNA marker #5940.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 675
ID AAH70049 standard; cDNA; 300 BP.
DE Human cervical cancer marker nucleic acid 1323.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 676
ID AAS29128 standard; cDNA; 304 BP.
DE cDNA encoding for human DNA-binding protein #99.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 5; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 677
ID ABS68268 standard; cDNA; 304 BP.
DE cDNA encoding human DNA-binding protein #99.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.5%; Score 53; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 678
ID ADC25262 standard; cDNA; 304 BP.
DE Human cDNA from extracellular matrix gene 99.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 679
ID ABX37505 standard; cDNA; 313 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2670.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 680
ID ABV15175 standard; cDNA; 317 BP.
DE Human prostate expression marker cDNA 15166.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 681
ID ADI73647 standard; cDNA; 318 BP.
DE Human ovarian cancer DNA marker #6389.
PN WO200170979-A2.

PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 682
ID ADL38776 standard; DNA; 318 BP.
DE Human ovarian cancer DNA marker #12666.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 683
ID AA184550 standard; cDNA; 320 BP.
DE Human polynucleotide SEQ ID NO 4610.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 684
ID ABV60996 standard; cDNA; 323 BP.
DE Human prostate expression marker cDNA 60987.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 685
ID ADL43688 standard; DNA; 328 BP.
DE Human ovarian cancer DNA marker #17578.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 686
ID ABT22555 standard; DNA; 331 BP.
DE Breast cancer marker gene SEQ ID No 928.
PN WO200285298-A2.
PD 31-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 687
ID ADI72852 standard; DNA; 332 BP.
DE Human ovarian cancer DNA marker #5594.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 688
ID ADL37991 standard; DNA; 332 BP.
DE Human ovarian cancer DNA marker #11881.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 689
ID ADL37149 standard; DNA; 336 BP.
DE Human ovarian cancer DNA marker #11039.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 690
ID ADI72000 standard; DNA; 336 BP.
DE Human ovarian cancer DNA marker #4742.
PN WO200170979-A2.
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 691
ID ABQ86019 standard; DNA; 337 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 889.
PN US2002062014-A1.
PD 23-MAY-2002.
PA (GORL-) GORLACH J.
PA (ANYI-) AN Y.
PA (HAMI-) HAMILTON C M.
PA (PRIC-) PRICE J L.
PA (RAIN-) RAINES T M.
PA (YUYI-) YU Y.
PA (RAME-) RAMEAKA J G.
PA (PAGE-) PAGE A.
PA (MATH-) MATHAW A V.
PA (LEDF-) LEDFORD B L.
PA (WOES-) WOESSNER J P.
PA (HAAS-) HAAS W D.
PA (GARC-) GARCIA C A.
PA (KRIC-) KRICKER M.
PA (SLAT-) SLATER T.
PA (DAVI-) DAVIS K R.
PA (ALLE-) ALLEN K.
PA (HOFF-) HOFFMAN N.
PA (HURB-) HURBAN P.
Query Match 1.5%; Score 53; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 692
ID ABV48996 standard; cDNA; 338 BP.
DE Human prostate expression marker cDNA 48987.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 338;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 693
ID ABV60873 standard; cDNA; 338 BP.
DE Human prostate expression marker cDNA 60864.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 338;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 694
ID ABZ08610 standard; cDNA; 338 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8601.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 1.5%; Score 53; DB 6; Length 338;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 695
ID ABV60943 standard; cDNA; 343 BP.
DE Human prostate expression marker cDNA 60934.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 343;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 696
ID ACN47065 standard; cDNA; 344 BP.
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-F1, SEQ:1846.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK-) DEIKMAN J.
PA (FENG-) FENG P C.
PA (FINC-) FINCHER K L.
PA (ZIEG-) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 697

ID AAI93468 standard; cDNA; 346 BP.
DE Human polynucleotide SEQ ID NO 13528.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 698
ID ADL43786 standard; DNA; 346 BP.
DE Human ovarian cancer DNA marker #17676.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 699
ID AAI87539 standard; cDNA; 347 BP.
DE Human polynucleotide SEQ ID NO 7599.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 700
ID ABX38206 standard; cDNA; 347 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3371.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 701
ID ADI73011 standard; DNA; 350 BP.
DE Human ovarian cancer DNA marker #5753.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 702
ID ADL38146 standard; DNA; 350 BP.
DE Human ovarian cancer DNA marker #12036.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 703
ID ADI72157 standard; DNA; 351 BP.
DE Human ovarian cancer DNA marker #4899.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 704
ID ADL37304 standard; DNA; 351 BP.
DE Human ovarian cancer DNA marker #11194.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 705
ID ABV60857 standard; cDNA; 352 BP.
DE Human prostate expression marker cDNA 60848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 706
ID ABV56898 standard; cDNA; 352 BP.
DE Human prostate expression marker cDNA 56889.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 707
ID ADI73560 standard; DNA; 358 BP.
DE Human ovarian cancer DNA marker #6302.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 708
ID ADL38690 standard; DNA; 358 BP.
DE Human ovarian cancer DNA marker #12580.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 709
ID ABL85588 standard; cDNA; 361 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:8566.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 710
ID ABV54973 standard; cDNA; 367 BP.
DE Human prostate expression marker cDNA 54964.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 367;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 711
ID AAI83125 standard; cDNA; 369 BP.
DE Human polynucleotide SEQ ID NO 3185.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 712
ID ACN50919 standard; cDNA; 373 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-B10, SEQ:5700.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 373;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
RESULT 713
ID ABV44911 standard; cDNA; 375 BP.
DE Human prostate expression marker cDNA 44902.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 714
ID ADL44584 standard; DNA; 375 BP.
DE Human ovarian cancer DNA marker #18474.
PN WO200170979-A2.
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 715
ID ADL43601 standard; DNA; 380 BP.
DE Human ovarian cancer DNA marker #17491.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 716
ID ABV42927 standard; cDNA; 382 BP.
DE Human prostate expression marker cDNA 42918.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 717
ID ABV24060 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 34051.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 718
ID ADL44116 standard; DNA; 383 BP.
DE Human ovarian cancer DNA marker #18006.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 719
ID ADL44714 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #18604.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 720
ID ADL45160 standard; DNA; 385 BP.
DE Human ovarian cancer DNA marker #19050.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 385;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 721
ID ABV57076 standard; cDNA; 386 BP.
DE Human prostate expression marker cDNA 57067.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 722
ID ADL44375 standard; DNA; 386 BP.
DE Human ovarian cancer DNA marker #18265.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 723
ID ADL43635 standard; DNA; 388 BP.
DE Human ovarian cancer DNA marker #17525.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 1.5%; Score 53; DB 5; Length 388;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 724
ID AAL20088 standard; cDNA; 389 BP.
DE Human breast cancer expressed polynucleotide 12545.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 725
ID ABX47205 standard; cDNA; 389 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12370.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 726
ID ADL43918 standard; DNA; 390 BP.
DE Human ovarian cancer DNA marker #17808.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 727
ID ABX37469 standard; cDNA; 392 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2634.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 392;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 728
ID ABX39417 standard; cDNA; 393 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4582.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 729
ID ACN86032 standard; DNA; 393 BP.
DE Breast cancer related marker, seq id 7182.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 11; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 730
ID ABX36090 standard; cDNA; 395 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1255.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 731
ID AAF94819 standard; cDNA; 396 BP.
DE Human ovarian cancer associated coding sequence SEQ ID NO: 10.

PN WO200118046-A2.
PD 15-MAR-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 732
ID ABL48769 standard; cDNA; 396 BP.
DE Ovarian carcinoma sequence isolate 21921.
PD US2002004491-A1.
PD 10-JAN-2002.
PA (XUJJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALCA/) ALGATE P A.
PA (FLIN/) FLING S P.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 733
ID ABT03086 standard; cDNA; 396 BP.
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 10.
PD WO200239885-A2.
PD 23-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 734
ID ADM10679 standard; cDNA; 396 BP.
DE Human ovarian carcinoma-associated cDNA 21921.
PD US2003206918-A1.
PD 06-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 735
ID ADJ11009 standard; cDNA; 396 BP.
DE Representative human ovarian carcinoma cDNA SeqID 10.
PD US2003232056-A1.
PD 18-DEC-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 736
ID ADM43270 standard; cDNA; 396 BP.
DE Human ovarian carcinoma cDNA #10.
PD US2003129192-A1.
PD 10-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 53; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 737
ID AA182664 standard; cDNA; 397 BP.
DE Human polynucleotide SEQ ID NO 2724.
PD WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 738
ID ABZ08435 standard; cDNA; 402 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8426.
PD WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 739
ID ABV56394 standard; cDNA; 404 BP.
DE Human prostate expression marker cDNA 56385.
PD WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 740
ID AAI83931 standard; cDNA; 405 BP.
DE Human polynucleotide SEQ ID NO 3991.
PD WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 741
ID ABV60840 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 60831.
PD WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 742
ID ABV60716 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 60707.
PD WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 407;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 743
ID ABX41098 standard; cDNA; 408 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5263.
PD US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHALAGAN N.
PA (TRON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 744
ID ADL37087 standard; DNA; 410 BP.
DE Human ovarian cancer DNA marker #10977.
PD WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 745
ID ADI71936 standard; DNA; 410 BP.
DE Human ovarian cancer DNA marker #4678.
PD WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 746
ID ACN52913 standard; cDNA; 411 BP.
DE Cotton androscium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ: 7694.
PD US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 747
ID AAI85186 standard; cDNA; 413 BP.
DE Human polynucleotide SEQ ID NO 5246.
PD WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 748
ID ADL44101 standard; DNA; 414 BP.
DE Human ovarian cancer DNA marker #17991.
PD WO200170979-A2.

PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 749
ID ABX39680 standard; cDNA; 418 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4845.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 53; DB 8; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 750
ID ABV56833 standard; cDNA; 420 BP.
DE Human prostate expression marker cDNA 56824.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 751
ID AAI89729 standard; cDNA; 422 BP.
DE Human polynucleotide SEQ ID NO 9789.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 752
ID ABV38062 standard; cDNA; 425 BP.
DE Human prostate expression marker cDNA 38053.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 753
ID AAI87325 standard; cDNA; 426 BP.
DE Human polynucleotide SEQ ID NO 7385.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 754
ID ABV44823 standard; cDNA; 426 BP.
DE Human prostate expression marker cDNA 44814.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 755
ID ABV39037 standard; cDNA; 426 BP.
DE Human prostate expression marker cDNA 39028.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
RESULT 756
ID ABK62058 standard; cDNA; 428 BP.
DE Human EST from P450TEC cDNA #24.
PN WO200181585-A2.
PD 01-NOV-2001.
PA (CYTO-) CYTOCHROMA INC.
Query Match 1.5%; Score 53; DB 6; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 757
ID ABV83644 standard; cDNA; 430 BP.
DE Human breast specific gene SEQ ID NO 87.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 53; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 758
ID ADL37205 standard; DNA; 433 BP.
DE Human ovarian cancer DNA marker #11095.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 759
ID ADL44530 standard; DNA; 433 BP.
DE Human ovarian cancer DNA marker #18420.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 760
ID ADI72056 standard; DNA; 433 BP.
DE Human ovarian cancer DNA marker #4798.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 761
ID ADL44027 standard; DNA; 434 BP.
DE Human ovarian cancer DNA marker #17917.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 762
ID ABV35678 standard; cDNA; 436 BP.
DE Human prostate expression marker cDNA 35669.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 763
ID ACN50643 standard; cDNA; 436 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-H2, SEQ:5424.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 764
ID ABV44483 standard; cDNA; 437 BP.
DE Human prostate expression marker cDNA 44474.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 765
ID ADI70485 standard; DNA; 440 BP.
DE Human ovarian cancer DNA marker #3227.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;

RESULT 766
ID ADI76810 standard; DNA; 440 BP.
DE Human ovarian cancer DNA marker #9552.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 440;
Pred. No. 2.4e-05;
RESULT 767
ID ACN49982 standard; cDNA; 441 BP.
DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F1, SEQ:4763.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 441;
Pred. No. 2.4e-05;
RESULT 768
ID ABV56410 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 56401.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 443;
Pred. No. 2.4e-05;
RESULT 769
ID ABV05431 standard; cDNA; 445 BP.
DE Human prostate expression marker cDNA 5422.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 445;
Pred. No. 2.4e-05;
RESULT 770
ID AA183049 standard; cDNA; 447 BP.
DE Human polynucleotide SEQ ID NO 3109.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 447;
Pred. No. 2.4e-05;
RESULT 771
ID ABZ08656 standard; cDNA; 450 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8647.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 450;
Pred. No. 2.4e-05;
RESULT 772
ID ACN91903 standard; DNA; 450 BP.
DE Breast cancer related marker, seq id 13053.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 11; Length 450;
Pred. No. 2.4e-05;
RESULT 773
ID AA187364 standard; cDNA; 453 BP.
DE Human polynucleotide SEQ ID NO 7424.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 453;
Pred. No. 2.4e-05;
RESULT 774
ID AA119946 standard; cDNA; 457 BP.
DE Human breast cancer expressed polynucleotide 12403.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 457;
Pred. No. 2.4e-05;
RESULT 775
ID ABV48620 standard; cDNA; 457 BP.
DE Human prostate expression marker cDNA 48611.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 457;
Pred. No. 2.4e-05;
RESULT 776
ID ABV54284 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 54275.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 459;
Pred. No. 2.4e-05;
RESULT 777
ID ADR60402 standard; cDNA; 460 BP.
DE Cotton cDNA sequence, SEQ ID 1183.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 460;
Pred. No. 2.4e-05;
RESULT 778
ID ACN61220 standard; cDNA; 460 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-033-Q1-N6-H12, SEQ:16001.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 460;
Pred. No. 2.4e-05;
RESULT 779
ID ABV34102 standard; cDNA; 462 BP.
DE Human prostate expression marker cDNA 34093.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 462;
Pred. No. 2.4e-05;
RESULT 780
ID ABV42965 standard; cDNA; 462 BP.
DE Human prostate expression marker cDNA 42956.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 462;
Pred. No. 2.4e-05;
RESULT 781
ID AA110366 standard; cDNA; 463 BP.
DE Human breast cancer expressed polynucleotide 2823.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 463;
Pred. No. 2.4e-05;
RESULT 782
ID ADL40902 standard; DNA; 463 BP.
DE Human ovarian cancer DNA marker #14792.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 463;
Pred. No. 2.4e-05;
RESULT 783
ID ACN51887 standard; cDNA; 469 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 784
ID ACN50594 standard; cDNA; 469 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-B6, SEQ:5375.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 785
ID ACN62049 standard; cDNA; 469 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 786
ID ABV14952 standard; cDNA; 472 BP.
DE Human prostate expression marker cDNA 14943.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 787
ID ABV61434 standard; cDNA; 474 BP.
DE Human prostate expression marker cDNA 61425.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 788
ID ACN51912 standard; cDNA; 477 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-E5, SEQ:6693.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 789
ID ABV7607 standard; cDNA; 478 BP.
DE Human prostate expression marker cDNA 7598.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 790
ID ACN51993 standard; cDNA; 478 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 791
ID ABV56511 standard; cDNA; 479 BP.
DE Human prostate expression marker cDNA 56502.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 792
ID ACN51787 standard; cDNA; 480 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-N6-A12, SEQ:6568.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 793
ID ACN52021 standard; cDNA; 485 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 794
ID ABV39079 standard; cDNA; 486 BP.
DE Human prostate expression marker cDNA 39070.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
RESULT 795
ID ADL43471 standard; DNA; 491 BP.
DE Human ovarian cancer DNA marker #17361.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 796
ID ABV56664 standard; cDNA; 496 BP.
DE Human prostate expression marker cDNA 56655.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 797
ID ACN62281 standard; cDNA; 496 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 798
ID ABV12935 standard; cDNA; 498 BP.
DE Human prostate expression marker cDNA 12926.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 799
ID ACN46935 standard; cDNA; 499 BP.
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 800
ID ACN58816 standard; cDNA; 499 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-012-Q6-N6-D11, SEQ:13597.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 801
ID ACN61218 standard; cDNA; 500 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-033-Q1-N6-H10, SEQ:15999.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 802
ID ABV56694 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 56685.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 803
ID ACN57794 standard; cDNA; 506 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-005-Q6-N6-H9, SEQ:12575.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 804
ID ACN61287 standard; cDNA; 512 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-035-Q1-N6-E12, SEQ:16068.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 805
ID ABV57086 standard; cDNA; 516 BP.
DE Human prostate expression marker cDNA 57077.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 1.5%; Score 53; DB 5; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 806
ID ACN61335 standard; cDNA; 517 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-036-Q1-N6-H9, SEQ:16116.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 517;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 807
ID ACN56421 standard; cDNA; 521 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-D4, SEQ:11202.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 808
ID ADL45090 standard; DNA; 522 BP.
DE Human ovarian cancer DNA marker #18980.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 809
ID ABO59079 standard; cDNA; 522 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:2774.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 1.5%; Score 53; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 810
ID ABV60707 standard; cDNA; 524 BP.
DE Human prostate expression marker cDNA 60698.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 811
ID ADL42046 standard; DNA; 524 BP.
DE Human ovarian cancer DNA marker #15936.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 812
ID ACN61425 standard; cDNA; 527 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 813
ID ACN47028 standard; cDNA; 528 BP.
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 528;
Pred. No. 2.3e-05;
RESULT 814
ID ACN53350 standard; cDNA; 528 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 528;
Pred. No. 2.3e-05;
RESULT 815
ID ADR64205 standard; cDNA; 529 BP.
DE Cotton cDNA sequence, SEQ ID 4986.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 529;
Pred. No. 2.3e-05;
RESULT 816
ID ACN46946 standard; cDNA; 529 BP.
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-E12, SEQ:1727.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 529;
Pred. No. 2.3e-05;
RESULT 817
ID ACN50477 standard; cDNA; 530 BP.
DE Cotton mature seed EST Clone ID: LIB3827-001-Q1-N6-C4, SEQ:5258.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 530;
Pred. No. 2.3e-05;
RESULT 818
ID ABV56527 standard; cDNA; 531 BP.
DE Human prostate expression marker cDNA 56518.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 531;
Pred. No. 2.3e-05;
RESULT 819
ID ADI75666 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #8408.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 531;
Pred. No. 2.3e-05;
RESULT 820
ID ADI69320 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #2062.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 531;
Pred. No. 2.3e-05;
RESULT 821
ID ACN62126 standard; cDNA; 533 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 533;
Pred. No. 2.3e-05;
RESULT 822
ID ACN58719 standard; cDNA; 534 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-011-Q6-N6-B7, SEQ:13500.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 534;
Pred. No. 2.3e-05;
RESULT 823
ID ABV03766 standard; cDNA; 535 BP.
DE Human prostate expression marker cDNA 3757.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 535;
Pred. No. 2.3e-05;
RESULT 824
ID ABV37538 standard; cDNA; 536 BP.
DE Human prostate expression marker cDNA 37529.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 536;
Pred. No. 2.3e-05;
RESULT 825
ID ACN52447 standard; cDNA; 537 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-015-Q1-N6-E10, SEQ:7228.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 537;
Pred. No. 2.3e-05;
RESULT 826
ID ACN62214 standard; cDNA; 538 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-026-Q6-N6-F2, SEQ:16995.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 100.0%; Score 53; DB 13; Length 538;
Pred. No. 2.3e-05;
RESULT 827
ID ADL43972 standard; DNA; 539 BP.
DE Human ovarian cancer DNA marker #17862.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 5; Length 539;
Pred. No. 2.3e-05;
RESULT 828
ID ACN55798 standard; cDNA; 539 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-F7, SEQ:10579.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 539;
Pred. No. 2.3e-05;
RESULT 829
ID ACN57165 standard; cDNA; 541 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-014-Q6-N6-G1, SEQ:11946.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 541;
Pred. No. 2.3e-05;
RESULT 830
ID ACN49713 standard; cDNA; 542 BP.
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-G12, SEQ:4494.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 542;
Pred. No. 2.3e-05;
RESULT 831
ID ABK11289 standard; cDNA; 545 BP.
DE Human cDNA encoding novel secreted protein from clone HMWBT59 #1.
PN WO200155207-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 545;
Pred. No. 2.3e-05;
RESULT 832
ID ADC06720 standard; cDNA; 545 BP.
DE Human TM4SF clone HMWBT59 cDNA - SEQ ID 12.
PN US2003039993-A1.
PD 27-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 545;
Pred. No. 2.3e-05;
RESULT 833
ID ABX16283 standard; cDNA; 545 BP.
DE Human cDNA encoding partial tetraspan superfamily member #2.
PN US2002151479-A1.
PD 17-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 545;
Pred. No. 2.3e-05;
RESULT 834
ID ACN58252 standard; cDNA; 546 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-N6-A9, SEQ:13033.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 546;
Pred. No. 2.3e-05;
RESULT 835
ID ACN62109 standard; cDNA; 547 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 547;
Pred. No. 2.3e-05;
RESULT 836
ID ACN45312 standard; cDNA; 552 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-C5, SEQ:93.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 552;
Pred. No. 2.3e-05;
RESULT 837
ID AAL10265 standard; cDNA; 554 BP.
DE Human breast cancer expressed polynucleotide 2722.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 554;
Pred. No. 2.3e-05;
RESULT 838
ID ACN47785 standard; cDNA; 557 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:2566.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 557;
Pred. No. 2.3e-05;
RESULT 839
ID ACN47210 standard; cDNA; 557 BP.
DE Cotton primed seed EST Clone ID: LIB3825-008-Q1-N6-D6, SEQ:1991.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 557;
Pred. No. 2.3e-05;
RESULT 840
ID ABT08060 standard; cDNA; 558 BP.
DE Human breast specific coding sequence SEQ ID NO: 6.
PN WO200266607-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 558;
Pred. No. 2.3e-05;
RESULT 841
ID ACN56272 standard; cDNA; 561 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E6, SEQ:11053.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 561;
Pred. No. 2.3e-05;
RESULT 842
ID ACN47476 standard; cDNA; 563 BP.
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-E7, SEQ:2257.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 563;
Pred. No. 2.3e-05;

RESULT 843
ID ACN56344 standard; cDNA; 565 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:111125.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 844
ID ACN45417 standard; cDNA; 565 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-G5, SEQ:198.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 845
ID ABV57082 standard; cDNA; 567 BP.
DE Human prostate expression marker cDNA 57073.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 846
ID ACN53005 standard; cDNA; 569 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-N6-E7, SEQ:7786.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 847
ID ADI73065 standard; DNA; 570 BP.
DE Human ovarian cancer DNA marker #5807.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 848
ID ADL38200 standard; DNA; 570 BP.
DE Human ovarian cancer DNA marker #12090.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 849
ID ACN52610 standard; cDNA; 574 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 850
ID ACN56366 standard; cDNA; 574 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-D1, SEQ:111147.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 851
ID ACN45381 standard; cDNA; 577 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-C7, SEQ:162.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 577;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 852
ID ACN53147 standard; cDNA; 578 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-E3, SEQ:7928.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 578;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 853
ID ACN51300 standard; cDNA; 593 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 854
ID ACN52339 standard; cDNA; 593 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F10, SEQ:7120.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 53; DB 13; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 855
ID AAH71472 standard; cDNA; 597 BP.
DE Human cervical cancer marker nucleic acid 2746.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 856
ID ACN88304 standard; DNA; 597 BP.
DE Breast cancer related marker, seq id 9454.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 11; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 857
ID AAH71474 standard; cDNA; 612 BP.
DE Human cervical cancer marker nucleic acid 2748.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 612;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 858
ID AAH71551 standard; cDNA; 621 BP.
DE Human cervical cancer marker nucleic acid 2825.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 859
ID ABV12980 standard; cDNA; 629 BP.
DE Human prostate expression marker cDNA 12971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 629;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 860
ID ADI72791 standard; DNA; 638 BP.
DE Human ovarian cancer DNA marker #5533.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 861
ID ADI37930 standard; DNA; 638 BP.
DE Human ovarian cancer DNA marker #11820.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 862
ID AAL23651 standard; cDNA; 644 BP.
DE Human breast cancer expressed polynucleotide 16108.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
RESULT 863
ID AAL14804 standard; cDNA; 693 BP.
DE Human breast cancer expressed polynucleotide 7261.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 864
ID ABQ65666 standard; DNA; 704 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 243.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.

Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 704;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 865
ID ADI72280 standard; DNA; 705 BP.
DE Human ovarian cancer DNA marker #5022.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 866
ID ADI37424 standard; DNA; 705 BP.
DE Human ovarian cancer DNA marker #11314.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 705;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 867
ID AAL24889 standard; cDNA; 722 BP.
DE Human breast cancer expressed polynucleotide 17346.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 868
ID ADI71984 standard; DNA; 723 BP.
DE Human ovarian cancer DNA marker #4726.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 869
ID ADI37134 standard; DNA; 723 BP.
DE Human ovarian cancer DNA marker #11024.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 5; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 870
ID AAL25251 standard; cDNA; 731 BP.
DE Human breast cancer expressed polynucleotide 17708.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 731;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 871
ID ABI90099 standard; cDNA; 735 BP.
DE Human polynucleotide SEQ ID NO 661.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 735;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 872
ID AAC78154 standard; cDNA; 736 BP.
DE Human cancer associated gene sequence SEQ ID NO:548.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 873
ID AAL24897 standard; cDNA; 739 BP.
DE Human breast cancer expressed polynucleotide 17354.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 739;

Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 874
ID ADL44766 standard; DNA; 752 BP.
DE Human ovarian cancer DNA marker #18656.
PN WO200170979-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 752;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 875
ID ADL43864 standard; DNA; 755 BP.
DE Human ovarian cancer DNA marker #17754.
PN WO200170979-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 755;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
RESULT 876
ID AAH71500 standard; cDNA; 764 BP.
DE Human cervical cancer marker nucleic acid 2774.
PN WO200142467-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 764;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 877
ID AAX27402 standard; DNA; 826 BP.
DE Human secreted protein gene 92 clone HLYAF80.
PN WO9902546-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 2; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 878
ID ADAJ9947 standard; cDNA; 826 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 8; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 879
ID ADA07281 standard; cDNA; 826 BP.
DE Human cDNA from secreted protein gene 92.
PN US2003064412-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match 1.5%; Score 53; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 880
ID ADD37625 standard; cDNA; 826 BP.
DE Human secreted protein encoding sequence #107.
PN WO200290526-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 881
ID ADA56135 standard; DNA; 826 BP.
DE Gene encoding human secreted protein #314.
PN WO2002102994-A2.

PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 882
ID ADN40950 standard; cDNA; 826 BP.
DE Novel human secreted protein cDNA seqid 72.
PN US2004044191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 1.5%; Score 53; DB 12; Length 826;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 883
ID ABV14600 standard; cDNA; 830 BP.
DE Human prostate expression marker cDNA 14591.
PN WO200160860-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 5; Length 830;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 884
ID ABV83628 standard; cDNA; 844 BP.
DE Human breast specific gene SEQ ID NO 71.
PN WO200286605-A2.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 53; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 885
ID AAL19845 standard; cDNA; 852 BP.
DE Human breast cancer expressed polynucleotide 12302.
PN WO200151628-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 53; DB 4; Length 852;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 886
ID ABT22217 standard; DNA; 857 BP.
DE Breast cancer marker gene SEQ ID NO 590.
PN WO200285298-A2.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 10; Length 857;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 887
ID ACN84830 standard; DNA; 874 BP.
DE Breast cancer related marker, seq id 5980.
PN US200309974-A1.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 11; Length 874;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 888
ID AAA87690 standard; cDNA; 892 BP.
DE Human secreted protein gene 25 SEQ ID NO:35.
PN WO200043495-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 3; Length 892;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 889

ID ABV83635 standard; cDNA; 895 BP.
DE Human breast specific gene SEQ ID NO 78.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 53; DB 6; Length 895;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 890
ID AAH33168 standard; cDNA; 896 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:224.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 2e-05;
RESULT 891
ID ACN80464 standard; DNA; 933 BP.
DE Breast cancer related marker, seq id 1614.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 11; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 892
ID ABV83640 standard; cDNA; 954 BP.
DE Human breast specific gene SEQ ID NO 83.
PN WO200266605-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 53; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 893
ID AA252527 standard; cDNA; 1034 BP.
DE Human secreted protein clone ya66_1 nucleotide sequence SEQ ID NO:105.
PN WO958642-A2.
PD 18-NOV-1999.
PA (GENY-) GENETICS INST INC.
Query Match 1.5%; Score 53; DB 3; Length 1034;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 894
ID AAA26358 standard; cDNA; 1052 BP.
DE Human secreted protein gene 13 SEQ ID NO:23.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 3; Length 1052;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 895
ID ADC73847 standard; DNA; 1052 BP.
DE Human secreted protein-related DNA - SEQ ID 480.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 1052;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 896
ID ADD37736 standard; cDNA; 1052 BP.
DE Human secreted protein encoding sequence #218.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 1052;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 897
ID ADA56496 standard; DNA; 1052 BP.
DE Gene encoding human secreted protein #172.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 1052;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
ID ADL71419 standard; cDNA; 1052 BP.

DE Novel human secreted protein cDNA seqid 23.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.5%; Score 53; DB 12; Length 1052;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
RESULT 899
ID ABT08073 standard; cDNA; 1074 BP.
DE Human breast specific coding sequence SEQ ID NO: 19.
PN WO200266607-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.5%; Score 53; DB 6; Length 1074;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 900
ID ADR60456 standard; cDNA; 1083 BP.
DE Cotton cDNA sequence, SEQ ID 1237.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 1.5%; Score 53; DB 13; Length 1083;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 901
ID AAS72542 standard; cDNA; 1087 BP.
DE DNA encoding novel human diagnostic protein #8346.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 53; DB 5; Length 1087;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 902
ID AAS26600 standard; cDNA; 1095 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 779.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 4; Length 1095;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 903
ID ABX73941 standard; DNA; 1095 BP.
DE Human novel polynucleotide #769.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.5%; Score 53; DB 8; Length 1095;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 904
ID AAS26184 standard; cDNA; 1096 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 363.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 4; Length 1096;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 905
ID ABX73525 standard; DNA; 1096 BP.
DE Human novel polynucleotide #353.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match 1.5%; Score 53; DB 8; Length 1096;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 906
ID ABO54863 standard; cDNA; 1145 BP.
DE Human ovarian antigen HVCAA65 cDNA, SEQ ID NO:743.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 6; Length 1145;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 907
ID ADO25557 standard; DNA; 1185 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8377.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 12; Length 1185;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 908
ID AAX25130 standard; cDNA; 1223 BP.
DE Soybean isoflavone reductase cDNA clone seq3.pk0034.g5.
PN WO9914351-A1.
PD 25-MAR-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 53; DB 2; Length 1223;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 909
ID AAX38425 standard; cDNA; 1223 BP.
DE Soybean isoflavone reductase cDNA clone seq3.pk0034.g5.
PN US6054636-A.
PD 25-APR-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 53; DB 3; Length 1223;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 910
ID ADJ32833 standard; cDNA; 1223 BP.
DE Soybean isoflavone reductase cDNA.
PN US6817493-B1.
PD 09-SEP-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.5%; Score 53; DB 10; Length 1223;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
RESULT 911
ID AAH49320 standard; cDNA; 1300 BP.
DE V. vinifera aquaporin PIP2-1 cDNA.
PN WO200166793-A2.
PD 13-SEP-2001.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 1.5%; Score 53; DB 5; Length 1300;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 912
ID AAC85035 standard; DNA; 1355 BP.
DE Soybean HES1 homologue DNA sequence (clone ID 701010572CPR9854).
PN WO200104314-A2.
PD 18-JAN-2001.
PA (PHAA) PHARMACIA CORP.
Query Match 1.5%; Score 53; DB 5; Length 1355;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 913
ID AAS00834 standard; cDNA; 1369 BP.
DE Human cDNA clone HOFMU69 encoding cancer related protein 8.
PN WO200118014-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 5; Length 1369;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 914
ID ADO26094 standard; DNA; 1371 BP.
DE Cotton lDox polynucleotide seqid 132.
PN WO2004046336-A2.
PD 03-JUN-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 1.5%; Score 53; DB 12; Length 1371;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 915
ID AAX04325 standard; DNA; 1376 BP.
DE Human secreted protein gene 15 clone HSD504.
PN WO9856804-A1.
PD 17-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 2; Length 1376;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 916
ID ABO54525 standard; cDNA; 1442 BP.
DE Human ovarian antigen HOFMU69 cDNA, SEQ ID NO:405.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 6; Length 1442;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 917
ID AAC82696 standard; cDNA; 1445 BP.
DE Murine variant Zalpha32 cDNA.
PN WO200071717-A1.
PD 30-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.5%; Score 53; DB 4; Length 1445;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 918
ID ADG42426 standard; cDNA; 1445 BP.
DE Mouse cDNA encoding variant Zalpha-32.
PN US2003207793-A1.
PD 06-NOV-2003.
PA (CONK/) CONKLIN D C.
PA (GAOZ/) GAO Z.
Query Match 1.5%; Score 53; DB 12; Length 1445;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 919
ID AAS41436 standard; cDNA; 1516 BP.
DE cDNA encoding novel human enzyme polypeptide #652.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 4; Length 1516;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 920
ID ADO05149 standard; DNA; 1550 BP.
DE Citrus X paradisi epsilon cyclase homologue H5 DNA.
PN WO2004027869-A1.
PD 01-APR-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 1.5%; Score 53; DB 12; Length 1550;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
RESULT 921
ID AAT28255 standard; cDNA; 1558 BP.
DE Survival motor neuron gene, clone T-BCD541.
PN EP708178-A1.
PD 24-APR-1996.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 1.5%; Score 53; DB 2; Length 1558;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
RESULT 922
ID AAT18828 standard; cDNA; 1560 BP.
DE Human survival motor neuron gene cDNA clone T-BCD541.
PN EP711833-A2.
PD 15-MAY-1996.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 1.5%; Score 53; DB 2; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
RESULT 923
ID AAT18831 standard; cDNA; 1582 BP.
DE Human survival motor neuron variant gene cDNA clone C-BCD541.
PN EP711833-A2.
PD 15-MAY-1996.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 1.5%; Score 53; DB 2; Length 1582;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 924
 ID AAT28259 standard; cDNA; 1582 BP.
 DE Survival motor neuron gene, clone C-BCD541.
 PN EP708178-A1.
 PD 24-APR-1996.
 PA (INRM) INSERM NAT SANTE & RECH MEDICALE.
 Query Match 1.5%; Score 53; DB 2; Length 1582;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 925
 ID ADI43284 standard; DNA; 1585 BP.
 DE Plant transcription factor polynucleotide #1178.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER) SHERMAN B K.
 PA (RIEC) RIECHMANN J L.
 PA (JIAN) JIANG C.
 PA (HEAR) HEARD J E.
 PA (HAAR) HAAKE V.
 PA (CREE) CREELMAN R A.
 PA (RATC) RATCLIFFE O.
 PA (ADAM) ADAM L J.
 PA (REUB) REUBER T L.
 PA (KEDD) KEDDIE J.
 PA (BROU) BROUN P E.
 PA (PILG) PILGRIM M L.
 PA (DUBE) DUBELL A N.
 PA (PINE) PINEDA O.
 PA (YUGG) YU G.
 Query Match 1.5%; Score 53; DB 12; Length 1585;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 926
 ID ADE55267 standard; DNA; 1589 BP.
 DE Human gene AL137271, SEQ ID NO 1081.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 927
 ID ADE55264 standard; DNA; 1589 BP.
 DE Human gene AL137271, SEQ ID NO 1078.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 928
 ID ADE58406 standard; DNA; 1591 BP.
 DE Toxicity-related gene, SEQ ID 3432.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 1.5%; Score 53; DB 10; Length 1591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 929
 ID ADE52986 standard; DNA; 1591 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3528.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 1.5%; Score 53; DB 10; Length 1591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 930
 ID ABR42053 standard; DNA; 1591 BP.
 DE Toxicity modelling related rat gene SEQ ID No 1755.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 1.5%; Score 53; DB 10; Length 1591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;

RESULT 931
 ID AAV33190 standard; cDNA; 1694 BP.
 DE Secreted protein BD380_1 cDNA.
 PN WO9838209-A2.
 PD 03-SEP-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 2; Length 1694;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 932
 ID AA252500 standard; cDNA; 1707 BP.
 DE Human secreted protein clone yb124_1 nucleotide sequence SEQ ID NO:51.
 PN WO9958642-A2.
 PD 18-NOV-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 3; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 933
 ID AAA27151 standard; cDNA; 1763 BP.
 DE Human p52 cDNA.
 PN WO200029578-A1.
 PD 25-MAY-2000.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 1.5%; Score 53; DB 3; Length 1763;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 934
 ID AA200457 standard; cDNA; 1772 BP.
 DE Human secreted protein cDNA encoding gene 48.
 PN WO9938881-A1.
 PD 05-AUG-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 53; DB 2; Length 1772;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 935
 ID AAA16649 standard; cDNA; 1812 BP.
 DE Human secreted protein clone pw460_5 nucleotide sequence SEQ ID NO:63.
 PN WO200009552-A1.
 PD 24-FEB-2000.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 53; DB 3; Length 1812;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 936
 ID ADQ24551 standard; DNA; 1816 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7371.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 1.5%; Score 53; DB 12; Length 1816;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 937
 ID ABR88010 standard; cDNA; 1827 BP.
 DE cDNA encoding human 83378 metal transporter protein.
 PN WO200240656-A2.
 PD 23-MAY-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.5%; Score 53; DB 6; Length 1827;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 938
 ID AAF21914 standard; DNA; 1882 BP.
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 301.
 PN WO200055173-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 53; DB 3; Length 1882;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 RESULT 939
 ID ADM47920 standard; DNA; 1882 BP.
 DE Polynucleotide sequence #338 useful in producing transgenic plants.
 PN US2003233670-A1.
 PD 18-DEC-2003.
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.
 Query Match 1.5%; Score 53; DB 12; Length 1882;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
RESULT 940
ID ABA06572 standard; cDNA; 1926 BP.
DE Human cDNA SEQ ID NO: 238.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 4; Length 1926;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 941
ID ABV83909 standard; cDNA; 1926 BP.
DE Human polynucleotide SEQ ID NO 238.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 1926;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 942
ID ABL90817 standard; cDNA; 1975 BP.
DE Human polynucleotide SEQ ID NO 1379.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 1975;
RESULT 943
ID AAX27383 standard; DNA; 1977 BP.
DE Human secreted protein gene 73 clone HCUPZ62.
PN WO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 2; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 944
ID ADA07262 standard; cDNA; 1977 BP.
DE Human cDNA from secreted protein gene 73.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHI/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R. A.
PA (BREW/) BREWER L A.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 945
ID ADNA1003 standard; cDNA; 1977 BP.
DE Novel human secreted protein cDNA seqid 125.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHI/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R. A.
PA (BIRS/) BIRSE C E.

Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 946
ID AD062413 standard; DNA; 2039 BP.
DE Transcription factor G916 orthologous sequence, SEQ ID 880.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDE-) MENDEL BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 2039;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 947
ID ABL90496 standard; cDNA; 2062 BP.
DE Human polynucleotide SEQ ID NO 1058.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 6; Length 2062;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 948
ID ADQ23447 standard; DNA; 2087 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6267.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 2087;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 949
ID AAA26375 standard; cDNA; 2103 BP.
DE Human secreted protein gene 30 SEQ ID NO:40.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 3; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 950
ID ADA39984 standard; cDNA; 2103 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 951
ID ACC50546 standard; cDNA; 2103 BP.
DE Human secreted protein coding sequence, SEQ ID 213.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 952
ID ABZ71300 standard; cDNA; 2103 BP.
DE Secreted protein-encoding gene 111 cDNA clone HNFPC43, SEQ ID NO:121.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 953
ID ADB91216 standard; cDNA; 2103 BP.
DE Human secreted protein cDNA #SEQ ID 162.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 954
ID ADC73608 standard; DNA; 2103 BP.
DE Human secreted protein-related DNA - SEQ ID 241.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 2103;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 955
ID ADA56173 standard; DNA; 2103 BP.
DE Gene encoding human secreted protein #352.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 10; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 956
ID ADL71436 standard; cDNA; 2103 BP.
DE Novel human secreted protein cDNA seqid 40.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KONA/) KOMATSOULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 1.5%; Score 53; DB 12; Length 2103;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 957
ID ADQ24823 standard; DNA; 2178 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7643.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.5%; Score 53; DB 12; Length 2178;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 958
ID ADP54455 standard; cDNA; 2222 BP.
DE Human PRO cDNA sequence SEQ ID NO:431.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 13; Length 2222;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 959
ID AAA47455 standard; cDNA; 2272 BP.
DE Human TANGO 197 coding sequence.
PN WO20039284-A1.
PD 06-JUL-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 3; Length 2272;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 960
ID ADI00533 standard; cDNA; 2272 BP.
DE Human TANGO 197 cDNA.
PN US2003144193-A1.
PD 31-JUL-2003.
PA (ROTT/) ROTTMAN J B.
PA (ORKE/) O'KEEFE T L.
PA (OZKA/) OZKAYNAK E.
PA (HEAL/) HEALEY J J.
Query Match 1.5%; Score 53; DB 10; Length 2272;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 961
ID ADM64567 standard; cDNA; 2272 BP.
DE Human von Willebrand factor A-like domain protein TANGO197 cDNA.
PN US2003134786-A1.
PD 17-JUL-2003.
PA (ROTT/) ROTTMAN J B.
PA (ORKE/) O'KEEFE T L.
PA (OZKA/) OZKAYNAK E.
PA (HEAL/) HEALEY J J.
Query Match 1.5%; Score 53; DB 11; Length 2272;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 962
ID AAC77021 standard; cDNA; 2273 BP.
DE Human ORFX ORF2576 polynucleotide sequence SEQ ID NO:5151.

PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 1.5%; Score 53; DB 3; Length 2273;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 963
ID ABL90769 standard; cDNA; 2317 BP.
DE Human polynucleotide SEQ ID NO 1331.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 6; Length 2317;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 964
ID ADO25966 standard; DNA; 2330 BP.
DE Corn chalcone synthase (CHS) polynucleotide seqid 4.
PN WO2004046336-A2.
PD 03-JUN-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 1.5%; Score 53; DB 12; Length 2330;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 965
ID ACH88807 standard; DNA; 2353 BP.
DE Breast cancer related marker, seq id 9957.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 53; DB 11; Length 2353;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
RESULT 966
ID ADF82123 standard; DNA; 2384 BP.
DE Leukaemia-related DNA sequence #2679.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYIU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 1.5%; Score 53; DB 10; Length 2384;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 967
ID ADF82124 standard; DNA; 2384 BP.
DE Leukaemia-related DNA sequence #2680.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYIU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 1.5%; Score 53; DB 10; Length 2384;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 968
ID AAC98119 standard; cDNA; 2461 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:129.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 3; Length 2461;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 969
ID AAH33223 standard; cDNA; 2461 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:279.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 53; DB 4; Length 2461;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 970
ID AAA27988 standard; cDNA; 2498 BP.
DE Wheat CCR4 transcription factor nucleotide sequence #1.
PN WO200032783-A1.

PD 08-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.5%; Score 53; DB 3; Length 2498;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 971
 ID ABS57567 standard; cDNA; 2619 BP.
 DE Human SECP-23 cDNA from clone 7503641CD1 SEQ ID 23.
 PN WO200279441-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.5%; Score 53; DB 8; Length 2619;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 972
 ID AAH33733 standard; cDNA; 2630 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:789.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUNA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 53; DB 4; Length 2630;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 973
 ID ACF34468 standard; DNA; 2712 BP.
 DE Gene encoding angiotensin protein BNO67.
 PN WO2003027285-A1.
 PD 03-APR-2003.
 PA (BION-) BIONOMICS LTD.
 Query Match 1.5%; Score 53; DB 8; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 974
 ID ABV75070 standard; DNA; 2712 BP.
 DE Human Dev20 homologue protein encoding DNA.
 PN WO200279238-A2.
 PD 10-OCT-2002.
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 Query Match 1.5%; Score 53; DB 8; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 975
 ID ADF81962 standard; DNA; 2712 BP.
 DE Leukaemia-related DNA sequence #2518.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAPE/) HAPERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match 1.5%; Score 53; DB 10; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 976
 ID ADO20179 standard; cDNA; 2712 BP.
 DE Human PRO polynucleotide #544.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.5%; Score 53; DB 12; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 977
 ID ADP55359 standard; cDNA; 2712 BP.
 DE Human PRO cDNA sequence SEQ ID NO:1335.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.5%; Score 53; DB 13; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 978
 ID ADP25232 standard; cDNA; 2712 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:2410.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.5%; Score 53; DB 13; Length 2712;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 979

ID AAD15455 standard; cDNA; 2838 BP.
 DE Human 26583 serine/threonine phosphatase cDNA.
 PN WO200166765-A2.
 PD 13-SEP-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.5%; Score 53; DB 4; Length 2838;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 980
 ID ADE38448 standard; DNA; 2838 BP.
 DE Human protein 26583 gene sequence.
 PN WO2003065006-A2.
 PD 07-AUG-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.5%; Score 53; DB 10; Length 2838;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 981
 ID ADD45824 standard; DNA; 2857 BP.
 DE Human gene AL050155, SEQ ID NO 11493.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 2857;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 982
 ID ADE60246 standard; DNA; 2857 BP.
 DE Human gene AL050155, SEQ ID NO 6152.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 2857;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 983
 ID ADE60248 standard; DNA; 2857 BP.
 DE Human gene AL050155, SEQ ID NO 6154.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 2857;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 984
 ID ADE60252 standard; DNA; 2857 BP.
 DE Human gene AL050155, SEQ ID NO 6158.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 2857;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 985
 ID ADE60250 standard; DNA; 2857 BP.
 DE Human gene AL050155, SEQ ID NO 6156.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 1.5%; Score 53; DB 10; Length 2857;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 RESULT 986
 ID AAC61886 standard; cDNA; 3030 BP.
 DE cDNA encoding a human secreted protein.
 PN WO200061755-A2.
 PD 19-OCT-2000.
 PA (CHIR) CHIRON CORP.
 Query Match 1.5%; Score 53; DB 3; Length 3030;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 987
 ID ADI42179 standard; DNA; 3118 BP.
 DE Plant transcription factor polynucleotide #364.
 PN US2004019927-A1.
 PD 29-JAN-2004.

PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIANG/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAR/) HAAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 988
 ID ADO02686 standard; cDNA; 3118 BP.
 DE Soybean orthologue of Thalecress transcription factor, cDNA #69.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMAHA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 989
 ID ADO62303 standard; DNA; 3118 BP.
 DE Transcription factor G438 orthologous sequence, SEQ ID 770.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 12; Length 3118;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 990
 ID AAS21262 standard; cDNA; 3501 BP.
 DE Human cDNA sequence encoding for PRO4985 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 4; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 991
 ID ACAD3621 standard; cDNA; 3501 BP.
 DE cDNA encoding human PRO polypeptide #19.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 992
 ID ABX89159 standard; cDNA; 3501 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO4985.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 993
 ID ACD41813 standard; cDNA; 3501 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #19.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 994
 ID ACA04042 standard; cDNA; 3501 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 37.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 8; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 995
 ID ADA45556 standard; cDNA; 3501 BP.
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.
 PN US200302328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 996
 ID ADA75987 standard; cDNA; 3501 BP.
 DE Human PRO polynucleotide #19.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 997
 ID ADA18637 standard; cDNA; 3501 BP.
 DE Human PRO polynucleotide #19.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 998
 ID ADA61260 standard; cDNA; 3501 BP.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 999
 ID ADB19045 standard; cDNA; 3501 BP.
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 1000
 ID ADB27586 standard; cDNA; 3501 BP.
 DE cDNA encoding human PRO polypeptide #19.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 RESULT 1001
 ID ADA86065 standard; cDNA; 3501 BP.
 DE Novel human secreted and transmembrane protein PRO4985 cDNA.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

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RESULT 1002
ID ADB15629 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1003
ID ADA47415 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1004
ID ADA67210 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1005
ID ADB30217 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1006
ID ADA95513 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1007
ID ADA96725 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1008
ID ADA79029 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1009
ID ADA87168 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1010
ID ADB16370 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1011
ID ADA81920 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1012
ID ADB14525 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1013
ID ADB18486 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1014
ID ADA93701 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1015
ID ADB19597 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1016
ID ADB12909 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1017
ID ACD98442 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1018
ID ADA74163 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1019
ID ADB24396 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
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DE Human PRO polynucleotide #19.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1021
ID ADA74883 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1022
ID ADA84961 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1023
ID ADA84409 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1024
ID ADB29665 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1025
ID ADA80193 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1026
ID ADA75435 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1027
ID ADA46660 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1028
ID ADB24956 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1029
ID ADA93132 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.

PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1030
ID ADB26482 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1031
ID ADB30769 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1032
ID ADA60697 standard; cDNA; 3501 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1033
ID ADB23844 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1034
ID ADA96173 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1035
ID ADA80745 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1036
ID ADA95621 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1037
ID ADB25930 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; DB 9; Length 3501;
Score 53; Pred. No. 1.3e-05;
RESULT 1038
ID ADB21415 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082765-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1039
ID ADA77194 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1040
ID ADB17934 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1041
ID ADA86617 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1042
ID ADA87720 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1043
ID ADA46108 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1044
ID ADB28138 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1045
ID ADB28690 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1046
ID ADA76642 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1047
ID ADA88272 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1048
ID ADA97277 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1049
ID ADB27034 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1050
ID ADB21967 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1051
ID ADA66658 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1052
ID ADB22519 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1053
ID ADB23292 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1054
ID ADA92014 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1055
ID ADB15077 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1056
ID ADB38329 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 9; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;

RESULT 1057
ID ADB37777 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 9; Length 3501;
RESULT 1058
ID ADB66249 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1059
ID ADB93329 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1060
ID ADB90061 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1061
ID ADB39162 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1062
ID ADB46785 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1063
ID ADB86392 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1064
ID ADB76997 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1065
ID ADB34154 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1066
ID ADB35258 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1067
ID ADB33602 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1068
ID ADB34706 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1069
ID ADB35810 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide SEQ ID NO 37.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1070
ID ADB46205 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1071
ID ADC50078 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1072
ID ADC71625 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1073
ID ADC59604 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1074
ID ADC52611 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 53; DB 10; Length 3501;
RESULT 1075
ID ADC56965 standard; cDNA; 3501 BP.

DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1076
ID ADC60156 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1077
ID ADC50631 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1078
ID ADC65158 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1079
ID ADC54256 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1080
ID ADC53217 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1081
ID ADC58740 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1082
ID ADC55618 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1083
ID ADC58188 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID37.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1084
ID ADD02862 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.

PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1085
ID ADC89854 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1086
ID ADC69273 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1087
ID ADC48162 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1088
ID ADD09691 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1089
ID ADD04266 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1090
ID ADC80222 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1091
ID ADD10729 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1092
ID ADC47610 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1093
ID ADC79670 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087358-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1094
ID ADD091139 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1095
ID ADD40852 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1096
ID ADD51991 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1097
ID ADD52731 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1098
ID ADD53283 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1099
ID ADD51439 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1100
ID ADD02238 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1101
ID ADD01672 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1102
ID ADD53854 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1103
ID ADD92171 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1104
ID ADD91067 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1105
ID ADE03681 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1106
ID ADE31978 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1107
ID ADE21910 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1108
ID ADD79134 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1109
ID ADE41670 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1110
ID ADE17487 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1111
ID ADD91619 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1112
ID ADE33082 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1113
ID ADE33634 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1114
ID ADD79686 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1115
ID ADD92723 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1116
ID ADE19143 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1117
ID ADE18591 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1118
ID ADE42787 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1119
ID ADD95576 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1120
ID ADE22462 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1121
ID ADD78580 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1122
ID ADE32530 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1123
ID ADE42222 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1124
ID ADD80238 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1125
ID ADD89266 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1126
ID ADE40550 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1127
ID ADE04349 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1128
ID ADE32478 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1129
ID ADG21187 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 3501;
RESULT 1130
ID ADE22462 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1121
ID ADD78580 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1122
ID ADE32530 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1123
ID ADE42222 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1124
ID ADD80238 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1125
ID ADD89266 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1126
ID ADE40550 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1127
ID ADE04349 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1128
ID ADE32478 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1129
ID ADG21187 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1130
ID ADE22462 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

RESULT 1130
ID ADG2828 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1131
ID ADG97163 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1132
ID ADG80227 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1133
ID ADG79675 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1134
ID ADH54967 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1135
ID ADH55519 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1136
ID ADI63738 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1137
ID ADI64687 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1138
ID ADI63186 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1139

ID ADH81600 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1140
ID ADH81048 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1141
ID ACD23871 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1142
ID ACA67012 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 10; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1143
ID ADM82217 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 11; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1144
ID ADN15616 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 11; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1145
ID ADN16245 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 11; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1146
ID ADN15064 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 11; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1147
ID ADN14512 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 11; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1148
ID ADC80774 standard; cDNA; 3501 BP.

DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1149
ID ADD76222 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1150
ID ADD87586 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1151
ID ADD85990 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1152
ID ADE75438 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1153
ID ADE23014 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1154
ID ADE23566 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1155
ID ADE24209 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1156
ID ADD87034 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1157
ID ADE88900 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.

PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1158
ID ADE18039 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1159
ID ADE88348 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1160
ID ADE94368 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1161
ID ADE90779 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1162
ID ADE94920 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1163
ID ADE93030 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1164
ID ADF34611 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1165
ID ADE91926 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1166
ID ADE90227 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003199063-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1167
ID ADE91374 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1168
ID ADG01953 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1169
ID ADG21739 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1170
ID ADG19809 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1171
ID ADF97715 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1172
ID ADG23932 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1173
ID ADF98286 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1174
ID ADG03117 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1175
ID ADF98838 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207353-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1176
ID ADG16423 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1177
ID ADG04882 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1178
ID ADG19149 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1179
ID ADG12986 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1180
ID ADG08043 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1181
ID ADG15213 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1182
ID ADF96611 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1183
ID ADG05796 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1184
ID ADG23380 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1194
ID ADG56570 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1195
ID ADG55466 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1196
ID ADG58226 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1197
ID ADG70592 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1198
ID ADG57674 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1199
ID ADG53258 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1200
ID ADG71144 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1201
ID ADG61331 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1202
ID ADH30293 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1203

ID ADH11660 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1204
ID ADG52082 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1205
ID ADG53810 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1206
ID ADG80779 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1207
ID ADG56018 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1208
ID ADH12284 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1209
ID ADG61130 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1210
ID ADH28217 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1211
ID ADG54362 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1212
ID ADG59402 standard; cDNA; 3501 BP.

DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1213
ID ADI80826 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1214
ID ADG09569 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1215
ID ADI15040 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1216
ID ADG08917 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1217
ID ADI14372 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1218
ID ADI17967 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1219
ID ADJ63248 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1220
ID ADJ77143 standard; cDNA; 3501 BP.
DE Human PRO polynucleotide #19.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 53; DB 12; Length 3501;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
RESULT 1221
ID ADJ65265 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.

PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1222
ID ADM27401 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1223
ID ADM42125 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1224
ID ADM27987 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3501;
RESULT 1225
ID ADI95469 standard; cDNA; 3501 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 3501;
RESULT 1226
ID ADI96021 standard; cDNA; 3501 BP.
DE Novel human secreted and transmembrane protein PRO4985 cDNA.
PN US200307354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 3501;
RESULT 1227
ID AAQ44391 standard; cDNA to mRNA; 3581 BP.
DE Sequence of murine OSF-4 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FAB) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 1.5%; Score 53; DB 2; Length 3581;
RESULT 1228
ID ADQ23054 standard; DNA; 3650 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5874.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 12; Length 3650;
RESULT 1229
ID ADP54957 standard; cDNA; 4090 BP.
DE Human PRO cDNA sequence SEQ ID NO:933.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 4090;
RESULT 1230
ID ADS88644 standard; cDNA; 4090 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:187.
PN WO2004035785-A1.

PD 29-APR-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match
Best Local Similarity 1.5%; Score 53; DB 13; Length 4090;
RESULT 1231
ID ADL06652 standard; cDNA; 4557 BP.
DE Human 3T3 cell conversion promoter PP13850 cDNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 4557;
RESULT 1232
ID ADL06654 standard; DNA; 4557 BP.
DE Human 3T3 cell conversion promoter PP13850 DNA.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 4557;
RESULT 1233
ID ADL15662 standard; DNA; 4816 BP.
DE Human structural and cytoskeleton-associated protein (SCAP) gene #10.
PN WO2003062391-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 1.5%; Score 53; DB 10; Length 4816;
RESULT 1234
ID ABZ26080 standard; DNA; 40116 BP.
DE Mouse DNaseX encoding genomic DNA SEQ ID NO 7.
PN EP1249495-A1.
PD 16-OCT-2002.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
Query Match
Best Local Similarity 1.5%; Score 53; DB 8; Length 40116;
RESULT 1235
ID AAZ23902 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 4.
PN WO950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Query Match
Best Local Similarity 1.5%; Score 53; DB 2; Length 49999;
RESULT 1236
ID ABK55207 standard; cDNA; 56 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 677.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 56;
RESULT 1237
ID ADT94789 standard; cDNA; 68 BP.
DE Colon cancer associated human cDNA sequence #308.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.5%; Score 52; DB 11; Length 68;
RESULT 1238
ID ABK54873 standard; cDNA; 72 BP.
DE Human colon cancer-associated cDNA, SEQ ID NO 343.
PN WO200212280-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 72;
RESULT 1239
ID ACN50126 standard; cDNA; 142 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-E5, SEQ:4907.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
RESULT 1240
ID ADT94954 standard; cDNA; 146 BP.
DE Colon cancer associated human cDNA sequence #473.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 52; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
RESULT 1241
ID ADF57474 standard; cDNA; 153 BP.
DE Urogenital sinus-derived expressed sequence tag, SEQ ID No 793.
PN WO958665-A2.
PD 18-NOV-1999.
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
Query Match 1.5%; Score 52; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
RESULT 1242
ID ABX46255 standard; cDNA; 165 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11420.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 52; DB 8; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
RESULT 1243
ID ADL45094 standard; DNA; 193 BP.
DE Human ovarian cancer DNA marker #18984.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
RESULT 1244
ID ABX45180 standard; cDNA; 210 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10345.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 52; DB 8; Length 210;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
RESULT 1245
ID ABX60856 standard; DNA; 215 BP.
DE Arabidopsis thaliana polynucleotide #202.
PN US2002142319-A1.
PD 03-OCT-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (HARG/) HARGISS T R.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
Query Match 1.5%; Score 52; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
RESULT 1246

ID AHH69412 standard; cDNA; 226 BP.
DE Human cervical cancer marker nucleic acid 686.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 4; Length 226;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
RESULT 1247
ID ABX54617 standard; cDNA; 229 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4546.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 52; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
RESULT 1248
ID AAD05356 standard; cDNA; 233 BP.
DE Human secreted protein-encoding gene 14 cDNA clone HCRNO87, SEQ ID NO:67.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
RESULT 1249
ID ABX46273 standard; cDNA; 239 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11438.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 52; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
RESULT 1250
ID ACN45492 standard; cDNA; 256 BP.
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-K6-G3, SEQ:273.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
RESULT 1251
ID ADK61479 standard; DNA; 260 BP.
DE Ovarian cancer-related DNA #634 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 1.5%; Score 52; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
RESULT 1252
ID ABV56597 standard; cDNA; 267 BP.
DE Human prostate expression marker cDNA 56588.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
RESULT 1253
ID AAL16362 standard; cDNA; 271 BP.
DE Human breast cancer expressed polynucleotide 8819.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;

RESULT 1254
ID ABV58412 standard; cDNA; 276 BP.
DE Human prostate expression marker cDNA 58403.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 276;
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
RESULT 1255
ID ADL43567 standard; DNA; 282 BP.
DE Human ovarian cancer DNA marker #17457.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 282;
PA (BYAT/) BYATT J C.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
RESULT 1256
ID ABV56381 standard; cDNA; 294 BP.
DE Human prostate expression marker cDNA 56372.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 294;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1257
ID ADL37508 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #11398.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 294;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1258
ID ADI72364 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #5106.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 294;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1259
ID ABV19977 standard; cDNA; 295 BP.
DE Human prostate expression marker cDNA 19968.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 295;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1260
ID ACN50415 standard; cDNA; 298 BP.
DE Cotton mature seed EST Clone ID: LTB3827-001-Q1-K6-C7, SEQ:5196.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 52; DB 13; Length 298;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1261
ID ABV49738 standard; cDNA; 303 BP.
DE Human prostate expression marker cDNA 49729.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 303;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1262
ID ABZ08725 standard; cDNA; 306 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8716.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.

Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 306;
RESULT 1263
ID ADK61477 standard; DNA; 306 BP.
DE Ovarian cancer-related DNA #632 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USOK) SLOAN KETTERING INST CANCER RES.
Query Match
Best Local Similarity 1.5%; Score 52; DB 10; Length 306;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
RESULT 1264
ID ABX42505 standard; cDNA; 308 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7670.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 308;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-05;
RESULT 1265
ID ABV04305 standard; cDNA; 314 BP.
DE Human prostate expression marker cDNA 4296.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 314;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-05;
RESULT 1266
ID ADQ21262 standard; DNA; 320 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4082.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 320;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-05;
RESULT 1267
ID ABX41000 standard; cDNA; 321 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6165.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 321;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-05;
RESULT 1268
ID ABV55706 standard; cDNA; 337 BP.
DE Human prostate expression marker cDNA 55697.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 5; Length 337;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
RESULT 1269
ID ACN45670 standard; cDNA; 341 BP.
DE Cotton primed seed EST Clone ID: LTB3825-007-Q1-K6-C8, SEQ:451.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.5%; Score 52; DB 13; Length 341;
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
RESULT 1270
ID ACN55002 standard; cDNA; 342 BP.
DE Cotton androecium tissue EST Clone ID: LTB3828-028-Q6-K6-A9, SEQ:9783.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 342;
 RESULT 1271
 ID ACN49021 standard; cDNA; 350 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-K6-A8, SEQ:3802.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 350;
 RESULT 1272
 ID ABX49592 standard; cDNA; 355 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #14757.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 8; Length 355;
 RESULT 1273
 ID ABX40295 standard; cDNA; 355 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #5460.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 8; Length 355;
 RESULT 1274
 ID ABV48348 standard; cDNA; 358 BP.
 DE Human prostate expression marker cDNA 48339.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 358;
 RESULT 1275
 ID ABV57991 standard; cDNA; 373 BP.
 DE Human prostate expression marker cDNA 57982.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 373;
 RESULT 1276
 ID AAS01025 standard; cDNA; 378 BP.
 DE Sugarcane plant gene promoter cDNA isolated from clone c32A.
 PN WO200118211-A1.
 PD 15-MAR-2001.
 PA (UYQU) UNIV QUEENSLAND.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 4; Length 378;
 RESULT 1277
 ID ABV49790 standard; cDNA; 380 BP.
 DE Human prostate expression marker cDNA 49781.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 380;
 RESULT 1278
 ID ABX44845 standard; cDNA; 380 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #10010.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 8; Length 380;
 RESULT 1279
 ID AAH70111 standard; cDNA; 384 BP.
 DE Human cervical cancer marker nucleic acid 1385.
 PN WO200142467-A2.
 PD 14-JUN-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 4; Length 384;
 RESULT 1280
 ID ABZ08601 standard; cDNA; 386 BP.
 DE Human leukocyte derived cDNA SEQ ID NO 8592.
 PN WO200257414-A2.
 PD 25-JUL-2002.
 PA (BIOC-) BIOCARDIA INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 6; Length 386;
 RESULT 1281
 ID ACH28736 standard; cDNA; 390 BP.
 DE Human adult ovary cDNA #7116.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 9; Length 390;
 RESULT 1282
 ID ABV47791 standard; cDNA; 391 BP.
 DE Human prostate expression marker cDNA 47782.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 391;
 RESULT 1283
 ID ABV49244 standard; cDNA; 394 BP.
 DE Human prostate expression marker cDNA 49235.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 394;
 RESULT 1284
 ID ABX34934 standard; cDNA; 395 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #99.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 8; Length 395;
 RESULT 1285
 ID AAF94851 standard; cDNA; 396 BP.
 DE Human ovarian cancer associated coding sequence SEQ ID NO: 42.
 PN WO200118046-A2.
 PD 15-MAR-2001.
 PA (CORI-) CORIXA CORP.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 4; Length 396;
 RESULT 1286

ID ABL48801 standard; cDNA; 396 BP.
DE Ovarian carcinoma sequence isolate 24356.
PD US200204491-A1.
PD 10-JAN-2002.
PA (XUJJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
Query Match 1.5%; Score 52; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1287
ID ABL03118 standard; cDNA; 396 BP.
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 42.
PD WO200239885-A2.
PD 23-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 52; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1288
ID ADM10711 standard; cDNA; 396 BP.
DE Human ovarian carcinoma-associated cDNA 24356.
PD US2003206918-A1.
PD 06-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 52; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1289
ID ADJ11041 standard; cDNA; 396 BP.
DE Representative human ovarian carcinoma cDNA SeqID 42.
PD US2003232056-A1.
PD 18-DEC-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 52; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1290
ID ADM43302 standard; cDNA; 396 BP.
DE Human ovarian carcinoma cDNA #42.
PD US2003129192-A1.
PD 10-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.5%; Score 52; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1291
ID ACN53082 standard; cDNA; 398 BP.
DE Cotton androecium tissue EST Clone ID: LTB3828-021-Q1-N6-P7, SEQ:7863.
PD US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1292
ID AAT13044 standard; cDNA; 399 BP.
DE Cotton fibre-specific cDNA clone A9.
PD US5495070-A.
PD 27-FEB-1996.
PA (CETU) AGRACETUS INC.
Query Match 1.5%; Score 52; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1293
ID AAT30261 standard; DNA; 399 BP.
DE Cotton fibre cell-specific cDNA clone CKFB10-A9.
PD US5521078-A.
PD 28-MAY-1996.
PA (CETU) AGRACETUS INC.
Query Match 1.5%; Score 52; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1294
ID AAT62620 standard; cDNA to mRNA; 399 BP.
DE Cotton fibre specific cDNA clone CKFB10-A9.
PD US5597718-A.
PD 10-JAN-1997.
PA (CETU) AGRACETUS INC.
Query Match 1.5%; Score 52; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1295
ID AAT70051 standard; cDNA; 399 BP.
DE Cotton fibre specific cDNA clone A9.
PD US5620882-A.
PD 15-APR-1997.
PA (CETU) AGRACETUS INC.
Query Match 1.5%; Score 52; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1296
ID AAZ35555 standard; DNA; 399 BP.
DE cDNA sequence a cotton fibre gene from clone CKFB10A9.
PD US5981834-A.
PD 09-NOV-1999.
PA (MONS) MONSANTO CO.
Query Match 1.5%; Score 52; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1297
ID AAI93256 standard; cDNA; 399 BP.
DE Human polynucleotide SEQ ID NO 13316.
PD WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.5%; Score 52; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1298
ID AAL19713 standard; cDNA; 402 BP.
DE Human breast cancer expressed polynucleotide 12170.
PD WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1299
ID ABZ08612 standard; cDNA; 402 BP.
DE Human leukocyte derived cDNA SEQ ID NO 8603.
PD WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 1.5%; Score 52; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
RESULT 1300
ID ABV49258 standard; cDNA; 404 BP.
DE Human prostate expression marker cDNA 49249.
PD WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
RESULT 1301
ID ABX45586 standard; cDNA; 404 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10751.
PD US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.5%; Score 52; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
RESULT 1302
ID ACH16113 standard; cDNA; 406 BP.
DE Human adult heart cDNA #427.
PD US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.

Query Match 1.5%; Score 52; DB 9; Length 406;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1303
 ID AAF81795 standard; cDNA; 410 BP.
 DE Human secreted protein gene 9 SEQ ID NO:19.
 PN WO200112775-A2.
 PD 22-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 52; DB 4; Length 410;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1304
 ID ADO63303 standard; DNA; 410 BP.
 DE Transcription factor G319 orthologous sequence, SEQ ID 1770.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 Query Match 1.5%; Score 52; DB 12; Length 410;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1305
 ID AAI88540 standard; cDNA; 418 BP.
 DE Human polynucleotide SEQ ID NO 8600.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 52; DB 4; Length 418;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1306
 ID ACH48626 standard; cDNA; 420 BP.
 DE Human leukocyte cDNA #220.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 1.5%; Score 52; DB 9; Length 420;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1307
 ID ACH28837 standard; cDNA; 424 BP.
 DE Human adult ovary cDNA #7217.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 1.5%; Score 52; DB 9; Length 424;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1308
 ID AAH33149 standard; cDNA; 425 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:205.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 52; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1309
 ID AAI88844 standard; cDNA; 426 BP.
 DE Human polynucleotide SEQ ID NO 8904.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 52; DB 4; Length 426;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1310
 ID ACH30520 standard; cDNA; 426 BP.
 DE Human testis cDNA #906.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 1.5%; Score 52; DB 9; Length 426;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1311
 ID ABV49095 standard; cDNA; 429 BP.
 DE Human prostate expression marker cDNA 49086.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 52; DB 5; Length 429;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 RESULT 1312
 ID AAI86320 standard; cDNA; 435 BP.
 DE Human polynucleotide SEQ ID NO 6380.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 52; DB 4; Length 435;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1313
 ID ACH18655 standard; cDNA; 435 BP.
 DE Human adult heart cDNA #2969.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 1.5%; Score 52; DB 9; Length 435;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1314
 ID AAH71214 standard; cDNA; 436 BP.
 DE Human cervical cancer marker nucleic acid 2488.
 PN WO200142467-A2.
 PD 14-JUN-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 52; DB 4; Length 436;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1315
 ID AAI87438 standard; cDNA; 441 BP.
 DE Human polynucleotide SEQ ID NO 7498.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 52; DB 4; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1316
 ID ABV56473 standard; cDNA; 442 BP.
 DE Human prostate expression marker cDNA 56464.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 52; DB 5; Length 442;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1317
 ID ABX43368 standard; cDNA; 447 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #8533.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 52; DB 8; Length 447;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 RESULT 1318
 ID ABL87269 standard; cDNA; 451 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:10247.
 PN WO200192581-A2.
 PD 06-DEC-2001.

PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
RESULT 1326
ID ADL42859 standard; DNA; 495 BP.
DE Human ovarian cancer DNA marker #16749.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 495;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
RESULT 1327
ID ABV56951 standard; cDNA; 496 BP.
DE Human prostate expression marker cDNA 56942.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
RESULT 1328
ID ACN49058 standard; cDNA; 514 BP.
DE Cotton primed seed EST Clone ID: LIB3825-029-Q6-K6-E7, SEQ:3839
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKWAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 514;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
RESULT 1329
ID ADI73400 standard; DNA; 515 BP.
DE Human ovarian cancer DNA marker #6142.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
RESULT 1330
ID ADL38531 standard; DNA; 515 BP.
DE Human ovarian cancer DNA marker #12421.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.5%; Score 52; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
RESULT 1331
ID ADP56917 standard; cDNA; 521 BP.
DE Urogenital sinus-derived expressed sequence tag, SEQ ID No 236.
PN WO9958665-A2.
PD 18-NOV-1999.
PA (UVVI-) UNIV VIRGINIA PATENT FOUND.
Query Match 1.5%; Score 52; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
RESULT 1332
ID ACN46717 standard; cDNA; 522 BP.
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-N6-C8, SEQ:1498
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKWAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.5%; Score 52; DB 13; Length 522;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
RESULT 1333
ID ACN61692 standard; cDNA; 522 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6_N6-H8, SEQ
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKWAN J.
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 522;
 RESULT 1334
 ID ACN59983 standard; cDNA; 526 BP.
 DE Cotton gynecium tissue EST Clone ID: LIB3829-036-Q1-N6-A4, SEQ:14764.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 526;
 RESULT 1335
 ID ACN53350 standard; cDNA; 528 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-P8, SEQ:8131.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 528;
 RESULT 1336
 ID AAS60058 standard; cDNA; 534 BP.
 DE Human cancer agent-sensitive marker #59.
 PN WO200179555-A2.
 PD 25-OCT-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 4; Length 534;
 RESULT 1337
 ID ACN55415 standard; cDNA; 536 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C9, SEQ:10196.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 536;
 RESULT 1338
 ID ADR62275 standard; cDNA; 546 BP.
 DE Cotton cDNA sequence, SEQ ID 3056.
 PN US2004181830-A1.
 PD 16-SEP-2004.
 PA (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAOY/) CAO Y.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 546;
 RESULT 1339
 ID ACN51414 standard; cDNA; 547 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 547;
 RESULT 1340
 ID ADG33016 standard; DNA; 552 BP.
 DE Human DNA differentially expressed in patients with SLE SeqID340.
 PN WO2003090694-A2.
 PD 06-NOV-2003.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 10; Length 552;

Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 RESULT 1341
 ID ACN62570 standard; cDNA; 552 BP.
 DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 552;
 RESULT 1342
 ID ABV40163 standard; cDNA; 556 BP.
 DE Human prostate expression marker cDNA 40154.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 556;
 RESULT 1343
 ID ABV40063 standard; cDNA; 556 BP.
 DE Human prostate expression marker cDNA 40054.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 556;
 RESULT 1344
 ID ABV42105 standard; cDNA; 556 BP.
 DE Human prostate expression marker cDNA 43592.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 556;
 RESULT 1345
 ID ABV43601 standard; cDNA; 556 BP.
 DE Human prostate expression marker cDNA 43592.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 556;
 RESULT 1346
 ID ACN56091 standard; cDNA; 573 BP.
 DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-K6-C10, SEQ:10872.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 573;
 RESULT 1347
 ID ABV57502 standard; cDNA; 574 BP.
 DE Human prostate expression marker cDNA 57493.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 5; Length 574;
 RESULT 1348
 ID ACN46463 standard; cDNA; 591 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-020-Q1-K6-D3, SEQ:1244.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match
 Best Local Similarity 1.5%; Score 52; DB 13; Length 591;

Best Local Similarity 100.0%; Pred. No. 4.1e-05;
RESULT 1349
ID AAF18206 standard; DNA; 601 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 225.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A. 1.5%; Score 52; DB 3; Length 601;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
RESULT 1350
ID ADC29847 standard; DNA; 619 BP.
DE Fertilization-independent endosperm protein gene #6.
PN WO2003026390-A2.
PD 03-APR-2003.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I. 1.5%; Score 52; DB 10; Length 619;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
RESULT 1351
ID AAS01161 standard; cDNA; 620 BP.
DE Fertilisation-independent endosperm cDNA clone hplc.pk003.e8.
PN WO200116325-A2.
PD 08-MAR-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC. 1.5%; Score 52; DB 4; Length 620;
Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
RESULT 1352
ID ADR63368 standard; cDNA; 670 BP.
DE Cotton cDNA sequence, SEQ ID 4149.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y. 1.5%; Score 52; DB 13; Length 723;
PA (CAOY/) CAO Y. 1.5%; Score 52; DB 13; Length 723;
Query Match
Best Local Similarity 100.0%; Pred. No. 4e-05;
RESULT 1353
ID ABV19321 standard; cDNA; 681 BP.
DE Human prostate expression marker cDNA 19312.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 1.5%; Score 52; DB 5; Length 681;
Query Match
Best Local Similarity 100.0%; Pred. No. 4e-05;
RESULT 1354
ID AAX30351 standard; DNA; 687 BP.
DE DNA encoding a human secreted protein.
PN WO9907891-A1.
PD 18-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC. 1.5%; Score 52; DB 2; Length 687;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1355
ID ADB47795 standard; cDNA; 687 BP.
DE Novel human secreted protein cDNA #68.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M. 1.5%; Score 52; DB 3; Length 785;
PA (SOPP/) SOPPET D R. 1.5%; Score 52; DB 3; Length 785;
PA (EBNE/) EBNER R. 1.5%; Score 52; DB 3; Length 785;
PA (OLSE/) OLSEN H S. 1.5%; Score 52; DB 3; Length 785;
PA (YOUN/) YOUNG P E. 1.5%; Score 52; DB 3; Length 785;
PA (GREE/) GREENE J M. 1.5%; Score 52; DB 3; Length 785;
PA (FERR/) FERRIE A M. 1.5%; Score 52; DB 3; Length 785;
PA (YUGG/) YU G. 1.5%; Score 52; DB 3; Length 785;
PA (NIJJ/) NI J. 1.5%; Score 52; DB 3; Length 785;
PA (ROSE/) ROSEN C A. 1.5%; Score 52; DB 3; Length 785;
PA (BREW/) BREWER L A. 1.5%; Score 52; DB 3; Length 785;
PA (JANA/) JANAT F. 1.5%; Score 52; DB 3; Length 785;
PA (BIRS/) BIRSE C E. 1.5%; Score 52; DB 3; Length 785;
Query Match

Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1356
ID ADJ55350 standard; cDNA; 687 BP.
DE Novel human secreted protein cDNA #68.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC. 1.5%; Score 52; DB 12; Length 687;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1357
ID ABL87011 standard; cDNA; 695 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:9989.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP. 1.5%; Score 52; DB 6; Length 695;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1358
ID ADR60499 standard; cDNA; 723 BP.
DE Cotton cDNA sequence, SEQ ID 1280.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y. 1.5%; Score 52; DB 13; Length 723;
PA (CAOY/) CAO Y. 1.5%; Score 52; DB 13; Length 723;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1359
ID ACN54305 standard; cDNA; 723 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-K6-F12, SEQ:9086.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J. 1.5%; Score 52; DB 4; Length 768;
PA (FENG/) FENG P C C. 1.5%; Score 52; DB 4; Length 768;
PA (FINC/) FINCHER K L. 1.5%; Score 52; DB 4; Length 768;
PA (ZIEG/) ZIEGLER T E. 1.5%; Score 52; DB 4; Length 768;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
RESULT 1360
ID AAL08093 standard; cDNA; 768 BP.
DE Human breast cancer expressed polynucleotide 550.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 1.5%; Score 52; DB 4; Length 768;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
RESULT 1361
ID AAL37842 standard; DNA; 783 BP.
DE Soybean KCP-like protein encoding DNA, SEQ ID NO 34.
PN WO200222821-A2.
PD 21-MAR-2002.
PA (PION-) PIONEER HI-BRED INT INC. 1.5%; Score 52; DB 6; Length 783;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
RESULT 1362
ID AAC77913 standard; cDNA; 785 BP.
DE Human cancer associated gene sequence SEQ ID NO:307.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC. 1.5%; Score 52; DB 3; Length 785;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
RESULT 1363
ID ABV13906 standard; cDNA; 814 BP.
DE Human prostate expression marker cDNA 13897.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 1.5%; Score 52; DB 5; Length 814;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
RESULT 1364
ID AAF91869 standard; cDNA; 840 BP.
DE Human secreted protein-encoding gene 12 cDNA clone HFKKS66, SEQ ID NO:22.
Query Match

PN WO200118022-A1.
 PD 15-MAR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; DB 4; Length 840;
 RESULT 1365
 ID AC660574 standard; cDNA; 878 BP.
 DE Polynucleotide relating to the invention SEQ ID NO: 151.
 PN WO200257460-A2.
 PD 25-JUL-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 100.0%; DB 6; Length 878;
 RESULT 1366
 ID AAL25029 standard; cDNA; 899 BP.
 DE Human breast cancer expressed polynucleotide 17486.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match
 Best Local Similarity 100.0%; DB 4; Length 899;
 RESULT 1367
 ID AAT65651 standard; cDNA to mRNA; 916 BP.
 DE cDNA encoding anti-coagulant protein A.
 PN JP09067396-A.
 PD 11-MAR-1997.
 PA (NORQ) NORINSUISANGSHO SANSHI KONCHU.
 Query Match
 Best Local Similarity 100.0%; DB 2; Length 916;
 RESULT 1368
 ID AAV62000 standard; cDNA; 916 BP.
 DE R. prolixus NO-r protein S cDNA.
 PN JP10265497-A.
 PD 06-OCT-1998.
 PA (NORQ) NORINSUISANGSHO SANSHI KONCHU.
 Query Match
 Best Local Similarity 100.0%; DB 2; Length 916;
 RESULT 1369
 ID AAI97661 standard; cDNA; 951 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3736.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match
 Best Local Similarity 100.0%; DB 4; Length 951;
 RESULT 1370
 ID AAC98222 standard; cDNA; 970 BP.
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:232.
 PN WO200055351-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; DB 3; Length 970;
 RESULT 1371
 ID ADF81829 standard; DNA; 976 BP.
 DE Leukemia-related DNA sequence #2385.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE/) HAFERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match
 Best Local Similarity 100.0%; DB 10; Length 976;
 RESULT 1372
 ID AAA53405 standard; cDNA; 991 BP.
 DE Clone asm.pk0067.g5 nucleotide sequence encoding GST type III.
 PN US6063570-A.
 PD 16-MAY-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 100.0%; DB 3; Length 991;

Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 RESULT 1373
 ID AA294961 standard; cDNA; 991 BP.
 DE Soybean glutathione-S-transferase cDNA clone asm.pk0067.g5.
 PN WO200018936-A1.
 PD 06-APR-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 100.0%; DB 3; Length 991;
 RESULT 1374
 ID AAA59469 standard; DNA; 991 BP.
 DE Nucleotide sequence of a soybean type III glutathione-S-transferase.
 PN WO200047728-A2.
 PD 17-AUG-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 100.0%; DB 3; Length 991;
 RESULT 1375
 ID AAF31584 standard; DNA; 991 BP.
 DE Soybean type III GST cDNA #6.
 PN US6171839-B1.
 PD 09-JAN-2001.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 100.0%; DB 4; Length 991;
 RESULT 1376
 ID AAF57531 standard; cDNA; 991 BP.
 DE Glycine max clone SSM.PK0067.G5 sequence.
 PN WO200121770-A2.
 PD 29-MAR-2001.
 PA (ZENE) ZENECA LTD.
 Query Match
 Best Local Similarity 100.0%; DB 4; Length 991;
 RESULT 1377
 ID AAQ12431 standard; DNA; 1013 BP.
 DE Fragment D of urate oxidase-encoding clone 9C.
 PN EP435776-A.
 PD 03-JUL-1991.
 PA (SNFI) SANOFI SA.
 PA (SNFI) ELF SANOFI.
 Query Match
 Best Local Similarity 100.0%; DB 2; Length 1013;
 RESULT 1378
 ID ADJ45542 standard; cDNA; 1022 BP.
 DE cDNA encoding LXR-ligand induced transcript seq id 73.
 PN US2004023276-A1.
 PD 05-FEB-2004.
 PA (WARD/) WARD T R.
 PA (MAOM/) MAO M.
 PA (LINS/) LINSLEY P S.
 PA (LUND/) LUND E.
 Query Match
 Best Local Similarity 100.0%; DB 12; Length 1022;
 RESULT 1379
 ID AAX30155 standard; DNA; 1032 BP.
 DE Human secreted protein gene 11.
 PN WO9910363-A1.
 PD 04-MAR-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 100.0%; DB 2; Length 1032;
 RESULT 1380
 ID ADP04740 standard; cDNA; 1052 BP.
 DE Sea squirt cDNA with tissue specific expression in development Seq 335.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match
 Best Local Similarity 100.0%; DB 12; Length 1052;
 RESULT 1381
 ID ADR65755 standard; cDNA; 1063 BP.
 DE Cotton cDNA sequence, SEQ ID 6536.
 PN US2004181830-A1.

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PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 13; Length 1063;
  Pred. No. 3.5e-05;
RESULT 1382
ID ABN98364 standard; DNA; 1072 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.
PD US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1072;
  Pred. No. 3.4e-05;
RESULT 1383
ID ADJ80201 standard; cDNA; 1103 BP.
DE Novel human nucleic acid-associated protein coding sequence #19.
PD WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 10; Length 1103;
  Pred. No. 3.4e-05;
RESULT 1384
ID AAV34315 standard; DNA; 1114 BP.
DE Human secreted protein gene 5 clone HELDY41.
PD WO9840483-A2.
PD 17-SEP-1998.
PA (HUNA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 2; Length 1114;
  Pred. No. 3.4e-05;
RESULT 1385
ID AAD44666 standard; cDNA; 1114 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HELDY41, SEQ ID NO:41.
PD US200207287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1114;
  Pred. No. 3.4e-05;
RESULT 1386
ID AAD44884 standard; cDNA; 1114 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HELDY41, SEQ ID NO:41.
PD US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 6; Length 1114;
  Pred. No. 3.4e-05;
RESULT 1387
ID ACC00855 standard; cDNA; 1130 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:500.
PD WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 8; Length 1130;
  Pred. No. 3.4e-05;
RESULT 1390
ID AAT39050 standard; cDNA; 1174 BP.
DE cDNA encoding cellulytic enzyme #4 of the invention.
PD WO9629397-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 12; Length 1114;
  Pred. No. 3.4e-05;
RESULT 1389
ID ACC00855 standard; cDNA; 1130 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:500.
PD WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
  Query Match
  Best Local Similarity 1.5%; Score 52; DB 8; Length 1130;
  Pred. No. 3.4e-05;
RESULT 1390
ID AAT39050 standard; cDNA; 1174 BP.
DE cDNA encoding cellulytic enzyme #4 of the invention.
PD WO9629397-A1.

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PD 26-SEP-1996.
PA (NOVO) NOVO-NORDISK AS.
Query Match 1.5%; Score 52; DB 2; Length 1174;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1391
ID AAV39096 standard; cDNA; 1174 BP.
DE Monocomponent endoglucanase encoding cDNA.
PN EP843041-A1.
PD 20-MAY-1998.
PA (NOVO) NOVO-NORDISK AS.
Query Match 1.5%; Score 52; DB 2; Length 1174;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1392
ID ADP73934 standard; DNA; 1174 BP.
DE DNA encoding the Thielavia terrestris cellulase protein SeqID 3.
PN WO2004053039-A2.
PD 24-JUN-2004.
PA (NOVO) NOVOZYMES AS.
Query Match 1.5%; Score 52; DB 12; Length 1174;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1393
ID AAX07565 standard; cDNA; 1230 BP.
DE Homo sapiens fetal kidney clone AK296 secreted protein gene.
PN WO9900405-A1.
PD 07-JAN-1999.
PA (GENY) GENETICS INST INC.
Query Match 1.5%; Score 52; DB 2; Length 1230;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1394
ID AAX25190 standard; cDNA; 1231 BP.
DE Nucleotide sequence of a human transferrin.
PN WO200146254-A1.
PD 28-JUN-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 4; Length 1231;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1395
ID AAA40490 standard; cDNA; 1248 BP.
DE Human fetal kidney cDNA fragment AK296_li.
PN WO200037630-A1.
PD 29-JUN-2000.
PA (GENY) GENETICS INST INC.
Query Match 1.5%; Score 52; DB 3; Length 1248;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1396
ID AAA53975 standard; cDNA; 1291 BP.
DE TRIB-AP53 tumour suppressor gene.
PN WO200055178-A1.
PD 21-SEP-2000.
PA (EXEL-) EXELIXIS INC.
Query Match 1.5%; Score 52; DB 3; Length 1291;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
RESULT 1397
ID ACC00641 standard; cDNA; 1301 BP.
DE Zea mays oil trait related cDNA sequence SEQ ID NO:31.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 1.5%; Score 52; DB 8; Length 1301;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1398
ID ABQ54352 standard; cDNA; 1319 BP.
DE Human ovarian antigen HNO5F50 cDNA, SEQ ID NO:232.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 6; Length 1319;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1399
ID AAC78172 standard; cDNA; 1334 BP.
DE Human cancer associated gene sequence SEQ ID NO:566.
PN WO200055350-A1.

PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 3; Length 1334;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1400
ID AAF21860 standard; DNA; 1336 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 3; Length 1336;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1401
ID ADI42533 standard; DNA; 1338 BP.
DE Plant transcription factor polynucleotide #631.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 1.5%; Score 52; DB 12; Length 1338;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1402
ID ADO02862 standard; cDNA; 1338 BP.
DE Soybean orthologue of Thalecress transcription factor, cDNA #139.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 1.5%; Score 52; DB 12; Length 1338;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
RESULT 1403
ID AAB05201 standard; cDNA; 1439 BP.
DE Human secreted protein-encoding gene 23 cDNA clone H15BL03, SEQ ID NO:91.
PN WO200134769-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 4; Length 1439;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1404
ID ADR63648 standard; cDNA; 1449 BP.
DE Cotton cDNA sequence, SEQ ID 4429.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.

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PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
  Query Match      1.5%; Score 52; DB 13; Length 1449;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1405
ID ACN92580 standard; DNA; 1453 BP.
DE Breast cancer related marker, seq id 13730.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match      1.5%; Score 52; DB 11; Length 1453;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1406
ID ABX92051 standard; cDNA; 1457 BP.
DE Lung specific nucleic acid (LSNA) #93.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
  Query Match      1.5%; Score 52; DB 6; Length 1457;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1407
ID AAS27566 standard; cDNA; 1462 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 601.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 4; Length 1462;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1408
ID ADB93744 standard; cDNA; 1462 BP.
DE Human cDNA encoding a novel protein #591.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match      1.5%; Score 52; DB 10; Length 1462;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1409
ID ACC62522 standard; cDNA; 1479 BP.
DE Human secreted protein #48 coding sequence SEQ ID 58.
PN WO200299066-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 8; Length 1479;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1410
ID AAX84967 standard; DNA; 1494 BP.
DE Human secreted protein gene No. 35.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 2; Length 1494;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1411
ID ADA39887 standard; cDNA; 1494 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 8; Length 1494;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1412
ID ACD18893 standard; cDNA; 1494 BP.
DE Novel human secreted protein cDNA #35.
PN US2003028003-A1.
PD 06-FEB-2003.
PA (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJU/) NI J.
  Query Match      1.5%; Score 52; DB 3; Length 1576;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1413
ID ADA56077 standard; DNA; 1494 BP.
DE Gene encoding human secreted protein #256.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 10; Length 1494;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1414
ID ADG78284 standard; cDNA; 1494 BP.
DE Human secreted protein cDNA #35.
PN US2003211472-A1.
PD 13-NOV-2003.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJU/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KIYAW/) KIYAW H.
PA (LAPL/) LAFLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
  Query Match      1.5%; Score 52; DB 8; Length 1494;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1415
ID ADN60575 standard; cDNA; 1494 BP.
DE Human secreted polynucleotide #35.
PN US2004038277-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 12; Length 1494;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1416
ID AAA27985 standard; cDNA; 1495 BP.
DE Corn CCR4 transcription factor nucleotide sequence #2.
PN WO200032783-A1.
PD 08-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
  Query Match      1.5%; Score 52; DB 3; Length 1495;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1417
ID AAC59407 standard; cDNA; 1576 BP.
DE Human secreted protein cDNA #16.
PN WO200056765-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 3; Length 1576;
  Best Local Similarity 100.0%; Pred. No. 3.1e-05;
RESULT 1418
ID ABL90003 standard; cDNA; 1612 BP.
DE Human polynucleotide SEQ ID NO 565.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      1.5%; Score 52; DB 6; Length 1612;
```

Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1419
ID AAC76111 standard; cDNA; 1644 BP.
DE Human ORFX ORF1666 polynucleotide sequence SEQ ID NO:3331.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 1.5%; Score 52; DB 3; Length 1644;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1420
ID ADQ22714 standard; DNA; 1661 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.5%; Score 52; DB 12; Length 1661;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1421
ID AAL60889 standard; cDNA; 1673 BP.
DE Human placental protein 11 splice variant (plap11) cDNA.
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GSET) GENSET SA.
Query Match 1.5%; Score 52; DB 9; Length 1673;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1422
ID AAC98165 standard; cDNA; 1689 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:175.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.5%; Score 52; DB 3; Length 1689;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1423
ID AAZ34311 standard; cDNA; 1738 BP.
DE Human PRO213-1 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 2; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1424
ID AAC78585 standard; cDNA; 1738 BP.
DE Human PRO213-1 nucleotide sequence SEQ ID NO:505.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 3; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1425
ID AAA75702 standard; cDNA; 1738 BP.
DE cDNA clone DNA30943-1163 encoding a PRO213 polypeptide.
PN WO200053752-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 3; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1426
ID AAC58226 standard; cDNA; 1738 BP.
DE Human PRO213 nucleotide sequence SEQ ID NO:3.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 3; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1427
ID ACA63879 standard; cDNA; 1738 BP.
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1428
ID ACA72043 standard; cDNA; 1738 BP.
DE Human secreted and transmembrane PRO polypeptide #33 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1429
ID ABX92683 standard; cDNA; 1738 BP.
DE cDNA encoding human PRO213-1 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1430
ID ACA66424 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO213-1.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1431
ID ADA25044 standard; cDNA; 1738 BP.
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 9; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1432
ID ACD30025 standard; cDNA; 1738 BP.
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 9; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1433
ID ADA12705 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO213-1.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 9; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1434
ID ACD29440 standard; cDNA; 1738 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #128.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 9; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1435
ID ADB74011 standard; cDNA; 1738 BP.
DE Human PRO polynucleotide sequence #128.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1436
ID ADB76727 standard; cDNA; 1738 BP.
DE Human PRO polynucleotide sequence #128.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1437
ID ADC44153 standard; cDNA; 1738 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1438
ID ADC61913 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1439
ID ADC63877 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1440
ID ADC66977 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1441
ID ADC69101 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1442
ID ADC63161 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1443
ID ADC68226 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1444
ID ADC41546 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1445
ID ADC67601 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1446
ID ADC62537 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1447
ID ADC42170 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1448
ID ADE49539 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1449
ID ADE35593 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1450
ID ADE16707 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1451
ID ADD73322 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1452
ID ADP72680 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1453
ID ADE17331 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1454
ID ADF47345 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 10; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1455
ID ADG53102 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003216561-A1.

PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;
RESULT 1456
ID ADG60422 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;
RESULT 1457
ID ADI61182 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;
RESULT 1458
ID ACD42844 standard; cDNA; 1738 BP.
DE Novel human secreted and transmembrane protein PRO213-1 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 10; Length 1738;
RESULT 1459
ID ADE48839 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1460
ID ADE89940 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1461
ID ADF61580 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.

PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1462
ID ADF40272 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1463
ID ADF46068 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1464
ID ADF24464 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1465
ID ADF40896 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1466
ID ADF23840 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1467
ID ADF33823 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1468
ID ADF27290 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1469
ID ADF27926 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 12; Length 1738;
RESULT 1470
ID ADF41520 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003199435-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1471
ID ADF33199 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1472
ID ADF25565 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1473
ID ADF26666 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1474
ID ADF34455 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1475
ID ADF46692 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1476
ID ADG50678 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1477
ID ADG50054 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1478
ID ADG51926 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1479
ID ADG49430 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003216305-A1.
PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1480
ID ADG48806 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1481
ID ADG51302 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1482
ID ADG59246 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1483
ID ADG62702 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1484
ID ADH25727 standard; cDNA; 1738 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:505.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1485
ID ADM17504 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1486
ID ADL07338 standard; cDNA; 1738 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO213-1.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1487
ID ADT92579 standard; cDNA; 1738 BP.
DE Human PRO213-1 cDNA sequence.
PN AU2002330288-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 1.5%; Score 52; DB 12; Length 1738;
Best Local Similarity 100.0%; Pred. No. 3e-05;
RESULT 1488
ID AAZ33891 standard; cDNA; 1743 BP.
DE Human PRO213 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 1.5%; Score 52; DB 2; Length 1743;
RESULT 1489
ID AAC78458 standard; cDNA; 1743 BP.
DE Human PRO213 (UNQ187) nucleotide sequence SEQ ID NO:1.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 3; Length 1743;
RESULT 1490
ID ABL98258 standard; cDNA; 1743 BP.
DE Human PRO1449 cDNA sequence SEQ ID NO:373.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;
RESULT 1491
ID AAL44159 standard; DNA; 1743 BP.
DE Beta vulgaris dihydroorotase gene sequence.
PN WO200252012-A2.
PD 04-JUL-2002.
PA (CROP-) CROPDISEIGN NV.
Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;
RESULT 1492
ID ABL95747 standard; cDNA; 1743 BP.
DE Human angiogenesis related cDNA PRO1449 SEQ ID NO: 373.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 1.5%; Score 52; DB 6; Length 1743;
RESULT 1493
ID ACA63459 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO213 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;
RESULT 1494
ID ACA71623 standard; cDNA; 1743 BP.
DE Human secreted and transmembrane polypeptide PRO213 cDNA.
PN US200217553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;
RESULT 1495
ID ABX92263 standard; cDNA; 1743 BP.
DE cDNA encoding human PRO213 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;
RESULT 1496
ID ACA66004 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO213.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 8; Length 1743;
RESULT 1497
ID ADA24540 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO213 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;
RESULT 1498
ID ACD29605 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane protein PRO213 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;
RESULT 1499
ID ADA12201 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO213.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;
RESULT 1500
ID ACD29020 standard; cDNA; 1743 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #1.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;

RESULT 1496
ID ACA66004 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO213.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
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RESULT 1497
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DE Novel human secreted and transmembrane protein PRO213 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;
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DE Novel human secreted and transmembrane protein PRO213 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;
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ID ADA12201 standard; cDNA; 1743 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO213.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
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DE Novel human secreted and transmembrane polypeptide cDNA #1.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 1.5%; Score 52; DB 9; Length 1743;

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OM nucleic - nucleic search, using sw model

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(without alignments)
9911.795 Million cell updates/sec

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Perfect score: 3580

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Scoring table: 01XG0_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

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- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	64	1.8	601	4	US-09-949-016-144200
5	64	1.8	601	4	US-09-949-016-144258
6	64	1.8	601	4	US-09-949-016-144316
7	64	1.8	53394	4	US-09-949-016-15817
8	64	1.8	53394	4	US-09-949-016-15818
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10	64	1.8	53394	4	US-09-949-016-15820
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14	59	1.6	201529	4	US-09-949-016-12740
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16	58	1.6	1023	4	US-09-229-947-38
17	58	1.6	1048	4	US-09-489-847-38
18	58	1.6	1057	4	US-09-716-129-16
19	58	1.6	1361	4	US-09-489-847-64
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21	58	1.6	1376	4	US-09-489-847-66
22	58	1.6	1411	3	US-08-964-127-5
23	58	1.6	1411	3	US-09-496-692-5
24	58	1.6	1411	4	US-10-000-273-5
25	58	1.6	1618	4	US-09-800-729-29
26	58	1.6	1733	3	US-09-073-569-1
27	58	1.6	1810	4	US-09-369-247-11

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1.6	2369	4	US-09-057-996-13	Sequence 13, Appl
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1.6	1069	3	US-09-372-422A-7	Sequence 7, Appl
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1.6	1375	3	US-09-372-422A-37	Sequence 37, Appl
1.6	1454	3	US-09-372-422A-19	Sequence 19, Appl
1.6	1485	3	US-09-372-422A-39	Sequence 39, Appl
1.6	2235	4	US-09-569-804-20	Sequence 20, Appl
1.6	2581	4	US-09-369-247-51	Sequence 51, Appl
1.6	2584	4	US-09-716-129-47	Sequence 47, Appl
1.6	487	3	US-09-257-179-22	Sequence 22, Appl
1.6	601	4	US-09-949-016-154650	Sequence 154650, A
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1.6	1138	4	US-09-800-729-44	Sequence 44, Appl
1.6	1722	4	US-09-482-273-102	Sequence 102, App
1.6	1825	3	US-09-461-697-75	Sequence 75, Appl
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1.5	28257	4	US-09-949-016-13076	Sequence 13076, A
1.5	112874	4	US-09-949-016-13180	Sequence 13180, A
1.5	247299	4	US-09-949-016-17590	Sequence 17590, A
1.5	144	1	US-08-702-344-26	Sequence 26, Appl
1.5	396	4	US-09-640-173-10	Sequence 10, Appl
1.5	396	4	US-09-713-550-10	Sequence 10, Appl
1.5	396	4	US-09-825-294-10	Sequence 10, Appl
1.5	396	4	US-09-970-966-10	Sequence 10, Appl
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1.5	396	4	US-09-640-173-42	Sequence 42, Appl
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1.5	396	4	US-09-970-966-42	Sequence 42, Appl
1.5	399	1	US-07-885-970A-13	Sequence 13, Appl
1.5	399	1	US-08-298-687A-13	Sequence 13, Appl
1.5	399	1	US-08-530-737-12	Sequence 12, Appl
1.5	399	1	US-08-298-829-13	Sequence 13, Appl
1.5	399	2	US-08-787-335-12	Sequence 12, Appl
1.5	612	4	US-09-270-767-11643	Sequence 11643, A
1.5	687	4	US-09-774-639-45	Sequence 45, Appl
1.5	991	3	US-08-924-747-25	Sequence 25, Appl
1.5	991	3	US-09-247-373B-25	Sequence 25, Appl

C 101	52	1.5	991	3	US-09-296-715-25	Sequence 25, Appl	174	51	1.4	13193	4	US-09-949-016-17515	Sequence 17515, A
C 102	52	1.5	1013	1	US-07-920-519-30	Sequence 30, Appl	175	51	1.4	14079	4	US-09-949-016-11993	Sequence 11993, A
C 103	52	1.5	1013	1	US-08-086-410-23	Sequence 30, Appl	176	51	1.4	80	3	US-09-284-627-15	Sequence 15, Appl
C 104	52	1.5	1013	1	US-08-314-586-30	Sequence 30, Appl	C 177	50	1.4	85	4	US-09-621-976-14741	Sequence 14741, A
C 105	52	1.5	1032	3	US-09-257-179-21	Sequence 21, Appl	C 178	50	1.4	100	4	US-09-621-976-12774	Sequence 12774, A
C 106	52	1.5	1114	3	US-09-152-060-41	Sequence 41, Appl	C 179	50	1.4	105	3	US-09-284-627-23	Sequence 23, Appl
C 107	52	1.5	1174	2	US-08-872-437-1	Sequence 1, Appl	C 180	50	1.4	138	4	US-09-621-976-9595	Sequence 9595, Ap
C 108	52	1.5	1174	2	US-08-651-136C-11	Sequence 11, Appl	C 181	50	1.4	141	4	US-09-621-976-9595	Sequence 9595, Ap
C 109	52	1.5	1174	3	US-09-229-911A-11	Sequence 11, Appl	C 182	50	1.4	185	4	US-09-513-999C-24016	Sequence 24016, A
C 110	52	1.5	1291	4	US-09-524-101D-5	Sequence 5, Appl	C 183	50	1.4	188	4	US-09-621-976-10364	Sequence 10364, A
C 111	52	1.5	1842	4	US-09-482-273-90	Sequence 90, Appl	C 184	50	1.4	194	4	US-09-621-976-15317	Sequence 15317, A
C 112	52	1.5	1976	4	US-09-920-759-10	Sequence 10, Appl	C 185	50	1.4	222	5	PCT-US93-00869-15	Sequence 15, Appl
C 113	52	1.5	2202	3	US-09-388-743-1	Sequence 1, Appl	C 186	50	1.4	222	3	US-09-782-594-11	Sequence 11, Appl
C 114	52	1.5	2202	4	US-10-044-543-1	Sequence 1, Appl	C 187	50	1.4	223	4	US-09-621-976-16456	Sequence 16456, A
C 115	52	1.5	2202	4	US-09-439-923-1	Sequence 1, Appl	C 188	50	1.4	231	4	US-09-621-976-10374	Sequence 10374, A
C 116	52	1.5	6200	3	US-09-439-923-1	Sequence 1, Appl	C 189	50	1.4	323	4	US-09-621-976-16131	Sequence 16131, A
C 117	52	1.5	6200	4	US-09-711-202A-1	Sequence 1, Appl	C 190	50	1.4	323	4	US-09-621-976-18858	Sequence 18858, A
C 118	51	1.4	94	3	US-09-711-205A-1	Sequence 1, Appl	C 191	50	1.4	391	4	US-09-640-173-33	Sequence 33, Appl
C 119	51	1.4	94	4	US-09-404-879A-261	Sequence 261, App	C 192	50	1.4	396	4	US-09-640-173-33	Sequence 33, Appl
C 120	51	1.4	94	4	US-09-338-933-261	Sequence 261, App	C 193	50	1.4	396	4	US-09-640-173-33	Sequence 33, Appl
C 121	51	1.4	94	4	US-09-215-681-261	Sequence 261, App	C 194	50	1.4	396	4	US-09-713-550-33	Sequence 33, Appl
C 122	51	1.4	94	4	US-09-215-003A-261	Sequence 261, App	C 195	50	1.4	396	4	US-09-713-550-33	Sequence 33, Appl
C 123	51	1.4	195	4	US-09-621-976-15314	Sequence 15314, A	C 196	50	1.4	396	4	US-09-825-294-33	Sequence 33, Appl
C 124	51	1.4	215	4	US-09-621-976-15321	Sequence 15321, A	C 197	50	1.4	396	4	US-09-825-294-33	Sequence 33, Appl
C 125	51	1.4	279	4	US-09-621-976-10220	Sequence 10220, A	C 198	50	1.4	396	4	US-09-970-966-57	Sequence 57, Appl
C 126	51	1.4	299	4	US-09-621-976-10211	Sequence 10211, A	C 199	50	1.4	458	1	US-09-524-757-1	Sequence 1, Appl
C 127	51	1.4	327	4	US-09-621-976-16141	Sequence 16141, A	C 200	50	1.4	540	1	US-09-313-434C-15	Sequence 15, Appl
C 128	51	1.4	341	4	US-09-621-976-16135	Sequence 16135, A	C 201	50	1.4	568	1	US-09-582-257-20	Sequence 20, Appl
C 129	51	1.4	347	4	US-09-621-976-16136	Sequence 16136, A	C 202	50	1.4	568	2	US-09-582-257-20	Sequence 20, Appl
C 130	51	1.4	351	4	US-09-621-976-16140	Sequence 16140, A	C 203	50	1.4	572	4	US-09-696-169A-12	Sequence 12, Appl
C 131	51	1.4	554	4	US-09-696-169A-14	Sequence 14, Appl	C 204	50	1.4	601	4	US-09-949-016-39835	Sequence 39835, A
C 132	51	1.4	569	4	US-09-461-325-44	Sequence 44, Appl	C 205	50	1.4	601	4	US-09-949-016-39836	Sequence 39836, A
C 133	51	1.4	569	4	US-10-012-542-44	Sequence 44, Appl	C 206	50	1.4	601	4	US-09-949-016-39837	Sequence 39837, A
C 134	51	1.4	569	4	US-10-115-123-44	Sequence 44, Appl	C 207	50	1.4	601	4	US-09-949-016-75976	Sequence 75976, A
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C 136	51	1.4	711	4	US-09-621-976-17854	Sequence 17854, A	C 209	50	1.4	601	4	US-09-949-016-109436	Sequence 109436, A
C 137	51	1.4	763	4	US-09-743-207-3	Sequence 3, Appl	C 210	50	1.4	601	4	US-09-949-016-109437	Sequence 109437, A
C 138	51	1.4	966	1	US-08-514-014-7	Sequence 7, Appl	C 211	50	1.4	601	4	US-09-949-016-112463	Sequence 112463, A
C 139	51	1.4	966	2	US-08-833-823-7	Sequence 7, Appl	C 212	50	1.4	601	4	US-09-949-016-116454	Sequence 116454, A
C 140	51	1.4	976	2	US-08-504-459-9	Sequence 9, Appl	C 213	50	1.4	601	4	US-09-949-016-123892	Sequence 123892, A
C 141	51	1.4	1117	3	US-09-247-373B-33	Sequence 33, Appl	C 214	50	1.4	601	4	US-09-949-016-160858	Sequence 160858, A
C 142	51	1.4	1632	4	US-09-912-628-3	Sequence 3, Appl	C 215	50	1.4	601	4	US-09-949-016-160859	Sequence 160859, A
C 143	51	1.4	1738	2	US-08-379-482A-2	Sequence 2, Appl	C 216	50	1.4	601	4	US-09-949-016-160860	Sequence 160860, A
C 144	51	1.4	1886	4	US-09-594-506-31	Sequence 31, Appl	C 217	50	1.4	601	4	US-09-949-016-164245	Sequence 164245, A
C 145	51	1.4	1910	2	US-09-009-438-1	Sequence 1, Appl	C 218	50	1.4	601	4	US-09-949-016-164317	Sequence 164317, A
C 146	51	1.4	1910	3	US-09-207-493-1	Sequence 1, Appl	C 219	50	1.4	675	4	US-09-621-976-2461	Sequence 2461, Ap
C 147	51	1.4	1949	4	US-09-461-325-26	Sequence 26, Appl	C 220	50	1.4	831	4	US-09-904-615-25	Sequence 25, Appl
C 148	51	1.4	1949	4	US-10-012-542-26	Sequence 26, Appl	C 221	50	1.4	844	4	US-09-690-942-3	Sequence 3, Appl
C 149	51	1.4	1949	4	US-10-115-123-26	Sequence 26, Appl	C 222	50	1.4	844	4	US-09-690-942-3	Sequence 3, Appl
C 150	51	1.4	1951	3	US-09-465-558-35	Sequence 35, Appl	C 223	50	1.4	911	3	US-09-248-335-9	Sequence 9, Appl
C 151	51	1.4	1963	4	US-09-482-273-91	Sequence 91, Appl	C 224	50	1.4	911	3	US-09-248-335-9	Sequence 9, Appl
C 152	51	1.4	1965	4	US-09-482-273-27	Sequence 27, Appl	C 225	50	1.4	981	4	US-09-780-717-4	Sequence 4, Appl
C 153	51	1.4	2060	4	US-09-345-473E-5	Sequence 5, Appl	C 226	50	1.4	997	4	US-09-907-794A-376	Sequence 376, App
C 154	51	1.4	2065	3	US-09-370-473-5	Sequence 5, Appl	C 227	50	1.4	997	4	US-09-905-125A-376	Sequence 376, App
C 155	51	1.4	2409	3	US-09-293-322C-8	Sequence 8, Appl	C 228	50	1.4	997	4	US-09-905-125A-376	Sequence 376, App
C 156	51	1.4	2409	4	US-09-839-497A-8	Sequence 8, Appl	C 229	50	1.4	997	4	US-09-906-700-376	Sequence 376, App
C 157	51	1.4	2589	3	US-08-569-749-1	Sequence 1, Appl	C 230	50	1.4	997	4	US-09-903-603A-376	Sequence 376, App
C 158	51	1.4	2589	4	US-09-689-366-1	Sequence 1, Appl	C 231	50	1.4	997	4	US-09-904-920A-376	Sequence 376, App
C 159	51	1.4	2589	5	PCT-US96-12860-1	Sequence 1, Appl	C 232	50	1.4	997	4	US-09-905-064-376	Sequence 376, App
C 160	51	1.4	2790	3	US-08-800-291B-1	Sequence 1, Appl	C 233	50	1.4	997	4	US-09-905-064-376	Sequence 376, App
C 161	51	1.4	2821	4	US-09-702-705-1669	Sequence 1669, Ap	C 234	50	1.4	1001	2	US-08-728-259A-10	Sequence 10, Appl
C 162	51	1.4	2821	4	US-09-736-457-1669	Sequence 1669, Ap	C 235	50	1.4	1001	2	US-08-473-486-10	Sequence 10, Appl
C 163	51	1.4	2821	4	US-09-671-325-1669	Sequence 1669, Ap	C 236	50	1.4	1024	4	US-09-328-475C-50	Sequence 50, Appl
C 164	51	1.4	2821	4	US-09-658-824-1669	Sequence 1669, Ap	C 237	50	1.4	1024	4	US-09-800-729-67	Sequence 67, Appl
C 165	51	1.4	2852	3	US-09-027-137-2	Sequence 2, Appl	C 238	50	1.4	1049	4	US-09-800-729-67	Sequence 67, Appl
C 166	51	1.4	3394	4	US-09-738-946-7	Sequence 7, Appl	C 239	50	1.4	1051	3	US-09-248-335-67	Sequence 67, Appl
C 167	51	1.4	4055	4	US-09-620-312D-706	Sequence 706, App	C 240	50	1.4	1051	4	US-09-893-238-10	Sequence 10, Appl
C 168	51	1.4	4064	4	US-09-873-737A-3	Sequence 3, Appl	C 241	50	1.4	1051	4	US-09-893-238-10	Sequence 10, Appl
C 169	51	1.4	4235	4	US-09-174-937-4	Sequence 4, Appl	C 242	50	1.4	1100	3	US-09-248-335-67	Sequence 67, Appl
C 170	51	1.4	8643	4	US-10-029-907-4	Sequence 4, Appl	C 243	50	1.4	1100	3	US-09-248-335-67	Sequence 67, Appl
C 171	51	1.4	9589	1	US-07-925-695-1	Sequence 1, Appl	C 244	50	1.4	1118	4	US-07-861-458C-4	Sequence 4, Appl
C 172	51	1.4	9589	1	US-07-925-695-1	Sequence 1, Appl	C 245	50	1.4	1118	4	US-09-614-912-181	Sequence 181, App
C 173	51	1.4	9589	1	US-07-925-695-2	Sequence 2, Appl	C 246	50	1.4	1123	3	US-09-152-060-15	Sequence 15, Appl

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C 248	50	1.4	1133	4	US-10-282-048-1	Sequence 1, Appli	C 321	50	1.4	2230	3	US-08-378-313-24	Sequence 24, Appl
C 249	50	1.4	1159	3	US-09-410-464-14	Sequence 14, Appl	C 322	50	1.4	2239	3	US-09-196-390-1	Sequence 1, Appli
C 250	50	1.4	1172	1	US-07-945-288-9	Sequence 9, Appli	C 323	50	1.4	2239	4	US-09-952-677-1	Sequence 1, Appli
C 251	50	1.4	1172	1	US-08-462-831-9	Sequence 9, Appli	C 324	50	1.4	2287	4	US-09-949-016-134	Sequence 134, App
C 252	50	1.4	1172	1	US-08-461-809-9	Sequence 9, Appli	C 325	50	1.4	2301	3	US-08-232-131-8	Sequence 8, Appli
C 253	50	1.4	1172	1	US-08-461-441-9	Sequence 9, Appli	C 326	50	1.4	2301	3	US-09-232-200-8	Sequence 8, Appli
C 254	50	1.4	1172	5	PCT-US93-08518-9	Sequence 9, Appli	C 327	50	1.4	2301	3	US-09-232-197-8	Sequence 8, Appli
C 255	50	1.4	1242	3	US-08-413-974-1	Sequence 1, Appli	C 328	50	1.4	2301	3	US-09-232-201-8	Sequence 8, Appli
C 256	50	1.4	1242	3	US-08-434-418-1	Sequence 1, Appli	C 329	50	1.4	2301	4	US-09-232-195-8	Sequence 8, Appli
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C 258	50	1.4	1242	3	US-08-174-739A-1	Sequence 1, Appli	C 331	50	1.4	2312	4	US-09-631-534-45	Sequence 45, Appl
C 259	50	1.4	1242	3	US-08-434-256-1	Sequence 1, Appli	C 332	50	1.4	2349	4	US-09-805-455-1	Sequence 1, Appli
C 260	50	1.4	1249	4	US-09-461-325-128	Sequence 128, App	C 333	50	1.4	2378	3	US-08-802-805D-20	Sequence 20, Appl
C 261	50	1.4	1249	4	US-10-012-542-128	Sequence 128, App	C 334	50	1.4	2378	4	US-08-860-370-1	Sequence 1, Appli
C 262	50	1.4	1249	4	US-10-115-123-128	Sequence 128, App	C 335	50	1.4	2550	6	5258287-23	Patent No. 5258287
C 263	50	1.4	1260	4	US-09-461-325-93	Sequence 93, Appl	C 336	50	1.4	2550	6	5258287-23	Patent No. 5258287
C 264	50	1.4	1260	4	US-10-012-542-93	Sequence 93, Appl	C 337	50	1.4	2625	4	US-09-270-767-10080	Sequence 10080, A
C 265	50	1.4	1260	4	US-10-115-123-93	Sequence 93, Appl	C 338	50	1.4	2710	3	US-09-232-200-44	Sequence 44, Appl
C 266	50	1.4	1281	4	US-09-436-521A-5	Sequence 5, Appli	C 339	50	1.4	2710	3	US-09-232-200-70	Sequence 70, Appl
C 267	50	1.4	1332	2	US-09-057-762-1	Sequence 1, Appli	C 340	50	1.4	2710	3	US-09-232-197-44	Sequence 44, Appl
C 268	50	1.4	1332	3	US-08-326-119A-1	Sequence 1, Appli	C 341	50	1.4	2710	3	US-09-232-197-70	Sequence 70, Appl
C 269	50	1.4	1364	1	US-08-265-087-3	Sequence 3, Appli	C 342	50	1.4	2710	3	US-09-232-201-44	Sequence 44, Appl
C 270	50	1.4	1364	1	US-08-621-493-3	Sequence 3, Appli	C 343	50	1.4	2710	3	US-09-232-201-70	Sequence 70, Appl
C 271	50	1.4	1364	2	US-08-965-688-3	Sequence 3, Appli	C 344	50	1.4	2710	4	US-09-232-195-44	Sequence 44, Appl
C 272	50	1.4	1414	3	US-09-260-173-3	Sequence 3, Appli	C 345	50	1.4	2710	4	US-09-232-195-70	Sequence 70, Appl
C 273	50	1.4	1414	4	US-09-501-115-5	Sequence 5, Appli	C 346	50	1.4	3299	4	US-09-800-729-68	Sequence 68, Appl
C 274	50	1.4	1474	3	US-08-821-994-64	Sequence 64, Appl	C 347	50	1.4	3366	4	US-09-596-141C-6	Sequence 6, Appli
C 275	50	1.4	1508	3	US-09-039-046-1	Sequence 1, Appli	C 348	50	1.4	3366	4	US-09-595-526C-6	Sequence 6, Appli
C 276	50	1.4	1546	4	US-09-901-151-1	Sequence 1, Appli	C 349	50	1.4	4239	4	US-09-815-048-1	Sequence 1, Appli
C 277	50	1.4	1579	4	US-09-403-466A-5	Sequence 5, Appli	C 350	50	1.4	5503	2	US-08-726-012B-1	Sequence 1, Appli
C 278	50	1.4	1604	1	US-08-665-966-9	Sequence 9, Appli	C 351	50	1.4	5503	4	US-09-023-655-989	Sequence 989, App
C 279	50	1.4	1604	3	US-09-041-780-9	Sequence 9, Appli	C 352	50	1.4	6065	4	US-09-800-729-35	Sequence 35, Appl
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C 281	50	1.4	1700	2	US-08-897-340-4	Sequence 4, Appli	C 354	50	1.4	7855	4	US-09-949-016-12431	Sequence 12431, A
C 282	50	1.4	1700	3	US-09-252-329-4	Sequence 4, Appli	C 355	50	1.4	10106	4	US-09-949-016-14269	Sequence 14269, A
C 283	50	1.4	1728	3	US-08-985-950-7	Sequence 7, Appli	C 356	50	1.4	10106	4	US-09-949-016-14270	Sequence 14270, A
C 284	50	1.4	1748	4	US-09-546-049-7	Sequence 7, Appli	C 357	50	1.4	10106	4	US-09-949-016-14271	Sequence 14271, A
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C 286	50	1.4	1771	4	US-09-907-794A-158	Sequence 158, App	C 359	50	1.4	10442	4	US-09-595-526C-1	Sequence 1, Appli
C 287	50	1.4	1771	4	US-09-866-028-36	Sequence 36, Appl	C 360	50	1.4	10474	4	US-09-596-141C-7	Sequence 7, Appli
C 288	50	1.4	1771	4	US-09-905-1425A-158	Sequence 158, App	C 361	50	1.4	10474	4	US-09-596-141C-7	Sequence 9, Appli
C 289	50	1.4	1771	4	US-09-902-775A-158	Sequence 158, App	C 362	50	1.4	10474	4	US-09-595-526C-7	Sequence 9, Appli
C 290	50	1.4	1771	4	US-09-906-700-158	Sequence 158, App	C 363	50	1.4	10474	4	US-09-595-526C-9	Sequence 9, Appli
C 291	50	1.4	1771	4	US-09-944-457-36	Sequence 36, Appl	C 364	50	1.4	13584	4	US-09-991-258-17	Sequence 17, Appl
C 292	50	1.4	1771	4	US-09-903-603A-158	Sequence 158, App	C 365	50	1.4	15450	4	US-09-470-661A-1	Sequence 1, Appli
C 293	50	1.4	1771	4	US-09-904-920A-158	Sequence 158, App	C 366	50	1.4	21360	4	US-09-949-016-12857	Sequence 12857, A
C 294	50	1.4	1771	4	US-09-903-064-158	Sequence 158, App	C 367	50	1.4	21361	4	US-09-949-016-16245	Sequence 16245, A
C 295	50	1.4	1771	4	US-09-905-381A-158	Sequence 158, App	C 368	50	1.4	24395	4	US-09-949-016-14758	Sequence 14758, A
C 296	50	1.4	1771	4	US-09-906-618-158	Sequence 158, App	C 369	50	1.4	24405	4	US-09-949-016-12040	Sequence 12040, A
C 297	50	1.4	1781	3	US-09-499-302A-1	Sequence 1, Appli	C 370	50	1.4	24405	4	US-09-949-016-17346	Sequence 17346, A
C 298	50	1.4	1813	5	PCT-US94-12883-3	Sequence 3, Appli	C 371	50	1.4	25969	4	US-09-949-016-13397	Sequence 13397, A
C 299	50	1.4	1883	4	US-09-419-679-13	Sequence 13, Appl	C 372	50	1.4	26760	4	US-09-949-016-15894	Sequence 15894, A
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C 302	50	1.4	1998	3	US-09-232-200-68	Sequence 68, Appl	C 375	50	1.4	36855	4	US-09-949-016-17095	Sequence 17095, A
C 303	50	1.4	1998	3	US-09-232-197-68	Sequence 68, Appl	C 376	50	1.4	36855	4	US-09-949-016-15700	Sequence 15700, A
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C 305	50	1.4	1998	4	US-09-232-195-68	Sequence 68, Appl	C 378	50	1.4	44248	4	US-09-949-016-11829	Sequence 11829, A
C 306	50	1.4	2083	4	US-09-716-129-41	Sequence 41, Appl	C 379	50	1.4	44249	4	US-09-949-016-14485	Sequence 14485, A
C 307	50	1.4	2087	3	US-09-232-191-6	Sequence 6, Appli	C 380	50	1.4	44249	4	US-09-949-016-14491	Sequence 14491, A
C 308	50	1.4	2087	3	US-09-232-200-6	Sequence 6, Appli	C 381	50	1.4	45314	4	US-09-949-016-14927	Sequence 14927, A
C 309	50	1.4	2087	3	US-09-232-197-6	Sequence 6, Appli	C 382	50	1.4	50797	4	US-09-949-016-16346	Sequence 16346, A
C 310	50	1.4	2087	3	US-09-232-201-6	Sequence 6, Appli	C 383	50	1.4	50797	4	US-09-949-016-16347	Sequence 16347, A
C 311	50	1.4	2087	3	US-09-232-195-6	Sequence 6, Appli	C 384	50	1.4	51822	4	US-09-949-016-15233	Sequence 15233, A
C 312	50	1.4	2206	4	US-09-907-794A-3	Sequence 3, Appli	C 385	50	1.4	52636	4	US-09-949-016-14839	Sequence 14839, A
C 313	50	1.4	2206	4	US-09-905-125A-3	Sequence 3, Appli	C 386	50	1.4	52598	4	US-09-491-356C-1	Sequence 1, Appli
C 314	50	1.4	2206	4	US-09-902-775A-3	Sequence 3, Appli	C 387	50	1.4	57811	4	US-09-949-016-13192	Sequence 13192, A
C 315	50	1.4	2206	4	US-09-906-700-3	Sequence 3, Appli	C 388	50	1.4	60304	4	US-09-949-016-12218	Sequence 12218, A
C 316	50	1.4	2206	4	US-09-903-603A-3	Sequence 3, Appli	C 389	50	1.4	60304	4	US-09-949-016-15791	Sequence 15791, A
C 317	50	1.4	2206	4	US-09-904-920A-3	Sequence 3, Appli	C 390	50	1.4	62804	3	US-08-800-960-3	Sequence 3, Appli
C 318	50	1.4	2206	4	US-09-909-064-3	Sequence 3, Appli	C 391	50	1.4	62804	3	US-10-096-960-3	Sequence 3, Appli
C 319	50	1.4	2206	4	US-09-905-381A-3	Sequence 3, Appli	C 392	50	1.4	63183	4	US-09-949-016-13047	Sequence 13047, A

393	50	1.4	63183	4	US-09-949-016-13048	Sequence 13048, A	c 466	49	1.4	216	3	US-09-175-928-34	Sequence 34, Appl
394	50	1.4	71863	4	US-09-949-016-15112	Sequence 15112, A	c 467	49	1.4	229	4	US-09-702-705-195	Sequence 195, App
395	50	1.4	84462	4	US-09-949-016-15116	Sequence 15116, A	c 468	49	1.4	229	4	US-09-736-457-195	Sequence 195, App
396	50	1.4	84425	4	US-09-949-016-17402	Sequence 17402, A	c 469	49	1.4	229	4	US-09-614-1248-195	Sequence 195, App
397	50	1.4	117391	4	US-09-949-016-13945	Sequence 13945, A	c 470	49	1.4	229	4	US-09-671-325-195	Sequence 195, App
398	50	1.4	118382	4	US-09-949-016-15996	Sequence 15996, A	c 471	49	1.4	229	4	US-09-589-184-195	Sequence 195, App
399	50	1.4	118382	4	US-09-949-016-15997	Sequence 15997, A	c 472	49	1.4	229	4	US-09-658-824-195	Sequence 195, App
400	50	1.4	137226	4	US-09-949-016-13763	Sequence 13763, A	c 473	49	1.4	240	1	US-08-628-417-6	Sequence 6, Appli
401	50	1.4	130049	4	US-09-949-016-17030	Sequence 17030, A	c 474	49	1.4	255	4	US-09-621-976-9406	Sequence 9406, Ap
402	50	1.4	139552	4	US-09-949-016-15300	Sequence 15300, A	c 475	49	1.4	270	4	US-09-621-976-17927	Sequence 17927, A
403	50	1.4	151256	4	US-09-949-016-12674	Sequence 12674, A	c 476	49	1.4	271	2	US-08-731-272A-29	Sequence 29, Appl
404	50	1.4	151261	4	US-09-949-016-13242	Sequence 13242, A	c 477	49	1.4	272	4	US-09-621-976-8353	Sequence 8353, Ap
405	50	1.4	157822	4	US-09-949-016-16723	Sequence 16723, A	c 478	49	1.4	289	1	US-08-341-568-3	Sequence 3, Appli
406	50	1.4	192506	4	US-09-949-016-15830	Sequence 15830, A	c 479	49	1.4	289	2	US-08-911-020-3	Sequence 3, Appli
407	50	1.4	192169	4	US-09-949-016-15091	Sequence 15091, A	c 480	49	1.4	289	4	US-09-621-976-10009	Sequence 10009, A
408	50	1.4	276237	4	US-09-949-016-17504	Sequence 17504, A	c 481	49	1.4	315	4	US-09-621-976-15329	Sequence 15329, A
409	50	1.4	636591	4	US-09-949-016-11808	Sequence 11808, A	c 482	49	1.4	351	4	US-09-621-976-927	Sequence 927, App
410	50	1.4	636591	4	US-09-949-016-13388	Sequence 13388, A	c 483	49	1.4	358	4	US-09-621-976-15134	Sequence 15134, A
411	49	1.4	57	4	US-09-621-976-12150	Sequence 12150, A	c 484	49	1.4	382	4	US-09-621-976-18855	Sequence 18855, A
412	49	1.4	61	3	US-09-457-959-7	Sequence 7, Appli	c 485	49	1.4	396	4	US-09-640-173-18	Sequence 18, Appl
413	49	1.4	61	4	US-10-079-178-7	Sequence 7, Appli	c 486	49	1.4	396	4	US-09-640-173-53	Sequence 53, Appl
414	49	1.4	63	4	US-09-621-976-12231	Sequence 12231, A	c 487	49	1.4	396	4	US-09-713-550-18	Sequence 18, Appl
415	49	1.4	63	4	US-09-621-976-13480	Sequence 13480, A	c 488	49	1.4	396	4	US-08-713-550-53	Sequence 53, Appl
416	49	1.4	68	4	US-09-621-976-11613	Sequence 11613, A	c 489	49	1.4	396	4	US-09-825-294-18	Sequence 18, Appl
417	49	1.4	68	4	US-09-621-976-11912	Sequence 11912, A	c 490	49	1.4	396	4	US-09-825-294-53	Sequence 53, Appl
418	49	1.4	68	4	US-09-621-976-12005	Sequence 12005, A	c 491	49	1.4	396	4	US-09-970-966-18	Sequence 18, Appl
419	49	1.4	69	4	US-09-621-976-12006	Sequence 12006, A	c 492	49	1.4	396	4	US-09-970-966-53	Sequence 53, Appl
420	49	1.4	70	4	US-09-621-976-13579	Sequence 13579, A	c 493	49	1.4	444	3	US-08-688-988-44	Sequence 44, Appl
421	49	1.4	75	4	US-09-621-976-12516	Sequence 12516, A	c 494	49	1.4	472	4	US-08-270-767-12212	Sequence 767, Appl
422	49	1.4	76	4	US-09-621-976-12446	Sequence 12446, A	c 495	49	1.4	474	3	US-08-516-859A-97	Sequence 97, Appl
423	49	1.4	81	4	US-09-513-999C-17324	Sequence 17324, A	c 496	49	1.4	474	3	US-09-586-472-97	Sequence 97, Appl
424	49	1.4	90	3	US-09-065-058-16	Sequence 16, Appl	c 497	49	1.4	474	3	US-09-528-706-97	Sequence 97, Appl
425	49	1.4	91	3	US-09-404-879A-201	Sequence 201, App	c 498	49	1.4	495	4	US-09-220-132-186	Sequence 186, App
426	49	1.4	91	4	US-09-338-933-201	Sequence 201, App	c 499	49	1.4	530	4	US-09-461-325-28	Sequence 28, Appl
427	49	1.4	91	4	US-09-215-681-201	Sequence 201, App	c 500	49	1.4	530	4	US-10-012-542-28	Sequence 28, Appl
428	49	1.4	91	4	US-09-621-976-14925	Sequence 14925, A	c 501	49	1.4	530	4	US-10-113-123-28	Sequence 28, Appl
429	49	1.4	91	4	US-09-216-003A-201	Sequence 201, App	c 502	49	1.4	570	1	US-07-885-970A-10	Sequence 10, Appl
430	49	1.4	91	4	US-09-667-857-201	Sequence 201, App	c 503	49	1.4	570	1	US-08-298-687A-10	Sequence 10, Appl
431	49	1.4	100	3	US-08-991-789A-30	Sequence 30, Appl	c 504	49	1.4	570	1	US-08-298-829-10	Sequence 10, Appl
432	49	1.4	100	3	US-09-062-451-30	Sequence 30, Appl	c 505	49	1.4	577	3	US-09-149-476-313	Sequence 313, App
433	49	1.4	100	3	US-09-598-326-30	Sequence 30, Appl	c 506	49	1.4	601	4	US-09-949-016-164575	Sequence 164575,
434	49	1.4	100	4	US-09-289-198-30	Sequence 30, Appl	c 507	49	1.4	601	4	US-09-949-016-164576	Sequence 164576,
435	49	1.4	100	4	US-09-429-755-30	Sequence 30, Appl	c 508	49	1.4	609	1	US-08-530-797-9	Sequence 9, Appli
436	49	1.4	100	4	US-09-699-295-30	Sequence 30, Appl	c 509	49	1.4	609	2	US-08-787-335-9	Sequence 9, Appli
437	49	1.4	101	3	US-09-404-879A-293	Sequence 293, App	c 510	49	1.4	612	4	US-09-902-540-1357	Sequence 1357, Ap
438	49	1.4	101	4	US-09-338-933-293	Sequence 293, App	c 511	49	1.4	612	3	US-09-105-542A-2	Sequence 2, Appli
439	49	1.4	101	4	US-09-215-681-293	Sequence 293, App	c 512	49	1.4	647	4	US-09-495-050A-54	Sequence 54, Appl
440	49	1.4	101	4	US-09-667-857-293	Sequence 293, App	c 513	49	1.4	728	3	US-09-091-097-5	Sequence 5, Appli
441	49	1.4	101	4	US-09-216-003A-293	Sequence 293, App	c 514	49	1.4	740	2	US-08-713-000-8	Sequence 8, Appli
442	49	1.4	102	4	US-09-621-976-11436	Sequence 11436, A	c 515	49	1.4	740	2	US-08-975-316-8	Sequence 8, Appli
443	49	1.4	110	4	US-09-621-976-12025	Sequence 12025, A	c 516	49	1.4	740	3	US-09-211-710-8	Sequence 8, Appli
444	49	1.4	120	1	US-08-153-058B-28	Sequence 28, Appl	c 517	49	1.4	740	3	US-09-615-192A-8	Sequence 8, Appli
445	49	1.4	120	1	US-08-060-952C-44	Sequence 44, Appl	c 518	49	1.4	740	4	US-09-169-789-8	Sequence 8, Appli
446	49	1.4	120	2	US-08-151-477A-28	Sequence 28, Appl	c 519	49	1.4	741	2	US-08-975-316-58	Sequence 58, Appl
447	49	1.4	120	3	US-08-819-867-58	Sequence 58, Appl	c 520	49	1.4	741	3	US-09-615-192A-58	Sequence 58, Appl
448	49	1.4	120	3	US-08-464-011B-44	Sequence 44, Appl	c 521	49	1.4	741	4	US-09-621-976-1894	Sequence 1894, Ap
449	49	1.4	120	4	US-09-378-535-58	Sequence 58, Appl	c 522	49	1.4	741	4	US-09-169-789-58	Sequence 58, Appl
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452	49	1.4	140	4	US-09-621-976-17449	Sequence 17449, A	c 525	49	1.4	748	1	US-08-484-332C-3	Sequence 3, Appli
453	49	1.4	141	3	US-08-737-078A-1	Sequence 1, Appli	c 526	49	1.4	785	4	US-09-518-036-9	Sequence 9, Appli
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455	49	1.4	145	4	US-09-621-976-16688	Sequence 16688, A	c 528	49	1.4	788	4	US-09-615-192A-96	Sequence 96, Appl
456	49	1.4	145	4	US-09-621-976-16691	Sequence 16691, A	c 529	49	1.4	788	4	US-09-169-789-96	Sequence 96, Appl
457	49	1.4	146	4	US-09-621-976-16686	Sequence 16686, A	c 530	49	1.4	795	4	US-09-270-767-14068	Sequence 14068, A
458	49	1.4	146	4	US-09-621-976-16695	Sequence 16695, A	c 531	49	1.4	796	1	US-08-104-073-2	Sequence 2, Appli
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460	49	1.4	148	4	US-09-621-976-17450	Sequence 17450, A	c 533	49	1.4	820	4	US-09-621-976-2725	Sequence 2725, Ap
461	49	1.4	153	4	US-09-621-976-17451	Sequence 17451, A	c 534	49	1.4	890	4	US-09-621-976-2725	Sequence 2725, Ap
462	49	1.4	184	4	US-09-621-976-12893	Sequence 12893, A	c 535	49	1.4	903	5	PCT-US95-06406A-21	Sequence 21, Appl
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464	49	1.4	214	4	US-09-621-976-9843	Sequence 9843, App	c 537	49	1.4	958	3	US-09-447-208-5	Sequence 5, Appli
465	49	1.4	216	1	US-08-686-878A-34	Sequence 34, Appl	c 538	49	1.4	958	3	US-09-135-988-5	Sequence 5, Appli

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C 550	49	1.4	1066	1	US-08-157-101A-4	Sequence 4, Appli	C 623	49	1.4	1878	3	US-09-465-558-39	Sequence 39, Appl
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C 570	49	1.4	1395	4	US-09-924-703-5	Sequence 5, Appli	C 643	49	1.4	2271	4	US-09-205-258-243	Sequence 243, App
C 571	49	1.4	1406	4	US-10-000-489-81	Sequence 81, Appl	C 644	49	1.4	2276	4	US-09-205-258-183	Sequence 183, App
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C 573	49	1.4	1461	5	PCT-US95-04258-4	Sequence 4, Appli	C 646	49	1.4	2280	4	US-09-546-553-1	Sequence 1, Appli
C 574	49	1.4	1483	3	US-09-262-749-1	Sequence 1, Appli	C 647	49	1.4	2311	4	US-09-720-317A-19	Sequence 19, Appl
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C 579	49	1.4	1490	3	US-09-734-719-5	Sequence 5, Appli	C 652	49	1.4	2434	4	US-09-489-847-67	Sequence 67, Appl
C 580	49	1.4	1492	4	US-09-369-247-23	Sequence 23, Appl	C 653	49	1.4	2483	4	US-09-205-258-58	Sequence 58, Appl
C 581	49	1.4	1505	2	US-08-909-965C-13	Sequence 13, Appl	C 654	49	1.4	2516	4	US-09-949-016-166	Sequence 166, App
C 582	49	1.4	1507	3	US-09-453-323-1	Sequence 1, Appli	C 655	49	1.4	2625	3	US-09-245-041-18	Sequence 18, Appl
C 583	49	1.4	1509	3	US-09-149-476-179	Sequence 179, App	C 656	49	1.4	2625	4	US-09-358-055B-18	Sequence 18, Appl
C 584	49	1.4	1522	3	US-09-413-574-1	Sequence 1, Appli	C 657	49	1.4	2625	4	US-09-893-238-18	Sequence 18, Appl
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C 586	49	1.4	1540	4	US-09-560-761B-3	Sequence 3, Appli	C 659	49	1.4	2671	6	5168051-9	Patent No. 5168051
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C 594	49	1.4	1641	4	US-08-988-197-8	Sequence 8, Appli	C 667	49	1.4	2836	3	US-09-005-051-24	Sequence 24, Appl
C 595	49	1.4	1641	4	US-10-385-072-8	Sequence 8, Appli	C 668	49	1.4	2836	3	US-09-005-051-26	Sequence 26, Appl
C 596	49	1.4	1660	4	US-09-722-971-9	Sequence 9, Appli	C 669	49	1.4	2836	4	US-09-403-942F-24	Sequence 24, Appl
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C 605	49	1.4	1736	3	US-09-182-816-24	Sequence 24, Appl	C 678	49	1.4	3350	5	PCT-US95-10245-1	Sequence 1, Appli
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C 607	49	1.4	1736	3	US-09-471-528-24	Sequence 24, Appl	C 680	49	1.4	3437	3	US-08-860-339-17	Sequence 17, Appl
C 608	49	1.4	1736	3	US-09-634-530-22	Sequence 22, Appl	C 681	49	1.4	3437	4	US-09-573-629-17	Sequence 17, Appl
C 609	49	1.4	1736	3	US-09-634-530-24	Sequence 24, Appl	C 682	49	1.4	3437	4	US-10-208-349-17	Sequence 17, Appl
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C 686	49	1.4	5173	1	US-08-242-677-1	Sequence 1, Appli	c 759	48	1.3	72	4	US-09-621-976-14842	Sequence 14842, A
C 687	49	1.4	5554	4	US-09-815-923-1	Sequence 1, Appli	c 760	48	1.3	72	4	US-09-621-976-15064	Sequence 15064, A
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C 690	49	1.4	7286	3	US-09-331-581-3	Sequence 3, Appli	c 763	48	1.3	74	4	US-09-621-976-14963	Sequence 14963, A
C 691	49	1.4	7938	3	US-09-331-581-14	Sequence 14, Appl	c 764	48	1.3	75	4	US-09-621-976-15073	Sequence 15073, A
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C 696	49	1.4	64190	4	US-09-949-016-14712	Sequence 14712, A	c 769	48	1.3	77	4	US-09-621-976-14176	Sequence 14176, A
C 697	49	1.4	64190	4	US-09-949-016-14713	Sequence 14713, A	c 770	48	1.3	77	4	US-08-781-986A-2883	Sequence 2883, Ap
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C 699	49	1.4	84171	4	US-09-949-016-16356	Sequence 16356, A	c 772	48	1.3	78	4	US-09-621-976-15092	Sequence 15092, A
C 700	49	1.4	86877	4	US-09-949-016-15491	Sequence 15491, A	c 773	48	1.3	79	4	US-09-621-976-15090	Sequence 15090, A
C 701	49	1.4	86877	4	US-09-949-016-15492	Sequence 15492, A	c 774	48	1.3	80	1	US-07-920-281C-25	Sequence 25, Appl
C 702	49	1.4	192506	4	US-09-949-016-15830	Sequence 15830, A	c 775	48	1.3	80	3	US-08-466-277-25	Sequence 25, Appl
C 703	49	1.4	193303	4	US-09-497-855A-37	Sequence 37, Appl	c 776	48	1.3	80	4	US-09-688-842-25	Sequence 25, Appl
C 704	49	1.4	193303	4	US-09-497-855A-44	Sequence 44, Appl	c 777	48	1.3	81	4	US-09-621-976-12198	Sequence 12198, A
C 705	48	1.3	50	1	US-08-420-443-1	Sequence 1, Appli	c 778	48	1.3	81	4	US-09-621-976-13152	Sequence 13152, A
C 706	48	1.3	50	4	US-09-621-976-14715	Sequence 14715, A	c 779	48	1.3	81	4	US-09-621-976-13601	Sequence 13601, A
C 707	48	1.3	52	4	US-09-621-976-13828	Sequence 13828, A	c 780	48	1.3	82	4	US-09-621-976-11689	Sequence 11689, A
C 708	48	1.3	53	4	US-09-621-976-12332	Sequence 12332, A	c 781	48	1.3	82	4	US-09-621-976-11841	Sequence 11841, A
C 709	48	1.3	53	4	US-09-621-976-14989	Sequence 14989, A	c 782	48	1.3	82	4	US-09-621-976-11864	Sequence 11864, A
C 710	48	1.3	54	4	US-09-621-976-14994	Sequence 14994, A	c 783	48	1.3	82	4	US-09-621-976-11888	Sequence 11888, A
C 711	48	1.3	55	4	US-09-621-976-14535	Sequence 14535, A	c 784	48	1.3	82	4	US-09-621-976-11944	Sequence 11944, A
C 712	48	1.3	55	4	US-09-621-976-14800	Sequence 14800, A	c 785	48	1.3	82	4	US-09-621-976-11949	Sequence 11949, A
C 713	48	1.3	56	4	US-09-621-976-12139	Sequence 12139, A	c 786	48	1.3	82	4	US-09-621-976-12015	Sequence 12015, A
C 714	48	1.3	56	4	US-09-621-976-13461	Sequence 13461, A	c 787	48	1.3	82	4	US-09-621-976-12088	Sequence 12088, A
C 715	48	1.3	56	4	US-09-621-976-14556	Sequence 14556, A	c 788	48	1.3	82	4	US-09-621-976-12103	Sequence 12103, A
C 716	48	1.3	57	4	US-09-621-976-11970	Sequence 11970, A	c 789	48	1.3	82	4	US-09-621-976-12127	Sequence 12127, A
C 717	48	1.3	57	4	US-09-621-976-13937	Sequence 13937, A	c 790	48	1.3	82	4	US-09-621-976-12131	Sequence 12131, A
C 718	48	1.3	58	4	US-09-621-976-8006	Sequence 8006, Ap	c 791	48	1.3	82	4	US-09-621-976-12137	Sequence 12137, A
C 719	48	1.3	58	4	US-09-621-976-14827	Sequence 14827, A	c 792	48	1.3	82	4	US-09-621-976-12322	Sequence 12322, A
C 720	48	1.3	59	4	US-09-621-976-13084	Sequence 13084, A	c 793	48	1.3	82	4	US-09-621-976-12434	Sequence 12434, A
C 721	48	1.3	59	4	US-09-621-976-13752	Sequence 13752, A	c 794	48	1.3	82	4	US-09-621-976-13499	Sequence 13499, A
C 722	48	1.3	60	3	US-09-457-959-8	Sequence 8, Appli	c 795	48	1.3	83	4	US-09-621-976-13526	Sequence 13526, A
C 723	48	1.3	60	4	US-09-621-976-12480	Sequence 12480, A	c 796	48	1.3	83	4	US-09-621-976-12087	Sequence 12087, A
C 724	48	1.3	60	4	US-09-621-976-13761	Sequence 13761, A	c 797	48	1.3	83	4	US-09-621-976-12175	Sequence 12175, A
C 725	48	1.3	60	4	US-09-621-976-14742	Sequence 14742, A	c 798	48	1.3	83	4	US-09-621-976-12195	Sequence 12195, A
C 726	48	1.3	60	4	US-09-621-976-14884	Sequence 14884, A	c 799	48	1.3	83	4	US-09-621-976-12429	Sequence 12429, A
C 727	48	1.3	60	4	US-10-079-178-8	Sequence 8, Appli	c 800	48	1.3	83	4	US-09-621-976-12450	Sequence 12450, A
C 728	48	1.3	61	4	US-09-621-976-11967	Sequence 11967, A	c 801	48	1.3	83	4	US-09-621-976-14751	Sequence 14751, A
C 729	48	1.3	61	4	US-09-621-976-1680	Sequence 1480, A	c 802	48	1.3	84	1	US-09-621-976-14959	Sequence 14959, A
C 730	48	1.3	61	4	US-09-621-976-14681	Sequence 14681, A	c 803	48	1.3	84	1	US-08-664-596B-3	Sequence 3, Appli
C 731	48	1.3	61	4	US-09-621-976-14754	Sequence 14754, A	c 804	48	1.3	84	1	US-08-738-357-3	Sequence 3, Appli
C 732	48	1.3	61	4	US-09-621-976-14799	Sequence 14799, A	c 805	48	1.3	84	4	US-09-621-976-14571	Sequence 14571, A
C 733	48	1.3	61	4	US-09-621-976-14834	Sequence 14834, A	c 806	48	1.3	84	4	US-09-621-976-14577	Sequence 14577, A
C 734	48	1.3	61	4	US-09-621-976-14948	Sequence 14948, A	c 807	48	1.3	85	4	US-09-621-976-13395	Sequence 13395, A
C 735	48	1.3	62	4	US-09-621-976-11091	Sequence 11091, A	c 808	48	1.3	85	4	US-09-621-976-14949	Sequence 14949, A
C 736	48	1.3	62	4	US-09-621-976-14130	Sequence 14130, A	c 809	48	1.3	87	4	US-09-621-976-14560	Sequence 14560, A
C 737	48	1.3	62	4	US-09-621-976-14825	Sequence 14825, A	c 810	48	1.3	87	4	US-09-621-976-14849	Sequence 14849, A
C 738	48	1.3	62	4	US-09-621-976-14936	Sequence 14936, A	c 811	48	1.3	89	4	US-09-621-976-14749	Sequence 14749, A
C 739	48	1.3	63	4	US-09-621-976-13842	Sequence 13842, A	c 812	48	1.3	89	4	US-09-621-976-14974	Sequence 14974, A
C 740	48	1.3	63	4	US-09-621-976-14756	Sequence 14756, A	c 813	48	1.3	90	1	US-08-677-944-1	Sequence 1, Appli
C 741	48	1.3	64	4	US-09-621-976-14858	Sequence 14858, A	c 814	48	1.3	90	1	US-08-677-944-2	Sequence 2, Appli
C 742	48	1.3	65	4	US-09-621-976-14743	Sequence 14743, A	c 815	48	1.3	90	3	US-09-254-048A-1	Sequence 1, Appli
C 743	48	1.3	65	4	US-09-621-976-14853	Sequence 14853, A	c 816	48	1.3	90	3	US-09-921-203-1	Sequence 1, Appli
C 744	48	1.3	66	4	US-09-621-976-12404	Sequence 12404, A	c 817	48	1.3	90	4	US-09-816-089A-2	Sequence 1, Appli
C 745	48	1.3	66	4	US-09-621-976-14819	Sequence 14819, A	c 818	48	1.3	90	4	US-10-106-832-1	Sequence 1, Appli
C 746	48	1.3	67	4	US-09-621-976-11909	Sequence 11909, A	c 819	48	1.3	91	4	US-09-621-976-12161	Sequence 12161, A
C 747	48	1.3	67	4	US-09-621-976-13917	Sequence 13917, A	c 820	48	1.3	92	4	US-09-621-976-13620	Sequence 13620, A
C 748	48	1.3	67	4	US-09-621-976-14753	Sequence 14753, A	c 821	48	1.3	92	4	US-09-621-976-14689	Sequence 14689, A
C 749	48	1.3	69	1	US-08-702-344-7	Sequence 7, Appli	c 822	48	1.3	93	4	US-09-816-089A-8	Sequence 8, Appli
C 750	48	1.3	69	4	US-09-621-976-14105	Sequence 14105, A	c 823	48	1.3	93	4	US-09-621-976-9086	Sequence 9086, Ap
C 751	48	1.3	69	4	US-09-621-976-14869	Sequence 14869, A	c 824	48	1.3	97	4	US-09-621-976-12430	Sequence 12430, A
C 752	48	1.3	69	4	US-09-573-080A-447	Sequence 447, App	c 825	48	1.3	97	1	US-08-088-658-42	Sequence 42, Appl
C 753	48	1.3	70	4	US-09-621-976-14750	Sequence 14750, A	c 826	48	1.3	98	2	US-08-471-907A-42	Sequence 42, Appl
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C 756	48	1.3	72	4	US-09-621-976-9837	Sequence 9837, Ap	c 829	48	1.3	98	4	US-09-621-976-15091	Sequence 15091, A
C 757	48	1.3	72	4	US-09-621-976-10145	Sequence 10145, A	c 830	48	1.3	102	4	US-09-621-976-14804	Sequence 14804, A

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979	48	1.3	470	3	US-09-030-607-102	Sequence 102, App	c1052	48	1.3	780	3	US-08-590-399-36	Sequence 36, Appl
980	48	1.3	470	3	US-09-433-313-102	Sequence 102, App	1053	48	1.3	789	3	US-09-020-956-32	Sequence 32, Appl
981	48	1.3	470	3	US-09-352-616A-102	Sequence 102, App	1054	48	1.3	789	3	US-09-030-607-32	Sequence 32, Appl
982	48	1.3	470	3	US-09-232-149A-102	Sequence 102, App	1055	48	1.3	789	3	US-09-352-616A-32	Sequence 32, Appl
983	48	1.3	470	3	US-09-159-812-102	Sequence 102, App	1056	48	1.3	789	3	US-09-232-149A-32	Sequence 32, Appl
984	48	1.3	470	4	US-09-636-215-102	Sequence 102, App	1057	48	1.3	789	3	US-09-159-812-32	Sequence 32, Appl
985	48	1.3	470	4	US-09-685-166A-102	Sequence 102, App	1058	48	1.3	789	4	US-09-636-215-32	Sequence 32, Appl
986	48	1.3	470	4	US-09-115-453-102	Sequence 102, App	1059	48	1.3	789	4	US-09-685-166A-32	Sequence 32, Appl
987	48	1.3	470	4	US-09-688-489-102	Sequence 102, App	1060	48	1.3	789	4	US-09-115-453-32	Sequence 32, Appl
988	48	1.3	470	4	US-09-679-426-102	Sequence 102, App	1061	48	1.3	789	4	US-09-688-489-32	Sequence 32, Appl
989	48	1.3	470	4	US-09-759-143-102	Sequence 102, App	1062	48	1.3	789	4	US-09-679-426-32	Sequence 32, Appl
990	48	1.3	470	4	US-09-651-236-102	Sequence 102, App	1063	48	1.3	789	4	US-09-759-143-32	Sequence 32, Appl
991	48	1.3	491	4	US-09-311-021-191	Sequence 191, App	1064	48	1.3	789	4	US-09-651-236-32	Sequence 32, Appl
992	48	1.3	508	4	US-09-621-976-17886	Sequence 17886, A	1065	48	1.3	803	4	US-09-800-729-60	Sequence 60, Appl
993	48	1.3	509	3	US-09-030-607-202	Sequence 202, App	1066	48	1.3	835	4	US-09-311-021-71	Sequence 71, Appl
994	48	1.3	509	3	US-09-433-313-202	Sequence 202, App	1067	48	1.3	835	4	US-08-308-883-1	Sequence 1, Appl
995	48	1.3	509	3	US-09-352-616A-202	Sequence 202, App	1068	48	1.3	857	1	US-08-730-163-1	Sequence 1, Appl
996	48	1.3	509	3	US-09-232-149A-202	Sequence 202, App	1069	48	1.3	857	1	US-08-730-163-1	Sequence 1, Appl
997	48	1.3	509	4	US-09-159-812-202	Sequence 202, App	1070	48	1.3	857	3	US-08-256-799-1	Sequence 1, Appl
998	48	1.3	509	4	US-09-636-215-202	Sequence 202, App	1071	48	1.3	857	3	US-08-462-437-1	Sequence 1, Appl
999	48	1.3	509	4	US-09-685-166A-202	Sequence 202, App	1072	48	1.3	872	3	US-09-248-335-63	Sequence 63, Appl
1000	48	1.3	509	4	US-09-115-453-202	Sequence 202, App	1073	48	1.3	873	3	US-09-475-316A-20	Sequence 20, Appl
1001	48	1.3	509	4	US-09-688-489-202	Sequence 202, App	1074	48	1.3	873	4	US-09-704-640-20	Sequence 20, Appl
1002	48	1.3	509	4	US-09-679-426-202	Sequence 202, App	1075	48	1.3	879	1	US-08-158-682A-1	Sequence 1, Appl
1003	48	1.3	509	4	US-09-759-143-202	Sequence 202, App	1076	48	1.3	879	1	US-08-015-203-1	Sequence 1, Appl
1004	48	1.3	509	4	US-09-651-236-202	Sequence 202, App	1077	48	1.3	882	2	US-08-909-965C-9	Sequence 9, Appl
1005	48	1.3	536	2	US-08-341-568-1	Sequence 1, Appl	1078	48	1.3	882	4	US-09-311-021-107	Sequence 107, App
1006	48	1.3	536	2	US-08-911-020-1	Sequence 1, Appl	1079	48	1.3	888	3	US-09-188-930-13	Sequence 13, Appl
1007	48	1.3	550	4	US-09-010-147B-5	Sequence 5, Appl	1080	48	1.3	888	4	US-09-312-283C-13	Sequence 13, Appl
1008	48	1.3	552	4	US-09-461-325-111	Sequence 111, App	1081	48	1.3	940	2	US-08-471-717-1	Sequence 1, Appl
1009	48	1.3	552	4	US-10-012-542-111	Sequence 111, App	1082	48	1.3	941	4	US-09-205-258-186	Sequence 186, App
1010	48	1.3	552	4	US-10-115-123-111	Sequence 111, App	1083	48	1.3	949	4	US-09-489-847-35	Sequence 35, Appl
1011	48	1.3	558	4	US-09-043-861-3	Sequence 3, Appl	1084	48	1.3	960	3	US-09-248-335-57	Sequence 57, Appl
1012	48	1.3	563	4	US-09-621-976-19183	Sequence 19183, A	1085	48	1.3	972	1	US-07-915-934-1	Sequence 1, Appl
1013	48	1.3	572	3	US-09-343-653-5	Sequence 5, Appl	1086	48	1.3	972	1	US-08-325-743-1	Sequence 1, Appl
1014	48	1.3	578	3	US-09-602-877A-95	Sequence 95, Appl	1087	48	1.3	972	3	US-09-549-831-5	Sequence 5, Appl
1015	48	1.3	588	4	US-09-205-258-64	Sequence 64, Appl	1088	48	1.3	974	2	US-08-504-459-13	Sequence 13, Appl
1016	48	1.3	593	4	US-09-904-615-59	Sequence 59, Appl	1089	48	1.3	985	4	US-09-322-409-25	Sequence 25, Appl
1017	48	1.3	600	4	US-09-774-639-44	Sequence 44, Appl	1090	48	1.3	985	4	US-09-322-409-27	Sequence 27, Appl
1018	48	1.3	601	4	US-09-949-016-64894	Sequence 64894, A	1091	48	1.3	985	4	US-09-451-527-25	Sequence 25, Appl
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1020	48	1.3	601	4	US-09-949-016-85308	Sequence 85308, A	1093	48	1.3	990	4	US-09-800-729-79	Sequence 79, Appl
1021	48	1.3	607	4	US-09-809-545A-19	Sequence 19, Appl	1094	48	1.3	1008	4	US-09-780-641-1	Sequence 1, Appl
1022	48	1.3	614	4	US-09-902-540-1318	Sequence 1318, App	1095	48	1.3	1013	4	US-09-322-409-6	Sequence 6, Appl
1023	48	1.3	619	4	US-09-489-847-58	Sequence 58, Appl	1096	48	1.3	1013	4	US-09-322-409-8	Sequence 8, Appl
1024	48	1.3	624	1	US-08-185-414E-1	Sequence 1, Appl	1097	48	1.3	1013	4	US-09-451-527-6	Sequence 6, Appl
1025	48	1.3	630	1	US-08-455-633A-35	Sequence 35, Appl	1098	48	1.3	1013	4	US-09-451-527-8	Sequence 8, Appl
1026	48	1.3	635	1	US-08-416-336-5	Sequence 35, Appl	1099	48	1.3	1020	4	US-09-328-475C-43	Sequence 43, Appl
1027	48	1.3	635	2	US-08-456-460C-35	Sequence 35, Appl	1100	48	1.3	1023	1	US-08-252-966B-16	Sequence 16, Appl
1028	48	1.3	635	5	PCT-US94-05334-35	Sequence 35, Appl	1101	48	1.3	1037	4	US-09-489-847-112	Sequence 112, App
1029	48	1.3	636	4	US-09-594-506-27	Sequence 27, Appl	1102	48	1.3	1039	4	US-09-464-535-23	Sequence 23, Appl
1030	48	1.3	639	4	US-09-482-273-49	Sequence 49, Appl	1103	48	1.3	1046	1	US-08-361-487B-4	Sequence 4, Appl
1031	48	1.3	639	4	US-09-904-615-66	Sequence 66, Appl	1104	48	1.3	1046	1	US-08-484-322C-4	Sequence 4, Appl
1032	48	1.3	664	4	US-09-620-405B-465	Sequence 465, App	1105	48	1.3	1050	4	US-09-482-273-58	Sequence 58, Appl
1033	48	1.3	674	4	US-09-433-828B-465	Sequence 465, App	1106	48	1.3	1062	4	US-09-796-766-3	Sequence 3, Appl
1034	48	1.3	674	4	US-09-604-287A-465	Sequence 465, App	1107	48	1.3	1069	4	US-09-205-258-74	Sequence 74, Appl
1035	48	1.3	674	4	US-09-834-759-465	Sequence 465, App	1108	48	1.3	1098	3	US-09-248-335-35	Sequence 35, Appl
1036	48	1.3	674	4	US-09-590-751A-465	Sequence 465, App	1109	48	1.3	1129	3	US-09-227-357-40	Sequence 40, Appl
1037	48	1.3	674	4	US-09-551-621-465	Sequence 465, App	1110	48	1.3	1129	3	US-09-149-476-119	Sequence 119, App
1038	48	1.3	687	4	US-09-774-639-106	Sequence 106, App	1111	48	1.3	1144	3	US-09-904-615-20	Sequence 20, Appl
1039	48	1.3	688	6	5498694-3	Patent No. 5498694	1112	48	1.3	1147	1	US-09-904-615-20	Sequence 1, Appl
1040	48	1.3	688	6	5498694-3	Patent No. 5498694	1113	48	1.3	1151	4	US-09-270-767-12633	Sequence 12633, A
1041	48	1.3	708	4	US-09-270-767-13081	Sequence 13081, A	1114	48	1.3	1151	3	US-09-149-476-41	Sequence 41, Appl
1042	48	1.3	708	4	US-09-270-767-14600	Sequence 14600, A	1115	48	1.3	1181	3	US-09-149-476-310	Sequence 310, Appl
1043	48	1.3	730	3	US-09-149-476-66	Sequence 66, Appl	1116	48	1.3	1184	4	US-09-489-847-76	Sequence 76, Appl
1044	48	1.3	732	3	US-09-949-016-413	Sequence 413, App	1117	48	1.3	1196	4	US-09-065-040-2	Sequence 2, Appl
1045	48	1.3	742	1	US-07-847-010-12	Sequence 12, Appl	1118	48	1.3	1206	3	US-09-465-558-53	Sequence 53, Appl
1046	48	1.3	742	1	US-09-614-912-93	Sequence 93, Appl	1119	48	1.3	1210	3	US-09-443-041A-29	Sequence 29, Appl
1047	48	1.3	756	4	US-09-465-559-5	Sequence 5, Appl	1120	48	1.3	1210	4	US-09-244-805-45	Sequence 45, Appl
1048	48	1.3	759	4	US-09-513-775B-5	Sequence 5, Appl	1121	48	1.3	1210	4	US-09-720-318A-3	Sequence 3, Appl
1049	48	1.3	769	4			1122	48	1.3	1212	3	US-09-149-476-186	Sequence 186, App

c1113	48	1.3	1214	4	US-09-780-717-28	Sequence 28, Appl	c1196	48	1.3	1534	4	US-08-988-197-6	Sequence 6, Appl
c1114	48	1.3	1215	4	US-09-646-693-1	Sequence 1, Appl	c1197	48	1.3	1534	4	US-10-385-072-6	Sequence 6, Appl
c1115	48	1.3	1230	4	US-09-244-805-6	Sequence 1, Appl	c1198	48	1.3	1538	4	US-09-205-258-193	Sequence 193, App
c1116	48	1.3	1248	4	US-09-489-847-101	Sequence 101, App	c1199	48	1.3	1544	4	US-09-187-999-14	Sequence 14, Appl
c1117	48	1.3	1273	4	US-09-270-767-14731	Sequence 14731, A	c1200	48	1.3	1545	4	US-09-559-023-1	Sequence 1, Appl
c1118	48	1.3	1279	3	US-09-248-335-25	Sequence 25, Appl	c1201	48	1.3	1559	4	US-09-489-847-42	Sequence 42, Appl
c1119	48	1.3	1296	4	US-09-461-325-29	Sequence 29, Appl	c1202	48	1.3	1560	4	US-09-500-495A-5	Sequence 5, Appl
c1120	48	1.3	1296	4	US-10-012-542-29	Sequence 29, Appl	c1203	48	1.3	1576	1	US-08-157-101A-6	Sequence 6, Appl
c1131	48	1.3	1296	4	US-10-115-123-29	Sequence 29, Appl	c1204	48	1.3	1602	1	US-08-530-950-3	Sequence 3, Appl
c1132	48	1.3	1297	4	US-09-800-729-80	Sequence 80, Appl	c1205	48	1.3	1602	1	US-08-888-429A-3	Sequence 3, Appl
c1133	48	1.3	1302	4	US-09-322-409-91	Sequence 91, Appl	c1206	48	1.3	1602	3	US-09-149-879-3	Sequence 3, Appl
c1134	48	1.3	1302	4	US-09-322-409-93	Sequence 93, Appl	c1207	48	1.3	1602	4	US-09-057-009-3	Sequence 3, Appl
c1135	48	1.3	1302	4	US-09-451-527-91	Sequence 91, Appl	c1208	48	1.3	1602	4	US-09-593-653-3	Sequence 3, Appl
c1136	48	1.3	1302	4	US-09-451-527-93	Sequence 93, Appl	c1209	48	1.3	1605	3	US-09-149-476-187	Sequence 187, App
c1137	48	1.3	1307	2	US-08-960-022-17	Sequence 17, Appl	c1210	48	1.3	1606	4	US-09-820-004-1	Sequence 1, Appl
c1138	48	1.3	1307	4	US-09-641-612-3	Sequence 3, Appl	c1211	48	1.3	1619	4	US-09-522-714-11	Sequence 11, Appl
c1139	48	1.3	1308	4	US-10-151-832-1	Sequence 1, Appl	c1212	48	1.3	1636	4	US-09-578-194-6	Sequence 6, Appl
c1140	48	1.3	1319	2	US-08-504-459-7	Sequence 7, Appl	c1213	48	1.3	1637	4	US-09-578-194-6	Sequence 6, Appl
c1141	48	1.3	1325	1	US-08-306-691B-51	Sequence 51, Appl	c1214	48	1.3	1639	2	US-08-737-524B-1	Sequence 1, Appl
c1142	48	1.3	1325	2	US-08-464-517-1	Sequence 1, Appl	c1215	48	1.3	1651	4	US-09-800-729-41	Sequence 41, Appl
c1143	48	1.3	1325	2	US-08-246-361A-1	Sequence 1, Appl	c1216	48	1.3	1653	3	US-09-345-469-2	Sequence 2, Appl
c1144	48	1.3	1325	3	US-08-463-772-1	Sequence 1, Appl	c1217	48	1.3	1666	3	US-09-822-862-1	Sequence 1, Appl
c1145	48	1.3	1325	5	PCT-US93-05000-1	Sequence 1, Appl	c1218	48	1.3	1683	3	US-09-347-803-11	Sequence 11, Appl
c1146	48	1.3	1332	3	US-09-333-423-1	Sequence 1, Appl	c1219	48	1.3	1692	4	US-09-821-803A-5	Sequence 5, Appl
c1147	48	1.3	1342	4	US-09-489-847-89	Sequence 89, Appl	c1220	48	1.3	1705	4	US-09-205-258-216	Sequence 216, App
c1148	48	1.3	1358	4	US-09-614-221A-1	Sequence 1, Appl	c1221	48	1.3	1708	4	US-09-859-053-31	Sequence 31, Appl
c1149	48	1.3	1358	4	US-09-949-016-463	Sequence 463, App	c1222	48	1.3	1721	5	PCT-US96-00994-3	Sequence 4, Appl
c1150	48	1.3	1359	3	US-09-387-574-11	Sequence 11, Appl	c1223	48	1.3	1725	4	US-09-668-097A-21	Sequence 21, Appl
c1151	48	1.3	1359	3	US-09-668-096-11	Sequence 11, Appl	c1224	48	1.3	1738	4	US-09-918-909A-27	Sequence 27, Appl
c1152	48	1.3	1386	2	US-08-897-340-1	Sequence 1, Appl	c1225	48	1.3	1740	4	US-09-709-103-45	Sequence 45, Appl
c1153	48	1.3	1386	3	US-09-252-329-1	Sequence 1, Appl	c1226	48	1.3	1746	4	US-09-439-410A-45	Sequence 45, App
c1154	48	1.3	1393	1	US-07-602-824A-1	Sequence 1, Appl	c1227	48	1.3	1746	4	US-09-485-529-57	Sequence 57, App
c1155	48	1.3	1393	1	US-07-983-451-1	Sequence 1, Appl	c1228	48	1.3	1768	4	US-09-485-529-13	Sequence 13, Appl
c1156	48	1.3	1393	1	US-08-261-577-6	Sequence 6, Appl	c1229	48	1.3	1780	3	US-09-202-548B-5	Sequence 5, Appl
c1157	48	1.3	1395	2	US-08-553-367A-1	Sequence 1, Appl	c1230	48	1.3	1780	4	US-09-942-858-5	Sequence 5, Appl
c1158	48	1.3	1395	3	US-09-295-306-1	Sequence 1, Appl	c1231	48	1.3	1780	4	US-10-461-180-5	Sequence 5, Appl
c1159	48	1.3	1395	3	US-09-734-719-1	Sequence 1, Appl	c1232	48	1.3	1790	4	US-09-866-028-31	Sequence 31, Appl
c1160	48	1.3	1405	4	US-09-244-111-9	Sequence 9, Appl	c1233	48	1.3	1790	3	US-09-944-457-31	Sequence 31, Appl
c1161	48	1.3	1412	4	US-09-614-912-197	Sequence 197, App	c1234	48	1.3	1798	3	US-09-797-906-1	Sequence 1, Appl
c1162	48	1.3	1441	3	US-08-821-994-63	Sequence 63, Appl	c1235	48	1.3	1804	2	US-08-504-459-5	Sequence 5, Appl
c1163	48	1.3	1443	4	US-09-904-615-21	Sequence 21, Appl	c1236	48	1.3	1810	4	US-09-800-729-73	Sequence 73, Appl
c1164	48	1.3	1443	3	US-09-697-367-19	Sequence 19, Appl	c1237	48	1.3	1811	4	US-09-800-729-77	Sequence 77, Appl
c1165	48	1.3	1445	3	US-09-814-951A-1	Sequence 1, Appl	c1238	48	1.3	1813	3	US-09-071-224-3	Sequence 3, Appl
c1166	48	1.3	1445	4	US-09-918-909A-19	Sequence 19, Appl	c1239	48	1.3	1827	4	US-09-720-318A-9	Sequence 9, Appl
c1167	48	1.3	1447	3	US-09-443-041A-27	Sequence 27, Appl	c1240	48	1.3	1829	4	US-09-885-723-4	Sequence 4, Appl
c1168	48	1.3	1459	4	US-09-537-654-3	Sequence 3, Appl	c1241	48	1.3	1844	4	US-10-003-352-7	Sequence 7, Appl
c1169	48	1.3	1478	4	US-09-216-393B-7	Sequence 7, Appl	c1242	48	1.3	1864	3	US-09-149-476-130	Sequence 130, App
c1170	48	1.3	1486	4	US-09-461-325-73	Sequence 73, Appl	c1243	48	1.3	1865	3	US-09-370-253-5	Sequence 5, Appl
c1171	48	1.3	1486	4	US-10-012-542-73	Sequence 73, Appl	c1244	48	1.3	1867	4	US-09-482-273-81	Sequence 81, Appl
c1172	48	1.3	1486	4	US-10-115-123-73	Sequence 73, Appl	c1245	48	1.3	1868	3	US-09-739-455-1	Sequence 1, Appl
c1173	48	1.3	1493	1	US-08-340-820-24	Sequence 24, Appl	c1246	48	1.3	1872	3	US-09-291-922-27	Sequence 27, Appl
c1174	48	1.3	1493	1	US-08-593-535-24	Sequence 24, Appl	c1247	48	1.3	1878	3	US-09-732-025-1	Sequence 1, Appl
c1175	48	1.3	1493	6	5340934-5	Sequence 6, Appl	c1248	48	1.3	1882	3	US-09-370-253-1	Sequence 1, Appl
c1176	48	1.3	1493	6	5340934-5	Sequence 6, Appl	c1249	48	1.3	1882	4	US-09-419-679-3	Sequence 3, Appl
c1177	48	1.3	1503	4	US-09-907-794A-220	Sequence 220, App	c1250	48	1.3	1895	3	US-09-444-336-7	Sequence 7, Appl
c1178	48	1.3	1503	4	US-09-905-125A-220	Sequence 220, App	c1251	48	1.3	1897	1	US-08-184-632-1	Sequence 1, Appl
c1179	48	1.3	1503	4	US-09-907-775A-220	Sequence 220, App	c1252	48	1.3	1925	4	US-09-148-545-128	Sequence 128, App
c1180	48	1.3	1503	4	US-09-906-700-220	Sequence 220, App	c1253	48	1.3	1927	3	US-09-336-536-66	Sequence 66, Appl
c1181	48	1.3	1503	4	US-09-903-603A-220	Sequence 220, App	c1254	48	1.3	1929	3	US-09-146-950-1	Sequence 1, Appl
c1182	48	1.3	1503	4	US-09-904-920A-220	Sequence 220, App	c1255	48	1.3	1933	3	US-09-920-759-3	Sequence 3, Appl
c1183	48	1.3	1503	4	US-09-909-064A-220	Sequence 220, App	c1256	48	1.3	1958	3	US-08-665-034A-3	Sequence 3, Appl
c1184	48	1.3	1503	4	US-09-905-381A-220	Sequence 220, App	c1257	48	1.3	1981	4	US-09-720-317A-3	Sequence 3, Appl
c1185	48	1.3	1503	4	US-09-906-618-220	Sequence 220, App	c1258	48	1.3	1985	4	US-09-907-779A-212	Sequence 212, App
c1186	48	1.3	1512	2	US-08-909-965C-8	Sequence 8, Appl	c1259	48	1.3	1985	4	US-09-905-125A-212	Sequence 212, App
c1187	48	1.3	1525	3	US-09-157-603-4	Sequence 4, Appl	c1260	48	1.3	1985	4	US-09-902-775A-212	Sequence 212, App
c1188	48	1.3	1525	3	US-09-587-436-4	Sequence 4, Appl	c1261	48	1.3	1985	4	US-09-906-700-212	Sequence 212, App
c1189	48	1.3	1525	3	US-08-927-165A-4	Sequence 4, Appl	c1262	48	1.3	1985	4	US-09-903-603A-212	Sequence 212, App
c1190	48	1.3	1525	4	US-09-461-325-110	Sequence 110, App	c1263	48	1.3	1985	4	US-09-904-920A-212	Sequence 212, App
c1191	48	1.3	1525	4	US-10-012-542-110	Sequence 110, App	c1264	48	1.3	1985	4	US-09-909-054-212	Sequence 212, App
c1192	48	1.3	1525	4	US-10-115-123-110	Sequence 110, App	c1265	48	1.3	1985	4	US-09-905-381A-212	Sequence 212, App
c1193	48	1.3	1527	4	US-09-244-111-7	Sequence 7, Appl	c1266	48	1.3	1985	4	US-09-906-618-212	Sequence 212, App
c1194	48	1.3	1530	4	US-09-811-361-19	Sequence 19, Appl	c1267	48	1.3	1993	4	US-09-889-463A-13	Sequence 13, Appl
c1195	48	1.3	1534	1	US-08-300-903A-6	Sequence 6, Appl	c1268	48	1.3	2010	1	US-07-864-475A-4	Sequence 4, Appl

c1269	48	1.3	2010	2	US-08-468-249A-4	Sequence 4, Appl	c1342	48	1.3	2539	4	US-10-144-198-21	Sequence 21, Appl
c1270	48	1.3	2017	4	US-09-690-454-45	Sequence 45, Appl	c1343	48	1.3	2540	4	US-09-949-016-431	Sequence 431, Appl
c1271	48	1.3	2025	3	US-09-149-476-316	Sequence 316, Appl	c1344	48	1.3	2567	3	US-08-993-260-4	Sequence 4, Appl
c1272	48	1.3	2028	2	US-09-211-930-12	Sequence 12, Appl	c1345	48	1.3	2604	2	US-08-630-118A-3	Sequence 3, Appl
c1273	48	1.3	2028	3	US-09-340-993-12	Sequence 12, Appl	c1346	48	1.3	2604	2	US-08-838-399-3	Sequence 3, Appl
c1274	48	1.3	2028	3	US-09-468-442-12	Sequence 12, Appl	c1347	48	1.3	2604	3	US-08-235-839-3	Sequence 3, Appl
c1275	48	1.3	2045	3	US-09-153-060-22	Sequence 22, Appl	c1348	48	1.3	2604	3	US-09-327-035-3	Sequence 3, Appl
c1276	48	1.3	2082	2	US-08-785-310A-2	Sequence 2, Appl	c1349	48	1.3	2608	4	US-09-904-615-16	Sequence 16, Appl
c1277	48	1.3	2091	3	US-09-813-818-1	Sequence 1, Appl	c1350	48	1.3	2610	3	US-09-545-814-1	Sequence 1, Appl
c1278	48	1.3	2091	4	US-10-199-333-1	Sequence 1, Appl	c1351	48	1.3	2610	3	US-09-545-814-3	Sequence 3, Appl
c1279	48	1.3	2096	3	US-09-008-481A-10	Sequence 10, Appl	c1352	48	1.3	2628	1	US-08-143-219-1	Sequence 1, Appl
c1280	48	1.3	2096	3	US-09-195-666A-16	Sequence 16, Appl	c1353	48	1.3	2634	3	US-09-463-238-3	Sequence 3, Appl
c1281	48	1.3	2096	3	US-09-309-592-10	Sequence 10, Appl	c1354	48	1.3	2648	3	US-09-417-255-6	Sequence 6, Appl
c1282	48	1.3	2096	3	US-09-633-705-16	Sequence 16, Appl	c1355	48	1.3	2648	3	US-09-348-942-6	Sequence 6, Appl
c1283	48	1.3	2096	3	US-09-634-858A-16	Sequence 16, Appl	c1356	48	1.3	2648	3	US-09-457-626-6	Sequence 6, Appl
c1284	48	1.3	2096	4	US-08-869-927C-16	Sequence 16, Appl	c1357	48	1.3	2648	4	US-09-576-008-6	Sequence 6, Appl
c1285	48	1.3	2114	1	US-07-803-622E-6	Sequence 6, Appl	c1358	48	1.3	2665	3	US-08-971-089-5	Sequence 5, Appl
c1286	48	1.3	2158	1	US-07-602-608-1	Sequence 1, Appl	c1359	48	1.3	2668	3	US-09-370-838-156	Sequence 156, Appl
c1287	48	1.3	2158	1	US-08-261-578-1	Sequence 1, Appl	c1360	48	1.3	2668	4	US-09-854-133-156	Sequence 156, Appl
c1288	48	1.3	2182	4	US-09-214-619-3	Sequence 3, Appl	c1361	48	1.3	2674	3	US-09-817-180-1	Sequence 1, Appl
c1289	48	1.3	2182	4	US-09-555-820A-11	Sequence 11, Appl	c1362	48	1.3	2674	4	US-10-003-295-1	Sequence 1, Appl
c1290	48	1.3	2184	3	US-08-953-918C-1	Sequence 1, Appl	c1363	48	1.3	2674	4	US-10-066-130-19	Sequence 19, Appl
c1291	48	1.3	2184	3	US-08-697-766A-1	Sequence 1, Appl	c1364	48	1.3	2677	4	US-09-733-634B-1	Sequence 1, Appl
c1292	48	1.3	2186	3	US-09-360-545-66	Sequence 66, Appl	c1365	48	1.3	2695	4	US-09-706-197-3	Sequence 3, Appl
c1293	48	1.3	2202	3	US-09-465-558-59	Sequence 59, Appl	c1366	48	1.3	2718	4	US-09-667-135-1	Sequence 1, Appl
c1294	48	1.3	2218	4	US-09-016-434-1157	Sequence 1157, Appl	c1367	48	1.3	2771	4	US-10-066-130-18	Sequence 18, Appl
c1295	48	1.3	2218	4	US-10-328-668-7	Sequence 7, Appl	c1368	48	1.3	2797	4	US-09-482-273-74	Sequence 74, Appl
c1296	48	1.3	2233	1	US-08-496-631-1	Sequence 1, Appl	c1369	48	1.3	2806	3	US-09-653-839-9	Sequence 9, Appl
c1297	48	1.3	2246	4	US-09-363-708-3	Sequence 3, Appl	c1370	48	1.3	2806	4	US-10-202-619-27	Sequence 27, Appl
c1298	48	1.3	2246	4	US-09-083-508-3	Sequence 3, Appl	c1371	48	1.3	2808	4	US-09-917-254-27	Sequence 27, Appl
c1299	48	1.3	2262	4	US-09-311-021-171	Sequence 171, Appl	c1372	48	1.3	2822	4	US-09-907-794A-48	Sequence 48, Appl
c1300	48	1.3	2269	3	US-09-394-645-1	Sequence 1, Appl	c1373	48	1.3	2822	4	US-09-905-125A-48	Sequence 48, Appl
c1301	48	1.3	2269	3	US-09-243-560B-1	Sequence 1, Appl	c1374	48	1.3	2822	4	US-09-902-775A-48	Sequence 48, Appl
c1302	48	1.3	2285	2	US-08-967-101-136	Sequence 136, Appl	c1375	48	1.3	2822	4	US-09-906-700-48	Sequence 48, Appl
c1303	48	1.3	2285	2	US-08-592-541-136	Sequence 136, Appl	c1376	48	1.3	2822	4	US-09-903-603A-48	Sequence 48, Appl
c1304	48	1.3	2285	3	US-09-124-698-136	Sequence 136, Appl	c1377	48	1.3	2822	4	US-09-904-920A-48	Sequence 48, Appl
c1305	48	1.3	2285	3	US-09-127-680-136	Sequence 136, Appl	c1378	48	1.3	2822	4	US-09-909-064-48	Sequence 48, Appl
c1306	48	1.3	2285	3	US-09-124-523-136	Sequence 136, Appl	c1379	48	1.3	2822	4	US-09-905-381A-48	Sequence 48, Appl
c1307	48	1.3	2285	4	US-09-636-796A-136	Sequence 136, Appl	c1380	48	1.3	2822	4	US-09-906-618-48	Sequence 48, Appl
c1308	48	1.3	2288	4	US-09-800-729-24	Sequence 24, Appl	c1381	48	1.3	2880	3	US-09-115-954-3	Sequence 3, Appl
c1309	48	1.3	2291	4	US-09-220-133-114	Sequence 114, Appl	c1382	48	1.3	2882	4	US-09-943-016-724	Sequence 724, Appl
c1310	48	1.3	2291	4	US-09-814-915A-95	Sequence 95, Appl	c1383	48	1.3	2908	4	US-09-904-615-35	Sequence 35, Appl
c1311	48	1.3	2311	4	US-08-496-841C-137	Sequence 137, Appl	c1384	48	1.3	2968	3	US-09-813-819-1	Sequence 1, Appl
c1312	48	1.3	2311	4	US-09-800-729-66	Sequence 66, Appl	c1385	48	1.3	2968	3	US-09-920-048-1	Sequence 1, Appl
c1313	48	1.3	2311	4	US-09-614-912-91	Sequence 91, Appl	c1386	48	1.3	2968	4	US-10-014-501-1	Sequence 1, Appl
c1314	48	1.3	2320	3	US-09-202-904A-13	Sequence 13, Appl	c1387	48	1.3	2989	6	5378464-1	Patent No. 5378464
c1315	48	1.3	2320	3	US-09-149-476-24	Sequence 24, Appl	c1388	48	1.3	2989	6	5378464-1	Patent No. 5378464
c1316	48	1.3	2327	4	US-10-066-130-20	Sequence 20, Appl	c1389	48	1.3	3007	4	US-09-810-268-1	Sequence 1, Appl
c1317	48	1.3	2346	3	US-09-149-476-193	Sequence 193, Appl	c1390	48	1.3	3040	1	US-08-446-794A-1	Sequence 1, Appl
c1318	48	1.3	2381	1	US-08-021-608D-9	Sequence 9, Appl	c1391	48	1.3	3040	2	US-08-750-007-2	Sequence 2, Appl
c1319	48	1.3	2381	1	US-08-726-160-9	Sequence 9, Appl	c1392	48	1.3	3040	2	US-08-945-024-1	Sequence 1, Appl
c1320	48	1.3	2381	5	PCT-US94-01782-9	Sequence 9, Appl	c1393	48	1.3	3047	3	US-09-873-737A-1	Sequence 1, Appl
c1321	48	1.3	2384	1	US-08-021-608D-1	Sequence 1, Appl	c1394	48	1.3	3080	3	US-09-099-081A-25	Sequence 25, Appl
c1322	48	1.3	2384	1	US-08-726-160-1	Sequence 1, Appl	c1395	48	1.3	3080	3	US-09-245-281-25	Sequence 25, Appl
c1323	48	1.3	2384	5	PCT-US94-01782-1	Sequence 1, Appl	c1396	48	1.3	3080	3	US-09-207-359B-25	Sequence 25, Appl
c1324	48	1.3	2394	4	US-09-800-729-33	Sequence 33, Appl	c1397	48	1.3	3080	4	US-09-340-620A-25	Sequence 25, Appl
c1325	48	1.3	2406	4	US-09-594-506-37	Sequence 37, Appl	c1398	48	1.3	3080	4	US-09-865-364-25	Sequence 25, Appl
c1326	48	1.3	2407	3	US-09-370-807-7	Sequence 7, Appl	c1399	48	1.3	3108	4	US-09-937-521-11	Sequence 11, Appl
c1327	48	1.3	2407	3	US-09-921-259-7	Sequence 7, Appl	c1400	48	1.3	3116	4	US-09-311-021-187	Sequence 187, Appl
c1328	48	1.3	2431	1	US-07-847-743B-25	Sequence 25, Appl	c1401	48	1.3	3124	3	US-09-734-030-1	Sequence 1, Appl
c1329	48	1.3	2431	1	US-08-456-201-25	Sequence 25, Appl	c1402	48	1.3	3124	4	US-10-153-921-1	Sequence 1, Appl
c1330	48	1.3	2431	2	US-08-456-241-25	Sequence 25, Appl	c1403	48	1.3	3136	4	US-09-689-728-1	Sequence 1, Appl
c1331	48	1.3	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	c1404	48	1.3	3136	4	US-09-680-689-1	Sequence 1, Appl
c1332	48	1.3	2438	4	US-09-393-634-4	Sequence 4, Appl	c1405	48	1.3	3136	4	US-10-017-066A-1	Sequence 1, Appl
c1333	48	1.3	2442	4	US-09-575-081B-3	Sequence 3, Appl	c1406	48	1.3	3145	4	US-09-949-016-1149	Sequence 1149, Appl
c1334	48	1.3	2445	4	US-09-949-016-781	Sequence 781, Appl	c1407	48	1.3	3200	1	US-08-444-405-1	Sequence 1, Appl
c1335	48	1.3	2447	2	US-09-014-969-14	Sequence 14, Appl	c1408	48	1.3	3200	1	US-08-384-850-1	Sequence 1, Appl
c1336	48	1.3	2481	2	US-08-630-118A-1	Sequence 1, Appl	c1409	48	1.3	3238	3	US-08-123-934A-5	Sequence 5, Appl
c1337	48	1.3	2481	2	US-08-838-399-1	Sequence 1, Appl	c1410	48	1.3	3238	5	US-09-874-638-5	Sequence 5, Appl
c1338	48	1.3	2481	3	US-09-235-839-1	Sequence 1, Appl	c1411	48	1.3	3238	5	PCT-US94-10080-5	Sequence 5, Appl
c1339	48	1.3	2481	3	US-09-327-035-1	Sequence 1, Appl	c1412	48	1.3	3268	4	US-09-688-188B-1	Sequence 1, Appl
c1340	48	1.3	2485	4	US-09-889-463A-9	Sequence 9, Appl	c1413	48	1.3	3268	4	US-09-291-417D-1	Sequence 1, Appl
c1341	48	1.3	2527	4	US-09-244-805-29	Sequence 29, Appl	c1414	48	1.3	3275	3	US-09-370-838-151	Sequence 151, Appl

1228 CAATTCCTATCTAGGCCCCCGCCAGACAGTACAGCTGAGAGAGGCGAGCTCGAAGG 1287
1375 CAATTCCTATCTAGGCCCCCGCCAGACAGTACAGCTGAGAGAGGCGAGCTCGAAGG 1434
1288 CTTTGCACATGCTGCTTCTTTGGAAGGAAGACTTTTCAAGGGCCCGTTCCCGTGCAG 1347
1435 CTTTGCACATGCTGCTTCTTTGGAAGGAAGACTTTTCAAGGGCCCGTTCCCGTGCAG 1494
1348 CTGCTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAGCCCAAGGAGTGGAC 1407
1495 CTGCTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAGCCCAAGGAGTGGAC 1554
1408 TTGCTGCTATTCTTCTAGCGGAGCTGCTGAGAAAGGCTCTGATGGACGATGAGATA 1467
1555 TTGCTGCTATTCTTCTCGGGAGCTGCTGAGAAAGGCTCTGATGGACGATGAGATA 1614
1468 GAGGCTGCTGAGGAGCTTCCACAGCCCAAGTGGCCAGGGGACTTTGCTGAAGAATTA 1527
1615 GAGGCTGCTGAGGAGCTTCCACAGCCCAAGTGGCCAGGGGACTTTGCTGAAGAATTA 1674
1528 GCACACATGCTTAATCTGTTTCTAGCCGAGCCCAAGTGGCCAGGACCCCAAGTGAAGCC 1587
1675 GCACACATGCTTAATCTGTTTCTAGCCGAGCCCAAGTGGCCAGGACCCCAAGTGAAGCC 1734
1588 TGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGGCTGAGAAGTG 1647
1735 TGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGGCTGAGAAGTG 1794
1648 GCGCTGCTTGGGCAATTCACAGAACCTTGAGACCCCGCTTCCAGAGAGGCCCAAGTG 1707
1795 GCGCTGCTTGGGCAATTCACAGAACCTTGAGACCCCGCTTCCAGAGAGGCCCAAGTG 1854
1708 CCCAATGAGACCCCTCACTGTTGGGTGTAGCTGGTCTACAGTCAGACTTCTGCTCT 1767
1855 CCCAATGAGACCCCTCACTGTTGGGTGTAGCTGGTCTACAGTCAGACTTCTGCTCT 1914
1768 AAGGCTGCTCACTGCTGGCATCCACACCGCAATCTTAGAGAAAGGAGAGTTGGCCCTGA 1827
1915 AAGGCTGCTCACTGCTGGCATCCACACCGCAATCTTAGAGAAAGGAGAGTTGGCCCTGA 1974
1828 TTTGGGATATGCGAGAAAGTCCAGAGATGCCAGTCTCTGGAGTGAAGAGGTGTGTTT 1887
1975 TTTGGGATATGCGAGAAAGTCCAGAGATGCCAGTCTCTGGAGTGAAGAGGTGTGTTT 2034
1888 GTTATCTCTTGGATTAATGAATGAGGTGTGGGTGTCTCAACACAGAAATTCAG 1947
2035 GTTATCTCTTGGATTAATGAATGAGGTGTGGGTGTCTCAACACAGAAATTCAG 2094
1948 CCTCATTTGCTATCCAGCATCTCTTAAACCTTTCTAGTCTTGGAAATTCATGACAGGC 2007
2095 CCTCATTTGCTATCCAGCATCTCTTAAACCTTTCTAGTCTTGGAAATTCATGACAGGC 2154
2008 AAATGACTCTGCTTAATTAATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTT 2067
2155 AAATGACTCTGCTTAATTAATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTT 2214
2068 TCTTATCACCAGAGCTGACTGCCA 2093
2215 TCTTATCACCAGAGCTGACTGCCA 2240

RESULT 2
US-09-799-451-817/c
; Sequence 817, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.

APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yuning
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radjoe T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL_genes Version 2.0
SEQ ID NO 817
LENGTH: 2223
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)..(2149)
US-09-799-451-817
Query Match 5.6%; Score 201; DB 4; Length 2223;
Best local Similarity 100.0%; Pred. No. 1.6e-55;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3380 ACAGGAAGTTGGGCTCCCGCACACACAGGCGGGGCTCCCGCGCGCGCGCCAC 3439
Db 1931 ACAGGAAGTTGGGCTCCCGCACACACAGGCGGGGCTCCCGCGCGCGCGCCAC 1872
QY 3440 CACGCTCAGGGCGCGGTAGACAAAGTGAAGTGGCTTGGCTTGGCTGCGCAGAGT 3499
Db 1871 CACGCTCAGGGCGCGGTAGACAAAGTGAAGTGGCTTGGCTTGGCTGCGCAGAGT 1812
QY 3500 AGCCCTTATGATGCGGCGCGGTGCTCGCCAGCTGGAAGCAGCGCGCTCCACCA 3559
Db 1811 AGCCCTTATGATGCGGCGCGGTGCTCGCCAGCTGGAAGCAGCGCGCTCCACCA 1752
QY 3560 GCACGAACAGCGGTCGCGCT 3580
Db 1751 GCACGAACAGCGGTCGCGCT 1731

RESULT 3
US-09-949-016-144142
; Sequence 144142, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144142
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144142

```
Query Match          1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||

QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 4
US-09-949-016-144200
; Sequence 144200, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144200
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144200

Query Match          1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||

QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 5
US-09-949-016-144258
; Sequence 144258, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144258
; LENGTH: 601
; TYPE: DNA
```

```
; ORGANISM: Human
US-09-949-016-144258

Query Match          1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||

QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 6
US-09-949-016-144316
; Sequence 144316, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144316
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144316

Query Match          1.8%; Score 64; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 2240
    |||||
Db 165 CCTGAGGTCAGGAATTCAGACACCGCTGGCCAAACATGCGCAAAACCCCATCTCTACTAAA 224
    |||||

QY 2241 AATA 2244
    |||||
Db 225 AATA 228

RESULT 7
US-09-949-016-15817
; Sequence 15817, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 15817
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15817

Query Match 1.8%; Score 64; DB 4; Length 53394;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240
|||
Db 45991 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050

QY 2241 AATA 2244
|||
Db 46051 AATA 46054

RESULT 8
US-09-949-016-15818
; Sequence 15818, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15818
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15818

Query Match 1.8%; Score 64; DB 4; Length 53394;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240
|||
Db 45991 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050

QY 2241 AATA 2244
|||
Db 46051 AATA 46054

RESULT 9
US-09-949-016-15819
; Sequence 15819, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15819
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15819

Query Match 1.8%; Score 64; DB 4; Length 53394;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240
|||
Db 45991 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050

QY 2241 AATA 2244
|||
Db 46051 AATA 46054

RESULT 10
US-09-949-016-15820
; Sequence 15820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15820
; LENGTH: 53394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(53394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15820

Query Match 1.8%; Score 64; DB 4; Length 53394;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 2240
|||
Db 45991 CCTGAGGTCAGGAATTCAGACCCCTGGCCCAACATGGCAAAACCCCATCTCTACTAAA 46050

QY 2241 AATA 2244
|||

Db 46051 AATA 46054

RESULT 11
US-09-949-016-15602/c
; Sequence 15602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15602
; LENGTH: 134890
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15602

Query Match 1.7%; Score 62; DB 4; Length 134890;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2183 TCAGTTCAGGAATTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAA 2242
Db 32159 TCAGTTCAGGAATTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAA 32100
Qy 2243 TA 2244
Db 32099 TA 32098

RESULT 12
US-09-372-422A-23/c
; Sequence 23, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)...(838)
US-09-372-422A-23

Query Match 1.6%; Score 59; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2583 GCGGCGCGCCCTTT 2641
Db 1193 GCGGCGCGCCCTTT 1135

RESULT 13

US-09-949-016-12928/c
; Sequence 12928, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12928
; LENGTH: 194537
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(194537)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12928

Query Match 1.6%; Score 59; DB 4; Length 194537;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2195 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 2253
Db 16281 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 16223

RESULT 14

US-09-949-016-12740/c
; Sequence 12740, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12740
; LENGTH: 201529
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(201529)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12740

Query Match 1.6%; Score 59; DB 4; Length 201529;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2195 TTCAGACACGCTGGCCACATGCGCAAAACCCCTCTCTACTAAAAAATTA 2253

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OM nucleic - nucleic search, using sw model

Run on: March 29, 2005, 04:09:43 ; Search time 5524 Seconds
(without alignments)
3862.130 Million cell updates/sec

Perfect score: 3580
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

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Post-processing: Listing first 1500 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 69	274	7.7	464	10	US-09-918-995-29372
C 70	201	5.6	2223	17	US-10-302-172-817
C 71	173	4.8	177	9	US-09-880-107-3886
72	152	4.2	441	17	US-10-242-355-187
73	82	2.3	1157	18	US-10-425-115-174016
74	79	2.2	403	18	US-10-425-115-155989
C 75	79	2.2	483	9	US-09-783-590-6515
C 76	76	2.1	2938	18	US-10-425-115-9664
77	74	2.1	1483	18	US-10-425-115-17547

Sequence 110917, A	1950	2.1	74	78	18	US-10-425-115-110917
Sequence 13888, A	5396	1.8	65	79	14	US-10-198-846-13888
Sequence 141959, A	1190	1.7	61	80	18	US-10-425-115-141959
Sequence 80981, A	1772	1.7	61	81	18	US-10-425-115-80981
Sequence 4953, Ap	60	1.7	60	82	10	US-09-908-975-4953
Sequence 23466, A	60	1.7	60	83	10	US-09-908-975-23466
Sequence 6405, Ap	397	1.7	60	84	9	US-09-960-352-6405
Sequence 100376, A	493	1.7	60	85	18	US-10-425-115-100376
Sequence 3, Appli	1408	1.7	60	86	9	US-09-745-605-3
Sequence 46816, A	1824	1.7	60	87	18	US-10-425-115-46816
Sequence 13051, A	246	1.6	59	88	18	US-10-437-963-13051
Sequence 93292, A	291	1.6	59	89	17	US-10-424-599-93292
Sequence 23886, A	307	1.6	59	90	18	US-10-425-115-23886
Sequence 69622, A	338	1.6	59	91	18	US-10-425-115-69622
Sequence 6394, Ap	358	1.6	59	92	18	US-10-425-115-6394
Sequence 53982, A	363	1.6	59	93	17	US-10-424-599-21016
Sequence 21016, A	363	1.6	59	94	18	US-10-425-115-95279
Sequence 95279, A	375	1.6	59	95	18	US-10-425-115-95279
Sequence 49666, A	377	1.6	59	96	17	US-10-424-599-49666
Sequence 13424, A	378	1.6	59	97	18	US-10-425-115-13424
Sequence 109809, A	382	1.6	59	98	18	US-10-425-115-109809
Sequence 182112, A	382	1.6	59	99	18	US-10-425-115-182112
Sequence 40806, A	389	1.6	59	100	18	US-10-425-115-40806
Sequence 90745, A	392	1.6	59	101	17	US-10-424-599-90745
Sequence 89348, A	401	1.6	59	102	18	US-10-425-115-89348
Sequence 67437, A	421	1.6	59	103	18	US-10-437-963-67437
Sequence 36699, A	437	1.6	59	104	17	US-10-424-599-36699
Sequence 131478, A	446	1.6	59	105	17	US-10-424-599-131478
Sequence 18960, A	461	1.6	59	106	18	US-10-767-701-18960
Sequence 80899, A	462	1.6	59	107	18	US-10-425-115-80899
Sequence 74761, A	464	1.6	59	108	17	US-10-424-599-74761
Sequence 156487, A	477	1.6	59	109	18	US-10-425-115-156487
Sequence 36374, A	481	1.6	59	110	18	US-10-425-115-36374
Sequence 48287, A	510	1.6	59	111	17	US-10-424-599-48287
Sequence 73854, A	569	1.6	59	112	18	US-10-425-115-73854
Sequence 14414, A	640	1.6	59	113	18	US-10-425-115-14414
Sequence 182620, A	643	1.6	59	114	18	US-10-425-115-182620
Sequence 42846, A	837	1.6	59	115	18	US-10-425-115-96026
Sequence 96026, A	859	1.6	59	116	18	US-10-425-115-42846
Sequence 60549, A	1076	1.6	59	117	18	US-10-425-115-60549
Sequence 105683, A	2063	1.6	59	118	18	US-10-425-115-105683
Sequence 754, App	81	1.6	58	119	14	US-10-066-543-754
Sequence 1308, Ap	81	1.6	58	120	14	US-10-066-543-1308
Sequence 589, App	89	1.6	58	121	14	US-10-066-543-589
Sequence 849, App	92	1.6	58	122	14	US-10-066-543-849
Sequence 5046, Ap	93	1.6	58	123	9	US-09-983-965-5046
Sequence 339, App	97	1.6	58	124	14	US-10-066-543-339
Sequence 906, App	100	1.6	58	125	9	US-09-770-696-906
Sequence 895, App	101	1.6	58	126	9	US-09-770-696-895
Sequence 890, App	102	1.6	58	127	9	US-09-770-696-890
Sequence 142, App	102	1.6	58	128	9	US-09-924-035A-142
Sequence 876, App	103	1.6	58	129	9	US-09-770-696-876
Sequence 878, App	103	1.6	58	130	9	US-09-770-696-878
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Sequence 880, App	103	1.6	58	132	9	US-09-770-696-880
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Sequence 875, App	103	1.6	58	134	9	US-09-924-035A-875
Sequence 1307, Ap	103	1.6	58	135	14	US-10-066-543-1307
Sequence 865, App	104	1.6	58	136	9	US-09-770-696-865
Sequence 866, App	104	1.6	58	137	9	US-09-770-696-866
Sequence 714, App	104	1.6	58	138	9	US-09-924-035A-714
Sequence 468, App	104	1.6	58	139	14	US-10-066-543-468
Sequence 855, App	105	1.6	58	140	9	US-09-770-696-855
Sequence 87, Appl	105	1.6	58	141	9	US-09-924-035A-87
Sequence 820, App	108	1.6	58	142	9	US-09-770-696-820
Sequence 821, App	108	1.6	58	143	9	US-09-770-696-821
Sequence 515, App	109	1.6	58	144	9	US-09-924-035A-515
Sequence 796, App	109	1.6	58	145	9	US-09-924-035A-796
Sequence 792, App	110	1.6	58	146	9	US-09-770-696-792
Sequence 784, App	110	1.6	58	147	9	US-09-770-696-784
Sequence 7296, Ap	111	1.6	58	148	9	US-09-960-352-7296
Sequence 471, App	112	1.6	58	149	9	US-09-924-035A-471
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152	58	1.6	113	9	US-09-924-035A-535	Sequence 535, App	225	58	1.6	330	11	US-09-922-293-42	Sequence 42, Appl
153	58	1.6	114	9	US-09-770-696-756	Sequence 756, App	226	58	1.6	335	18	US-10-425-115-159362	Sequence 159362, App
154	58	1.6	114	9	US-09-770-696-757	Sequence 757, App	227	58	1.6	337	9	US-09-960-352-6976	Sequence 6976, App
155	58	1.6	114	9	US-09-924-035A-747	Sequence 747, App	228	58	1.6	342	17	US-10-424-599-130104	Sequence 130104, App
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158	58	1.6	115	9	US-09-924-035A-258	Sequence 258, App	231	58	1.6	358	14	US-10-198-846-9603	Sequence 9603, App
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161	58	1.6	116	9	US-09-924-035A-466	Sequence 466, App	c 234	58	1.6	370	9	US-09-960-352-6169	Sequence 6169, App
162	58	1.6	116	14	US-10-066-543-761	Sequence 761, App	235	58	1.6	382	9	US-09-960-352-3209	Sequence 3209, App
163	58	1.6	117	14	US-10-066-543-763	Sequence 763, App	236	58	1.6	382	18	US-10-425-115-112847	Sequence 112847, App
164	58	1.6	118	9	US-09-770-696-706	Sequence 706, App	237	58	1.6	385	9	US-09-770-791-99	Sequence 99, Appl
165	58	1.6	118	9	US-09-770-696-708	Sequence 708, App	238	58	1.6	392	9	US-09-960-352-13003	Sequence 13003, A
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167	58	1.6	118	14	US-10-066-543-1097	Sequence 1097, App	240	58	1.6	401	9	US-09-983-965-3184	Sequence 3184, App
168	58	1.6	119	9	US-09-960-352-1069	Sequence 1069, App	c 241	58	1.6	403	18	US-10-425-115-155989	Sequence 155989, A
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171	58	1.6	121	9	US-09-770-696-684	Sequence 684, App	244	58	1.6	410	9	US-09-960-352-7492	Sequence 7492, App
172	58	1.6	121	9	US-09-924-035A-51	Sequence 51, Appl	245	58	1.6	414	9	US-09-960-352-9161	Sequence 9161, App
173	58	1.6	121	14	US-10-066-543-790	Sequence 790, App	246	58	1.6	415	9	US-09-960-352-6869	Sequence 6869, App
174	58	1.6	122	14	US-10-066-543-807	Sequence 807, App	247	58	1.6	415	9	US-09-960-352-4867	Sequence 4867, App
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189	58	1.6	145	14	US-10-066-543-1004	Sequence 1004, App	262	58	1.6	554	17	US-10-333-184-319	Sequence 319, App
190	58	1.6	145	14	US-10-066-543-1096	Sequence 1096, App	263	58	1.6	568	17	US-10-332-859-123	Sequence 123, App
191	58	1.6	152	9	US-09-960-352-6995	Sequence 6995, App	264	58	1.6	571	17	US-10-424-599-13254	Sequence 13254, A
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193	58	1.6	181	9	US-09-960-352-1301	Sequence 1301, App	266	58	1.6	589	16	US-10-231-417-62	Sequence 62, Appl
194	58	1.6	186	9	US-09-924-035A-789	Sequence 789, App	267	58	1.6	592	14	US-10-198-846-8340	Sequence 8340, App
195	58	1.6	196	9	US-09-924-035A-208	Sequence 208, App	268	58	1.6	592	14	US-10-198-846-8817	Sequence 8817, App
196	58	1.6	203	9	US-09-960-352-3742	Sequence 3742, App	269	58	1.6	631	14	US-10-198-846-2882	Sequence 2882, App
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203	58	1.6	228	9	US-09-960-352-10334	Sequence 10334, App	275	58	1.6	786	10	US-09-925-302-133	Sequence 133, App
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205	58	1.6	236	9	US-09-960-352-12183	Sequence 12183, A	c 277	58	1.6	836	9	US-09-770-445-613	Sequence 613, App
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213	58	1.6	283	9	US-09-960-352-12075	Sequence 12075, A	c 285	58	1.6	991	18	US-10-739-930-1451	Sequence 38, Appl
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217	58	1.6	301	9	US-09-924-035A-351	Sequence 351, App	c 289	58	1.6	1023	18	US-10-854-485-38	Sequence 1631, App
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221	58	1.6	312	9	US-09-960-352-6315	Sequence 6315, App	c 293	58	1.6	1064	10	US-09-974-879-124	Sequence 126, App
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223	58	1.6	316	18	US-10-425-115-127645	Sequence 127645, App	c 295	58	1.6	1064	10	US-09-818-683-126	Sequence 126, App

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C 301	1.6	1083	14	US-10-091-438-17	Sequence 17, Appl	C 374	58	1.6	2778	14	US-10-176-847-75	Sequence 75, Appl
C 302	1.6	1083	14	US-10-091-438-83	Sequence 83, Appl	C 375	58	1.6	2778	14	US-10-176-847-75	Sequence 75, Appl
C 303	1.6	1140	9	US-09-925-299-14	Sequence 14, Appl	C 376	58	1.6	2875	9	US-09-801-220-1	Sequence 1, Appl
C 304	1.6	1140	10	US-09-925-299-14	Sequence 14, Appl	C 377	58	1.6	2875	9	US-09-801-220-1	Sequence 1, Appl
C 305	1.6	1156	17	US-10-264-049-544	Sequence 544, App	C 378	58	1.6	2964	13	US-10-184-648-9	Sequence 9, Appl
C 306	1.6	1172	9	US-09-925-299-127	Sequence 127, App	C 379	58	1.6	2964	13	US-10-042-431-25	Sequence 25, Appl
C 307	1.6	1172	10	US-09-925-299-127	Sequence 127, App	C 380	58	1.6	3102	15	US-10-155-895-5	Sequence 5, Appl
C 308	1.6	1172	15	US-10-106-698-286	Sequence 286, App	C 381	58	1.6	3118	9	US-09-925-300-424	Sequence 424, App
C 309	1.6	1180	18	US-10-739-930-1332	Sequence 1332, App	C 382	58	1.6	3138	18	US-10-739-930-1391	Sequence 1391, App
C 310	1.6	1257	9	US-09-741-711-8	Sequence 8, Appl	C 383	58	1.6	3169	10	US-09-796-753-93	Sequence 93, Appl
C 311	1.6	1325	18	US-10-767-795-4065	Sequence 4065, App	C 384	58	1.6	3169	10	US-09-796-753-93	Sequence 107, App
C 312	1.6	1331	9	US-09-764-884-11	Sequence 11, Appl	C 385	58	1.6	3196	9	US-09-782-980-50	Sequence 50, Appl
C 313	1.6	1331	14	US-10-092-256-11	Sequence 11, Appl	C 386	58	1.6	3196	18	US-10-806-018-50	Sequence 50, Appl
C 314	1.6	1334	17	US-10-264-237-638	Sequence 638, App	C 387	58	1.6	3747	11	US-09-764-875-331	Sequence 331, App
C 315	1.6	1361	17	US-10-351-334-64	Sequence 64, Appl	C 388	58	1.6	4560	18	US-10-437-963-78114	Sequence 78114, A
C 316	1.6	1375	17	US-10-351-334-120	Sequence 120, App	C 389	58	1.6	4897	15	US-10-288-222A-23	Sequence 23, Appl
C 317	1.6	1376	17	US-10-351-334-66	Sequence 66, Appl	C 390	58	1.6	5109	14	US-10-170-102-1	Sequence 1, Appl
C 318	1.6	1411	13	US-10-000-273-5	Sequence 5, Appl	C 391	57	1.6	87	14	US-10-066-543-628	Sequence 628, App
C 319	1.6	1411	16	US-10-385-760-5	Sequence 5, Appl	C 392	57	1.6	108	14	US-10-066-543-470	Sequence 470, App
C 320	1.6	1459	17	US-10-264-237-744	Sequence 744, App	C 393	57	1.6	131	15	US-10-106-698-392	Sequence 392, App
C 321	1.6	1494	17	US-10-310-154-162	Sequence 162, App	C 394	57	1.6	155	14	US-10-091-483-28	Sequence 28, Appl
C 322	1.6	1551	17	US-10-264-049-852	Sequence 852, App	C 395	57	1.6	155	14	US-10-091-483-28	Sequence 28, Appl
C 323	1.6	1574	17	US-10-374-780A-1251	Sequence 1251, App	C 396	57	1.6	179	9	US-09-960-352-14191	Sequence 14191, A
C 324	1.6	1596	17	US-10-426-776-40	Sequence 40, Appl	C 397	57	1.6	226	17	US-10-131-827-8671	Sequence 8671, App
C 325	1.6	1618	9	US-09-800-729-29	Sequence 29, Appl	C 398	57	1.6	237	9	US-09-764-846-65	Sequence 65, Appl
C 326	1.6	1637	17	US-10-374-780A-840	Sequence 840, App	C 399	57	1.6	237	14	US-10-091-483-65	Sequence 65, Appl
C 327	1.6	1772	10	US-09-813-153-58	Sequence 58, Appl	C 400	57	1.6	269	18	US-10-437-963-80835	Sequence 80835, A
C 328	1.6	1779	10	US-09-802-668-103	Sequence 103, App	C 401	57	1.6	289	17	US-10-424-599-51278	Sequence 51278, A
C 329	1.6	1779	16	US-10-243-475-103	Sequence 103, App	C 402	57	1.6	303	15	US-10-106-698-709	Sequence 709, App
C 330	1.6	1810	14	US-10-062-548-11	Sequence 11, Appl	C 403	57	1.6	324	18	US-10-425-115-132897	Sequence 132897, A
C 331	1.6	1810	19	US-10-918-446-11	Sequence 11, Appl	C 404	57	1.6	329	17	US-10-424-599-64059	Sequence 64059, A
C 332	1.6	1834	9	US-09-934-289A-41	Sequence 41, Appl	C 405	57	1.6	369	9	US-09-960-352-3028	Sequence 3028, App
C 333	1.6	1834	19	US-10-932-991-41	Sequence 41, Appl	C 406	57	1.6	380	18	US-10-425-115-64692	Sequence 64692, A
C 334	1.6	1857	17	US-10-264-237-1103	Sequence 1103, App	C 407	57	1.6	385	18	US-10-425-115-54576	Sequence 54576, A
C 335	1.6	1865	16	US-10-243-475-118	Sequence 118, App	C 408	57	1.6	410	18	US-10-425-115-165149	Sequence 165149, A
C 336	1.6	1885	17	US-10-374-780A-849	Sequence 849, App	C 409	57	1.6	411	18	US-10-425-115-79198	Sequence 79198, A
C 337	1.6	1902	18	US-10-193-452-16	Sequence 16, Appl	C 410	57	1.6	415	9	US-09-770-423-487	Sequence 487, App
C 338	1.6	1920	17	US-10-310-154-60	Sequence 60, Appl	C 411	57	1.6	417	9	US-09-924-035A-250	Sequence 250, App
C 339	1.6	2022	9	US-09-925-298-22	Sequence 22, Appl	C 412	57	1.6	429	17	US-10-424-599-27791	Sequence 27791, A
C 340	1.6	2022	14	US-10-102-806-22	Sequence 22, Appl	C 413	57	1.6	430	18	US-10-425-115-99951	Sequence 99951, A
C 341	1.6	2034	16	US-10-047-855-2	Sequence 2, Appl	C 414	57	1.6	455	9	US-09-770-444-566	Sequence 566, App
C 342	1.6	2034	17	US-10-426-776-19	Sequence 19, Appl	C 415	57	1.6	457	9	US-09-924-035A-228	Sequence 228, App
C 343	1.6	2038	10	US-09-885-723-6	Sequence 6, Appl	C 416	57	1.6	460	18	US-10-425-115-73400	Sequence 73400, A
C 344	1.6	2073	15	US-10-106-698-433	Sequence 433, App	C 417	57	1.6	491	18	US-10-437-963-3643	Sequence 3643, App
C 345	1.6	2076	10	US-09-986-480-116	Sequence 116, App	C 418	57	1.6	503	18	US-10-425-115-41124	Sequence 41124, A
C 346	1.6	2093	10	US-09-796-753-85	Sequence 85, App	C 419	57	1.6	529	17	US-10-424-599-62243	Sequence 62243, A
C 347	1.6	2140	9	US-09-764-853-250	Sequence 250, App	C 420	57	1.6	552	18	US-10-425-115-102957	Sequence 102957, A
C 348	1.6	2202	16	US-10-372-686-3	Sequence 3, Appl	C 421	57	1.6	578	18	US-10-425-115-62108	Sequence 62108, A
C 349	1.6	2202	16	US-10-371-558-3	Sequence 3, Appl	C 422	57	1.6	580	18	US-10-425-115-168241	Sequence 168241, A
C 350	1.6	2202	16	US-10-375-553-3	Sequence 3, Appl	C 423	57	1.6	618	18	US-10-437-963-88030	Sequence 88030, A
C 351	1.6	2202	17	US-10-372-553-3	Sequence 3, Appl	C 424	57	1.6	738	9	US-09-925-300-606	Sequence 606, App
C 352	1.6	2236	10	US-09-814-353-19364	Sequence 19364, A	C 425	57	1.6	995	17	US-10-424-599-10204	Sequence 10204, A
C 353	1.6	2241	14	US-10-198-846-13592	Sequence 13592, A	C 426	57	1.6	1023	17	US-10-374-780A-1317	Sequence 1317, App
C 354	1.6	2242	18	US-10-357-930-22588	Sequence 22588, A	C 427	57	1.6	1023	17	US-10-412-699B-1465	Sequence 1465, App
C 355	1.6	2242	18	US-10-357-930-28429	Sequence 28429, A	C 428	57	1.6	1046	9	US-09-925-237-307	Sequence 307, App
C 356	1.6	2252	17	US-10-374-780A-1488	Sequence 1488, App	C 429	57	1.6	1102	18	US-10-425-115-15192	Sequence 15192, A
C 357	1.6	2252	17	US-10-412-699B-1576	Sequence 1576, App	C 430	57	1.6	1162	11	US-09-764-875-163	Sequence 163, App
C 358	1.6	2266	17	US-10-264-049-471	Sequence 471, App	C 431	57	1.6	1194	15	US-10-106-698-1692	Sequence 1692, App
C 359	1.6	2274	14	US-10-097-065-113	Sequence 113, App	C 432	57	1.6	1198	9	US-09-789-561-19	Sequence 19, Appl
C 360	1.6	2274	17	US-10-372-876-113	Sequence 113, App	C 433	57	1.6	1198	18	US-10-883-936-19	Sequence 19, Appl
C 361	1.6	2292	11	US-09-764-875-321	Sequence 321, App	C 434	57	1.6	1306	18	US-10-739-930-1378	Sequence 1378, App
C 362	1.6	2294	17	US-10-264-049-818	Sequence 818, App	C 435	57	1.6	1621	9	US-09-739-907-14	Sequence 14, Appl
C 363	1.6	2357	15	US-10-106-698-2037	Sequence 2037, App	C 436	57	1.6	1621	11	US-09-938-671-14	Sequence 14, Appl
C 364	1.6	2369	17	US-10-635-822-13	Sequence 13, Appl	C 437	57	1.6	1621	11	US-10-935-098-14	Sequence 14, Appl
C 365	1.6	2419	17	US-10-310-154-151	Sequence 151, App	C 438	57	1.6	1782	18	US-10-425-115-5454	Sequence 5454, App
C 366	1.6	2591	18	US-10-357-930-21265	Sequence 21265, A	C 439	57	1.6	1968	17	US-10-424-599-97293	Sequence 97293, A
C 367	1.6	2591	18	US-10-357-930-27107	Sequence 27107, A	C 440	57	1.6	2235	15	US-10-318-780-20	Sequence 20, Appl
C 368	1.6	2713	16	US-10-436-523-1	Sequence 1, Appl	C 441	57	1.6	2581	14	US-10-062-548-51	Sequence 51, Appl
C 369	1.6	2713	16	US-10-436-523-31	Sequence 31, Appl	C 442	57	1.6	2581	19	US-10-918-446-51	Sequence 51, Appl

C 443	57	1.6	2584	17	US-10-632-983-47	Sequence 47, Appl	56	1.6	895	18	US-10-767-701-9396	Sequence 9396, Ap
C 444	57	1.6	3160	13	US-10-098-841-273	Sequence 273, App	56	1.6	907	18	US-10-481-652-11	Sequence 11, Appl
C 445	56	1.6	72	9	US-09-919-580-221	Sequence 221, App	56	1.6	931	10	US-09-984-276-31	Sequence 31, Appl
C 446	56	1.6	73	9	US-09-919-580-542	Sequence 542, App	56	1.6	931	10	US-09-984-271-31	Sequence 31, Appl
C 447	56	1.6	74	9	US-09-919-580-262	Sequence 262, App	56	1.6	938	18	US-10-425-115-70736	Sequence 70736, A
C 448	56	1.6	74	9	US-09-919-580-394	Sequence 394, App	56	1.6	980	15	US-10-195-730-26	Sequence 26, Appl
C 449	56	1.6	74	18	US-10-021-323-9257	Sequence 9257, Ap	56	1.6	980	15	US-10-799-747-26	Sequence 26, Appl
C 450	56	1.6	77	9	US-09-919-580-135	Sequence 135, App	56	1.6	1039	18	US-10-739-930-1331	Sequence 1331, Ap
C 451	56	1.6	79	9	US-09-919-580-206	Sequence 206, App	56	1.6	1070	17	US-10-424-599-141566	Sequence 141566,
C 452	56	1.6	81	9	US-09-919-580-749	Sequence 749, App	56	1.6	1080	18	US-10-425-115-107267	Sequence 107267,
C 453	56	1.6	82	9	US-09-919-580-220	Sequence 220, App	56	1.6	1080	18	US-10-425-115-136900	Sequence 136900,
C 454	56	1.6	82	9	US-09-919-580-278	Sequence 278, App	56	1.6	1138	9	US-09-800-729-44	Sequence 44, Appl
C 455	56	1.6	90	9	US-09-919-580-157	Sequence 157, App	56	1.6	1342	18	US-10-425-115-150282	Sequence 150282,
C 456	56	1.6	95	9	US-09-919-580-246	Sequence 246, App	56	1.6	1362	15	US-10-050-882-44	Sequence 44, Appl
C 457	56	1.6	100	9	US-09-919-580-428	Sequence 428, App	56	1.6	1367	16	US-10-411-224-37	Sequence 37, Appl
C 458	56	1.6	105	14	US-10-066-543-872	Sequence 872, App	56	1.6	1367	17	US-10-047-021-37	Sequence 37, Appl
C 459	56	1.6	113	9	US-09-983-965-4693	Sequence 4693, Ap	56	1.6	1407	17	US-10-426-776-20	Sequence 20, Appl
C 460	56	1.6	117	9	US-09-919-580-762	Sequence 762, App	56	1.6	1408	18	US-10-425-115-104777	Sequence 104777,
C 461	56	1.6	128	14	US-10-066-543-1216	Sequence 1216, Ap	56	1.6	1421	16	US-10-411-224-24	Sequence 24, Appl
C 462	56	1.6	154	9	US-09-919-580-152	Sequence 152, App	56	1.6	1421	17	US-10-047-021-24	Sequence 24, Appl
C 463	56	1.6	160	9	US-09-960-352-11058	Sequence 11058, A	56	1.6	1524	9	US-09-925-302-193	Sequence 193, App
C 464	56	1.6	161	9	US-09-919-580-243	Sequence 243, App	56	1.6	1524	10	US-09-925-302-193	Sequence 193, App
C 465	56	1.6	208	17	US-10-424-599-123367	Sequence 123367,	56	1.6	1526	17	US-10-364-237-227	Sequence 227, App
C 466	56	1.6	244	18	US-10-425-115-88230	Sequence 88230, A	56	1.6	1548	18	US-10-425-115-88255	Sequence 88255, A
C 467	56	1.6	255	18	US-10-425-115-25874	Sequence 25874, A	56	1.6	1554	18	US-10-425-115-138108	Sequence 138108,
C 468	56	1.6	279	17	US-10-424-599-83996	Sequence 83996, A	56	1.6	1574	9	US-09-925-301-581	Sequence 581, App
C 469	56	1.6	286	9	US-09-960-352-8161	Sequence 8161, Ap	56	1.6	1657	9	US-09-925-301-134	Sequence 134, App
C 470	56	1.6	338	18	US-10-437-963-57609	Sequence 57609, A	56	1.6	1694	9	US-09-925-299-144	Sequence 144, App
C 471	56	1.6	353	18	US-10-425-115-113949	Sequence 113949,	56	1.6	1694	10	US-09-925-299-144	Sequence 144, App
C 472	56	1.6	366	18	US-10-425-115-130732	Sequence 130732,	56	1.6	1694	18	US-10-425-115-115253	Sequence 115253,
C 473	56	1.6	367	17	US-10-424-599-65070	Sequence 65070, A	56	1.6	1722	10	US-09-984-276-102	Sequence 102, App
C 474	56	1.6	370	18	US-10-437-963-26300	Sequence 26300, A	56	1.6	1722	10	US-09-984-271-102	Sequence 102, App
C 475	56	1.6	383	17	US-10-424-599-46064	Sequence 46064, A	56	1.6	1724	17	US-10-364-237-1239	Sequence 1239, Ap
C 476	56	1.6	398	17	US-10-424-599-13756	Sequence 13756, A	56	1.6	1732	17	US-10-424-599-61177	Sequence 61177, A
C 477	56	1.6	401	17	US-10-424-599-58129	Sequence 58129, A	56	1.6	1779	10	US-09-892-877-108	Sequence 108, App
C 478	56	1.6	408	9	US-09-960-352-11233	Sequence 11233, A	56	1.6	1779	10	US-09-948-783-109	Sequence 109, App
C 479	56	1.6	411	17	US-10-425-115-16531	Sequence 16531, A	56	1.6	1791	18	US-10-425-115-48559	Sequence 48559, A
C 480	56	1.6	417	18	US-10-424-599-117777	Sequence 117777,	56	1.6	1825	9	US-09-922-261-75	Sequence 75, Appl
C 481	56	1.6	424	9	US-09-960-352-13484	Sequence 13484, A	56	1.6	1892	17	US-10-364-237-1324	Sequence 1324, Ap
C 482	56	1.6	437	9	US-09-924-035A-152	Sequence 152, App	56	1.6	1977	17	US-10-364-237-1217	Sequence 1217, Ap
C 483	56	1.6	438	18	US-10-425-115-70695	Sequence 70695, A	56	1.6	2108	18	US-10-425-115-14255	Sequence 14255, A
C 484	56	1.6	456	18	US-10-425-115-59159	Sequence 59159, A	56	1.6	2539	18	US-10-425-115-140288	Sequence 140288,
C 485	56	1.6	464	18	US-10-437-963-19054	Sequence 19054, A	56	1.6	2755	17	US-10-264-049-222	Sequence 222, App
C 486	56	1.6	467	18	US-10-437-963-19054	Sequence 19054, A	56	1.6	3144	9	US-09-925-302-191	Sequence 191, App
C 487	56	1.6	467	18	US-10-437-963-598	Sequence 598, App	56	1.6	3144	10	US-09-925-302-191	Sequence 191, App
C 488	56	1.6	467	18	US-10-425-115-89331	Sequence 89331, A	56	1.6	3144	10	US-09-814-353-20006	Sequence 20006, A
C 489	56	1.6	485	18	US-10-357-930-55641	Sequence 55641, A	56	1.6	4773	14	US-10-066-543-1258	Sequence 1258, Ap
C 490	56	1.6	487	9	US-09-729-835-22	Sequence 22, Appl	55	1.5	94	14	US-10-066-543-713	Sequence 713, App
C 491	56	1.6	506	17	US-10-424-599-56636	Sequence 56636, A	55	1.5	96	14	US-10-066-543-342	Sequence 342, App
C 492	56	1.6	521	18	US-10-425-115-111585	Sequence 111585,	55	1.5	110	14	US-09-983-965-207	Sequence 207, App
C 493	56	1.6	522	18	US-10-425-115-123105	Sequence 123105,	55	1.5	138	9	US-09-815-343-1505	Sequence 1505, Ap
C 494	56	1.6	531	17	US-10-424-599-81285	Sequence 81285, A	55	1.5	172	17	US-10-097-105-1505	Sequence 1505, Ap
C 495	56	1.6	541	17	US-10-424-599-35290	Sequence 35290, A	55	1.5	210	9	US-09-960-352-3981	Sequence 3981, Ap
C 496	56	1.6	554	17	US-10-424-599-37944	Sequence 37944, A	55	1.5	252	18	US-10-425-115-100475	Sequence 100475,
C 497	56	1.6	554	17	US-10-424-599-37944	Sequence 37944, A	55	1.5	257	9	US-09-960-352-8890	Sequence 8890, App
C 498	56	1.6	554	18	US-10-021-323-5547	Sequence 5547, Ap	55	1.5	277	9	US-09-924-035A-585	Sequence 585, App
C 499	56	1.6	558	18	US-10-425-115-187527	Sequence 187527, A	55	1.5	278	18	US-10-425-115-105175	Sequence 105175,
C 500	56	1.6	565	18	US-10-425-115-37807	Sequence 37807, A	55	1.5	321	9	US-09-960-352-13013	Sequence 13013, A
C 501	56	1.6	565	18	US-10-425-115-37807	Sequence 37807, A	55	1.5	328	18	US-10-425-115-144615	Sequence 144615, A
C 502	56	1.6	569	18	US-10-425-115-31618	Sequence 31618, A	55	1.5	344	18	US-10-425-115-68510	Sequence 68510, A
C 503	56	1.6	569	17	US-10-424-599-34774	Sequence 34774, A	55	1.5	355	9	US-09-960-352-2945	Sequence 2945, Ap
C 504	56	1.6	571	18	US-10-425-115-89390	Sequence 89390, A	55	1.5	359	9	US-09-770-791-558	Sequence 558, App
C 505	56	1.6	575	18	US-10-425-115-70286	Sequence 70286, A	55	1.5	360	18	US-10-425-115-154595	Sequence 154595,
C 506	56	1.6	579	18	US-10-425-115-44286	Sequence 44286, A	55	1.5	365	17	US-10-424-599-120990	Sequence 120990,
C 507	56	1.6	585	18	US-10-425-115-175362	Sequence 175362,	55	1.5	381	10	US-09-918-995-8255	Sequence 8255, Ap
C 508	56	1.6	587	18	US-10-021-323-15513	Sequence 15513, A	55	1.5	382	18	US-10-767-701-16889	Sequence 16889, A
C 509	56	1.6	601	18	US-10-437-963-39474	Sequence 39474, A	55	1.5	392	18	US-10-425-115-13019	Sequence 13019, A
C 510	56	1.6	639	18	US-10-482-985-10	Sequence 10, Appl	55	1.5	393	18	US-10-425-115-122487	Sequence 122487,
C 511	56	1.6	659	18	US-10-425-115-45561	Sequence 45561, A	55	1.5	402	18	US-10-437-963-34549	Sequence 34549, A
C 512	56	1.6	669	17	US-10-424-599-141641	Sequence 141641,	55	1.5	426	18	US-10-425-115-54531	Sequence 54531, A
C 513	56	1.6	735	18	US-10-425-115-62884	Sequence 62884, A	55	1.5	439	9	US-09-764-869-332	Sequence 332, App
C 514	56	1.6	824	14	US-10-144-929-29	Sequence 29, Appl	55	1.5	439	14	US-10-091-504-332	Sequence 332, App
C 515	56	1.6	824	17	US-10-144-929-29	Sequence 29, Appl	55	1.5	439	17	US-10-227-577-332	Sequence 332, App

589	55	1.5	441	17	US-10-424-599-31092	Sequence 31092, A	c 662	54	1.5	354	18	US-10-425-115-26048	Sequence 26048, A
590	55	1.5	502	18	US-10-425-115-137010	Sequence 137010, A	c 663	54	1.5	360	9	US-09-770-791-532	Sequence 532, App
591	55	1.5	509	18	US-10-437-963-84504	Sequence 84504, A	c 664	54	1.5	367	18	US-10-425-115-49226	Sequence 49226, A
592	55	1.5	518	18	US-10-437-963-23217	Sequence 23217, A	c 665	54	1.5	369	18	US-10-425-115-52629	Sequence 52629, A
593	55	1.5	535	18	US-10-425-115-6513	Sequence 6513, App	c 666	54	1.5	380	18	US-10-425-115-60437	Sequence 60437, A
594	55	1.5	551	18	US-10-425-115-154555	Sequence 154555, A	c 667	54	1.5	381	18	US-10-425-115-78509	Sequence 78509, A
595	55	1.5	559	18	US-10-425-115-187633	Sequence 187633, A	c 668	54	1.5	382	18	US-10-767-701-16521	Sequence 16521, A
596	55	1.5	559	18	US-10-425-115-155836	Sequence 155836, A	c 669	54	1.5	384	18	US-10-425-115-180943	Sequence 180943, A
597	55	1.5	564	18	US-10-021-323-12971	Sequence 12971, A	c 670	54	1.5	385	9	US-09-924-035A-848	Sequence 848, App
598	55	1.5	568	18	US-10-021-323-8302	Sequence 8302, App	c 671	54	1.5	390	17	US-10-424-599-3459	Sequence 3459, App
599	55	1.5	579	18	US-10-021-323-17839	Sequence 17839, A	c 672	54	1.5	393	18	US-10-437-963-100408	Sequence 100408, A
600	55	1.5	598	17	US-10-424-599-89182	Sequence 89182, A	c 673	54	1.5	398	17	US-10-424-599-73667	Sequence 73667, A
601	55	1.5	603	18	US-10-021-323-5966	Sequence 5966, App	c 674	54	1.5	407	18	US-10-021-323-9680	Sequence 9680, App
602	55	1.5	604	14	US-10-144-929-15	Sequence 15, App	c 675	54	1.5	408	18	US-10-437-963-19491	Sequence 19491, A
603	55	1.5	604	17	US-10-144-929-15	Sequence 15, App	c 676	54	1.5	410	9	US-09-960-352-8969	Sequence 8969, App
604	55	1.5	621	18	US-10-425-115-82625	Sequence 82625, A	c 677	54	1.5	412	18	US-10-425-115-84156	Sequence 84156, A
605	55	1.5	638	18	US-10-425-115-112248	Sequence 112248, A	c 678	54	1.5	417	10	US-09-918-995-6724	Sequence 6724, App
606	55	1.5	756	18	US-10-425-115-51642	Sequence 51642, A	c 679	54	1.5	421	18	US-10-425-115-43004	Sequence 43004, A
607	55	1.5	832	10	US-09-774-639-57	Sequence 57, App	c 680	54	1.5	426	9	US-09-924-035A-817	Sequence 817, App
608	55	1.5	832	10	US-09-969-730-18	Sequence 18, App	c 681	54	1.5	428	17	US-10-424-599-15564	Sequence 15564, A
609	55	1.5	832	17	US-10-621-363-18	Sequence 18, App	c 682	54	1.5	432	17	US-10-424-599-107176	Sequence 107176, A
610	55	1.5	834	18	US-10-739-930-1368	Sequence 1368, App	c 683	54	1.5	432	18	US-10-425-115-167620	Sequence 167620, A
611	55	1.5	878	18	US-10-425-115-173677	Sequence 173677, A	c 684	54	1.5	440	17	US-10-425-115-22621	Sequence 22621, A
612	55	1.5	880	18	US-10-425-115-8129	Sequence 8129, App	c 685	54	1.5	448	17	US-10-424-599-6035	Sequence 6035, App
613	55	1.5	974	18	US-10-357-930-25629	Sequence 25629, A	c 686	54	1.5	450	17	US-10-424-599-108900	Sequence 108900, A
614	55	1.5	1001	10	US-09-986-480-93	Sequence 93, App	c 687	54	1.5	472	18	US-10-425-115-20833	Sequence 20833, A
615	55	1.5	1027	18	US-10-739-930-1883	Sequence 1883, App	c 688	54	1.5	472	18	US-10-425-115-40048	Sequence 40048, A
616	55	1.5	1040	18	US-10-425-115-131033	Sequence 131033, A	c 689	54	1.5	477	18	US-10-437-963-15271	Sequence 15271, A
617	55	1.5	1129	17	US-10-264-237-1241	Sequence 1241, App	c 690	54	1.5	478	18	US-10-425-115-23077	Sequence 23077, A
618	55	1.5	1142	10	US-09-397-945-88	Sequence 88, App	c 691	54	1.5	482	18	US-10-437-963-68155	Sequence 68155, A
619	55	1.5	1142	17	US-10-653-595-88	Sequence 88, App	c 692	54	1.5	484	10	US-09-918-995-11820	Sequence 11820, A
620	55	1.5	1259	17	US-10-264-049-886	Sequence 886, App	c 693	54	1.5	487	18	US-10-021-323-8739	Sequence 8739, App
621	55	1.5	1265	18	US-10-425-115-150426	Sequence 150426, A	c 694	54	1.5	487	18	US-10-767-795-6225	Sequence 6225, App
622	55	1.5	1355	18	US-10-425-115-125985	Sequence 125985, A	c 695	54	1.5	499	18	US-10-425-115-88302	Sequence 88302, A
623	55	1.5	1392	18	US-10-425-115-107438	Sequence 107438, A	c 696	54	1.5	510	10	US-09-814-353-18805	Sequence 18805, A
624	55	1.5	1418	18	US-10-425-115-110834	Sequence 110834, A	c 697	54	1.5	514	18	US-10-021-323-7651	Sequence 7651, App
625	55	1.5	1459	18	US-10-425-115-124308	Sequence 124308, A	c 698	54	1.5	523	18	US-10-425-115-129269	Sequence 129269, A
626	55	1.5	1473	10	US-09-796-753-47	Sequence 47, App	c 699	54	1.5	523	18	US-10-425-115-13607	Sequence 13607, A
627	55	1.5	1539	9	US-09-925-300-447	Sequence 447, App	c 700	54	1.5	523	18	US-10-425-115-44359	Sequence 44359, A
628	55	1.5	1794	18	US-10-425-115-76840	Sequence 76840, A	c 701	54	1.5	531	18	US-10-425-115-181362	Sequence 181362, A
629	55	1.5	1796	18	US-10-425-115-74502	Sequence 74502, A	c 702	54	1.5	535	17	US-10-424-599-117295	Sequence 117295, A
630	55	1.5	1945	18	US-10-425-115-65906	Sequence 65906, A	c 703	54	1.5	540	18	US-10-425-115-123478	Sequence 123478, A
631	55	1.5	2197	18	US-10-723-860-4898	Sequence 4898, App	c 704	54	1.5	545	18	US-10-437-963-89099	Sequence 89099, A
632	55	1.5	2224	17	US-10-424-599-10608	Sequence 10608, A	c 705	54	1.5	550	9	US-09-764-887-91	Sequence 91, App
633	55	1.5	2438	17	US-10-264-049-796	Sequence 796, App	c 706	54	1.5	550	14	US-10-073-961-91	Sequence 91, App
634	55	1.5	2888	17	US-10-443-622-33	Sequence 33, App	c 707	54	1.5	554	18	US-10-425-115-27542	Sequence 27542, A
635	55	1.5	2895	10	US-09-759-130B-271	Sequence 271, App	c 708	54	1.5	555	18	US-10-425-115-171087	Sequence 171087, A
636	55	1.5	2895	14	US-10-189-123-1	Sequence 1, App	c 709	54	1.5	556	17	US-10-424-599-74285	Sequence 74285, A
637	55	1.5	2895	16	US-10-188-495-1	Sequence 1, App	c 710	54	1.5	557	18	US-10-425-115-41747	Sequence 41747, A
638	55	1.5	2895	18	US-10-741-790-271	Sequence 271, App	c 711	54	1.5	562	17	US-10-424-599-87969	Sequence 87969, A
639	55	1.5	3036	17	US-10-264-049-931	Sequence 931, App	c 712	54	1.5	563	18	US-10-425-115-6781	Sequence 6781, App
640	55	1.5	3037	14	US-10-050-704-46	Sequence 46, App	c 713	54	1.5	563	18	US-10-425-115-110109	Sequence 110109, A
641	55	1.5	3037	18	US-10-798-512-46	Sequence 46, App	c 714	54	1.5	563	18	US-10-425-115-1869	Sequence 1869, App
642	55	1.5	3058	17	US-10-424-599-13614	Sequence 13614, A	c 715	54	1.5	588	18	US-10-021-323-8041	Sequence 8041, App
643	55	1.5	3234	18	US-10-425-115-74703	Sequence 74703, A	c 716	54	1.5	605	18	US-10-425-115-148026	Sequence 148026, A
644	55	1.5	3585	18	US-10-437-963-13180	Sequence 13180, A	c 717	54	1.5	635	17	US-10-424-599-70780	Sequence 70780, A
645	55	1.5	6023	17	US-10-138-588-51	Sequence 51, App	c 718	54	1.5	638	9	US-09-925-301-630	Sequence 630, App
646	55	1.5	7001	18	US-10-437-963-98673	Sequence 98673, A	c 719	54	1.5	652	18	US-10-425-115-74276	Sequence 74276, A
647	54	1.5	66	14	US-10-066-543-585	Sequence 585, App	c 720	54	1.5	653	17	US-10-424-599-46097	Sequence 46097, A
648	54	1.5	180	18	US-10-021-323-2502	Sequence 2502, App	c 721	54	1.5	682	18	US-10-425-115-157131	Sequence 157131, A
649	54	1.5	193	18	US-10-425-115-37812	Sequence 37812, A	c 722	54	1.5	684	18	US-10-425-115-118289	Sequence 118289, A
650	54	1.5	203	9	US-09-960-352-5438	Sequence 5438, App	c 723	54	1.5	752	18	US-10-767-795-2049	Sequence 2049, App
651	54	1.5	215	18	US-10-425-115-123101	Sequence 123101, A	c 724	54	1.5	772	18	US-10-425-115-152740	Sequence 152740, A
652	54	1.5	221	18	US-10-357-930-59145	Sequence 59145, A	c 725	54	1.5	796	17	US-10-333-184-311	Sequence 311, App
653	54	1.5	226	18	US-10-021-323-15685	Sequence 15685, A	c 726	54	1.5	812	16	US-10-425-115-97406	Sequence 97406, A
654	54	1.5	242	18	US-10-425-115-47703	Sequence 47703, A	c 727	54	1.5	818	14	US-10-198-846-8654	Sequence 8654, App
655	54	1.5	260	17	US-10-424-599-13375	Sequence 13375, A	c 728	54	1.5	848	16	US-10-231-417-55	Sequence 55, App
656	54	1.5	279	18	US-10-425-115-17712	Sequence 17712, A	c 729	54	1.5	854	13	US-10-001-887-25	Sequence 25, App
657	54	1.5	308	18	US-10-425-115-142042	Sequence 142042, A	c 730	54	1.5	854	19	US-10-958-863-25	Sequence 25, App
658	54	1.5	336	18	US-10-425-115-11658	Sequence 11658, A	c 731	54	1.5	866	18	US-10-425-115-76851	Sequence 76851, A
659	54	1.5	344	18	US-10-425-115-85675	Sequence 85675, A	c 732	54	1.5	883	17	US-10-264-049-416	Sequence 416, App
660	54	1.5	345	18	US-10-425-115-66223	Sequence 66223, A	c 733	54	1.5	927	18	US-10-739-930-1431	Sequence 1431, App
661	54	1.5	347	18	US-10-425-115-20886	Sequence 20886, A	c 734	54	1.5	928	18	US-10-425-115-5274	Sequence 5274, App

C 735	54	1.5	942	17	US-10-424-599-91119	Sequence 91119, A	808	53	1.5	263	18	US-10-425-115-174630	Sequence 174630,
C 736	54	1.5	973	18	US-10-767-795-4358	Sequence 4358, Ap	809	53	1.5	264	9	US-09-867-701-10185	Sequence 10185, A
C 737	54	1.5	998	18	US-10-739-930-1579	Sequence 1579, Ap	810	53	1.5	266	18	US-10-437-963-4817	Sequence 4817, Ap
C 738	54	1.5	1007	18	US-10-425-115-53453	Sequence 53453, A	C 811	53	1.5	266	18	US-10-425-115-88938	Sequence 88938, A
C 739	54	1.5	1046	18	US-10-425-115-80457	Sequence 80457, A	C 812	53	1.5	269	17	US-10-424-599-134367	Sequence 134367, A
C 740	54	1.5	1060	9	US-09-925-299-43	Sequence 43, Appl	C 813	53	1.5	269	18	US-10-357-930-7483	Sequence 7483, Ap
C 741	54	1.5	1060	10	US-09-925-299-43	Sequence 43, Appl	814	53	1.5	275	9	US-09-919-580-75	Sequence 75, Appl
C 742	54	1.5	1081	18	US-10-425-115-155277	Sequence 155277, A	815	53	1.5	275	18	US-10-425-115-180214	Sequence 180214, A
C 743	54	1.5	1123	18	US-10-739-930-3770	Sequence 3770, Ap	816	53	1.5	281	18	US-09-814-353-17383	Sequence 17383, A
C 744	54	1.5	1150	17	US-10-424-599-121759	Sequence 121759, Ap	817	53	1.5	281	18	US-10-357-930-35994	Sequence 35994, A
C 745	54	1.5	1194	18	US-10-744-572-13	Sequence 13, Appl	818	53	1.5	283	18	US-10-357-930-61322	Sequence 61322, A
C 746	54	1.5	1221	18	US-10-739-930-1833	Sequence 1833, Ap	819	53	1.5	285	18	US-10-425-115-34607	Sequence 34607, A
C 747	54	1.5	1269	15	US-10-180-375-135	Sequence 135, App	820	53	1.5	286	17	US-10-424-599-134048	Sequence 134048, A
C 748	54	1.5	1269	17	US-10-183-687-265	Sequence 265, App	821	53	1.5	290	18	US-10-437-963-51258	Sequence 51258, A
C 749	54	1.5	1298	18	US-10-425-115-81395	Sequence 81395, A	C 822	53	1.5	295	9	US-09-764-846-33	Sequence 33, Appl
C 750	54	1.5	1408	18	US-10-425-115-28249	Sequence 28249, A	C 823	53	1.5	295	14	US-10-091-483-33	Sequence 33, Appl
C 751	54	1.5	1723	14	US-10-012-542-98	Sequence 98, Appl	824	53	1.5	296	10	US-09-814-353-5940	Sequence 5940, Ap
C 752	54	1.5	1723	14	US-10-115-123-98	Sequence 98, Appl	825	53	1.5	296	10	US-09-814-353-12220	Sequence 12220, A
C 753	54	1.5	1774	18	US-10-425-115-117350	Sequence 117350, A	826	53	1.5	296	18	US-10-425-115-98517	Sequence 98517, A
C 754	54	1.5	1797	17	US-10-424-599-41191	Sequence 41191, A	827	53	1.5	298	17	US-10-424-599-120040	Sequence 120040, A
C 755	54	1.5	1847	17	US-10-264-049-820	Sequence 820, App	828	53	1.5	303	18	US-10-437-963-51951	Sequence 51951, A
C 756	54	1.5	1931	10	US-09-813-153-78	Sequence 78, Appl	C 829	53	1.5	304	9	US-09-764-846-109	Sequence 109, App
C 757	54	1.5	1932	10	US-09-813-153-12	Sequence 12, Appl	C 830	53	1.5	304	14	US-10-091-483-109	Sequence 109, App
C 758	54	1.5	2017	17	US-10-424-599-108607	Sequence 108607, A	831	53	1.5	304	17	US-10-424-599-133280	Sequence 133280, A
C 759	54	1.5	2029	18	US-10-437-963-91052	Sequence 91052, A	C 832	53	1.5	305	17	US-10-424-599-94601	Sequence 94601, A
C 760	54	1.5	2053	18	US-10-425-115-142365	Sequence 142365, A	C 833	53	1.5	310	17	US-10-424-599-69405	Sequence 69405, A
C 761	54	1.5	2088	17	US-10-424-599-63979	Sequence 63979, A	C 834	53	1.5	311	18	US-10-425-115-82662	Sequence 82662, A
C 762	54	1.5	2150	18	US-10-881-088-37	Sequence 37, Appl	C 835	53	1.5	312	18	US-10-425-115-125299	Sequence 125299, A
C 763	54	1.5	2254	17	US-10-424-599-3803	Sequence 3803, Ap	836	53	1.5	313	9	US-09-960-352-2670	Sequence 2670, Ap
C 764	54	1.5	2386	18	US-10-739-930-1418	Sequence 1418, Ap	837	53	1.5	317	18	US-10-357-930-15166	Sequence 15166, A
C 765	54	1.5	2506	18	US-10-425-115-95015	Sequence 95015, A	838	53	1.5	318	10	US-09-814-353-6389	Sequence 6389, Ap
C 766	54	1.5	2728	18	US-10-425-115-57309	Sequence 57309, A	839	53	1.5	318	10	US-09-814-353-12666	Sequence 12666, A
C 767	54	1.5	2753	18	US-10-437-963-78534	Sequence 78534, A	840	53	1.5	318	18	US-10-425-115-25520	Sequence 25520, A
C 768	54	1.5	2756	9	US-09-925-301-351	Sequence 351, App	841	53	1.5	318	18	US-10-425-115-26677	Sequence 26677, A
C 769	54	1.5	3006	9	US-09-962-678-1	Sequence 1, Appl	C 842	53	1.5	320	17	US-10-424-599-22672	Sequence 22672, A
C 770	54	1.5	3066	17	US-10-184-648-38	Sequence 38, Appl	C 843	53	1.5	321	18	US-10-425-115-169025	Sequence 169025, A
C 771	54	1.5	3552	10	US-09-814-353-19891	Sequence 19891, A	844	53	1.5	321	18	US-10-425-115-37134	Sequence 37134, A
C 772	54	1.5	3552	14	US-10-198-846-11479	Sequence 11479, A	845	53	1.5	323	18	US-10-357-930-61015	Sequence 61015, A
C 773	54	1.5	3552	18	US-10-357-930-21448	Sequence 21448, A	846	53	1.5	324	17	US-10-424-599-131074	Sequence 131074, A
C 774	54	1.5	3552	18	US-10-357-930-27289	Sequence 27289, A	847	53	1.5	327	18	US-10-425-115-130293	Sequence 130293, A
C 775	53	1.5	58	9	US-09-919-580-703	Sequence 703, App	848	53	1.5	328	10	US-09-814-353-17578	Sequence 17578, A
C 776	53	1.5	60	9	US-09-919-580-419	Sequence 419, App	849	53	1.5	331	17	US-10-125-968-928	Sequence 928, App
C 777	53	1.5	74	14	US-10-066-543-1108	Sequence 1108, Ap	850	53	1.5	332	10	US-09-814-353-5594	Sequence 5594, Ap
C 778	53	1.5	90	9	US-09-919-580-217	Sequence 217, App	851	53	1.5	332	10	US-09-814-353-11881	Sequence 11881, A
C 779	53	1.5	90	14	US-10-066-543-328	Sequence 328, App	852	53	1.5	336	10	US-09-814-353-4742	Sequence 4742, Ap
C 780	53	1.5	107	14	US-10-066-543-1787	Sequence 1787, Ap	853	53	1.5	336	10	US-09-814-353-11039	Sequence 11039, A
C 781	53	1.5	125	18	US-10-466-894-229	Sequence 229, App	854	53	1.5	337	9	US-09-770-791-889	Sequence 889, App
C 782	53	1.5	144	13	US-10-114-893-208	Sequence 208, App	855	53	1.5	337	18	US-10-357-930-60892	Sequence 60892, A
C 783	53	1.5	160	18	US-10-466-894-269	Sequence 269, App	856	53	1.5	337	18	US-10-131-827-8601	Sequence 8601, Ap
C 784	53	1.5	175	9	US-09-983-965-2999	Sequence 2999, Ap	C 857	53	1.5	338	18	US-10-425-115-22891	Sequence 22891, A
C 785	53	1.5	197	17	US-10-264-049-1247	Sequence 1247, Ap	C 858	53	1.5	338	18	US-10-357-930-49015	Sequence 49015, A
C 786	53	1.5	202	9	US-09-960-352-9114	Sequence 9114, Ap	C 859	53	1.5	339	18	US-10-425-115-80751	Sequence 80751, A
C 787	53	1.5	204	18	US-10-357-930-19212	Sequence 19212, A	860	53	1.5	339	18	US-10-425-115-126017	Sequence 126017, A
C 788	53	1.5	211	18	US-10-357-930-14987	Sequence 14987, A	861	53	1.5	340	18	US-10-425-115-3498	Sequence 3498, Ap
C 789	53	1.5	214	17	US-10-242-535A-15938	Sequence 15938, A	862	53	1.5	340	18	US-10-425-115-88133	Sequence 88133, A
C 790	53	1.5	214	17	US-10-085-783A-15938	Sequence 15938, A	863	53	1.5	341	18	US-10-425-115-14920	Sequence 14920, A
C 791	53	1.5	219	18	US-10-357-930-60860	Sequence 60860, A	C 864	53	1.5	342	18	US-10-425-115-53693	Sequence 53693, A
C 792	53	1.5	221	17	US-10-424-599-11732	Sequence 11732, A	C 865	53	1.5	343	18	US-10-425-115-49757	Sequence 49757, A
C 793	53	1.5	222	10	US-09-814-353-18350	Sequence 18350, A	866	53	1.5	343	18	US-10-357-930-60962	Sequence 60962, A
C 794	53	1.5	224	18	US-10-425-115-87153	Sequence 87153, A	C 867	53	1.5	344	17	US-10-424-599-97275	Sequence 97275, A
C 795	53	1.5	225	17	US-10-242-535A-46212	Sequence 46212, A	868	53	1.5	344	18	US-10-021-323-1846	Sequence 1846, Ap
C 796	53	1.5	225	17	US-10-085-783A-46212	Sequence 46212, A	869	53	1.5	346	10	US-09-814-353-17676	Sequence 17676, A
C 797	53	1.5	226	18	US-10-357-930-5818	Sequence 5818, Ap	870	53	1.5	347	9	US-09-960-352-3771	Sequence 3771, Ap
C 798	53	1.5	233	18	US-10-425-115-70230	Sequence 70230, A	871	53	1.5	350	10	US-09-814-353-5753	Sequence 5753, Ap
C 799	53	1.5	234	10	US-09-814-353-4810	Sequence 4810, Ap	872	53	1.5	350	10	US-09-814-353-12036	Sequence 12036, A
C 800	53	1.5	234	10	US-09-814-353-11107	Sequence 11107, A	C 873	53	1.5	350	17	US-10-424-599-41239	Sequence 41239, A
C 801	53	1.5	235	18	US-10-357-930-60948	Sequence 60948, A	874	53	1.5	351	10	US-09-814-353-4899	Sequence 4899, Ap
C 802	53	1.5	240	10	US-09-814-353-12780	Sequence 12780, A	875	53	1.5	351	10	US-09-814-353-11194	Sequence 11194, A
C 803	53	1.5	241	10	US-09-814-353-5827	Sequence 5827, Ap	876	53	1.5	351	17	US-10-424-599-115233	Sequence 115233, A
C 804	53	1.5	248	18	US-10-357-930-60895	Sequence 60895, A	C 877	53	1.5	352	18	US-10-357-930-56917	Sequence 56917, A
C 805	53	1.5	255	17	US-10-424-599-56737	Sequence 56737, A	878	53	1.5	352	18	US-10-357-930-60876	Sequence 60876, A
C 806	53	1.5	256	18	US-10-425-115-167530	Sequence 167530, A	879	53	1.5	354	18	US-10-425-115-53496	Sequence 53496, A
C 807	53	1.5	262	18	US-10-425-115-130837	Sequence 130837, A	880	53	1.5	358	10	US-09-814-353-6302	Sequence 6302, Ap

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c 883	53	1.5	359	18	US-10-437-963-37882	Sequence 37882, A	956	53	1.5	419	17	US-10-424-599-8	Sequence 8, Appl
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c 888	53	1.5	362	17	US-10-424-599-65278	Sequence 65278, A	961	53	1.5	422	17	US-10-424-599-82450	Sequence 82450, A
c 889	53	1.5	362	18	US-10-425-115-181680	Sequence 181680, A	962	53	1.5	422	18	US-10-425-115-178328	Sequence 178328, A
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c 891	53	1.5	367	18	US-10-357-930-54992	Sequence 54992, A	964	53	1.5	424	18	US-10-437-963-32593	Sequence 32593, A
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893	53	1.5	371	18	US-10-425-115-88000	Sequence 88000, A	966	53	1.5	426	18	US-10-357-930-39056	Sequence 39056, A
894	53	1.5	371	18	US-10-425-115-101688	Sequence 101688, A	967	53	1.5	426	18	US-10-357-930-44842	Sequence 44842, A
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c 896	53	1.5	373	18	US-10-767-701-12535	Sequence 12535, A	969	53	1.5	429	18	US-10-437-963-18973	Sequence 18973, A
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c 899	53	1.5	376	17	US-10-424-599-141998	Sequence 141998, A	972	53	1.5	430	17	US-10-424-599-98110	Sequence 98110, A
c 900	53	1.5	378	17	US-10-424-599-105378	Sequence 105378, A	973	53	1.5	430	17	US-10-437-963-19293	Sequence 19293, A
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c 911	53	1.5	388	10	US-09-814-353-17525	Sequence 17525, A	984	53	1.5	435	18	US-10-021-323-5424	Sequence 5424, Ap
c 912	53	1.5	388	17	US-10-424-599-74489	Sequence 74489, A	985	53	1.5	436	18	US-10-357-930-35696	Sequence 35696, A
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c 916	53	1.5	391	18	US-10-425-115-40878	Sequence 40878, A	c 989	53	1.5	438	18	US-10-425-115-91314	Sequence 91314, A
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932	53	1.5	404	18	US-10-437-963-57047	Sequence 57047, A	1005	53	1.5	446	18	US-10-425-115-50016	Sequence 50016, A
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1063	53	1.5	478	17	US-10-424-599-105242	Sequence 105242, A	1136	53	1.5	516	18	US-10-357-930-57105	Sequence 57105, A
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c 114	75	2.1	1099	4	BM467696	BM467696	AGENCOURT	C 187	60	1.7	658	4	BF968907	BF968907	602270874
c 115	75	2.1	1385	3	AY103744	AY103744	Zea may	C 188	60	1.7	675	7	C0891521	C0891521	BovGen_19
116	74	2.1	220	6	CB474275	CB474275	jns02_A12	C 189	60	1.7	686	7	C0894553	C0894553	BovGen_22
117	74	2.1	469	7	C0890709	C0890709	BovGen_19	C 190	60	1.7	718	7	CK172899	CK172899	EST762219
118	74	2.1	667	6	CA076217	CA076217	SCMCAM110	C 191	60	1.7	801	7	CV120758	CV120758	AGENCOURT
c 119	74	2.1	678	7	C0894416	C0894416	BovGen_22	C 192	60	1.7	817	7	CK172900	CK172900	EST762220
c 120	73	2.0	514	6	CD723758	CD723758	oj28b09.y	C 193	60	1.7	846	7	CK194390	CK194390	FGAS00381
c 121	72	2.0	743	7	C0878776	C0878776	BovGen_07	C 194	60	1.7	859	5	BUI70431	BUI70431	AGENCOURT
c 122	72	2.0	751	7	CF285041	CF285041	AGENCOURT	C 195	60	1.7	870	7	CF885064	CF885064	tr1c077xe
123	71	2.0	163	1	AI289747	AI289747	qv91e07.x	C 196	60	1.7	883	7	CF885106	CF885106	tr1c077x1
124	71	2.0	551	7	CK431019	CK431019	oj56h10.y	C 197	60	1.7	886	7	CK199049	CK199049	FGAS00754
c 125	71	2.0	635	7	C0878096	C0878096	BovGen_06	C 198	60	1.7	894	7	CF885605	CF885605	tr1c082x1
c 126	71	2.0	903	5	BUI72251	BUI72251	AGENCOURT	C 199	60	1.7	908	7	CF885585	CF885585	tr1c082xc
c 127	70	2.0	184	4	BM192204	BM192204	dai21g08.	C 200	60	1.7	910	7	CF886357	CF886357	tr1c086xx
c 128	70	2.0	301	4	BG513761	BG513761	dac18d09.	C 201	60	1.7	929	7	CF885679	CF885679	tr1c082xh
c 129	70	2.0	587	6	CA263211	CA263211	SCPLB203	C 202	60	1.7	938	7	CF886324	CF886324	tr1c086xg
c 130	69	1.9	551	7	CK431019	CK431019	oj56h10.y	C 203	60	1.7	946	6	CA987707	CA987707	AGENCOURT
c 131	68	1.9	520	7	CK235878	CK235878	SB0100240	C 204	60	1.7	990	7	CF871636	CF871636	tr1c005xg
c 132	67	1.9	314	7	C0874293	C0874293	BovGen_02	C 205	60	1.7	1083	5	BM905598	BM905598	AGENCOURT
c 133	67	1.9	495	5	BQ238068	BQ238068	TaE05008H	C 206	59	1.6	139	2	BF812963	BF812963	MR2-C1018
c 134	67	1.9	673	7	C0887800	C0887800	BovGen_16	C 207	59	1.6	158	4	BM632157	BM632157	170006875
135	67	1.9	695	7	C0878226	C0878226	BovGen_06	C 208	59	1.6	165	1	AI469764	AI469764	tm20f02.x
c 136	67	1.9	853	7	C0007895	C0007895	EST796230	C 209	59	1.6	325	1	AI801589	AI801589	to91d07.x
c 137	67	1.9	1057	5	B0506841	B0506841	AGENCOURT	C 210	59	1.6	358	4	BG781092	BG781092	SEADMC001
c 138	66	1.8	187	1	AU284592	AU284592	Xb16c02.x	C 211	59	1.6	360	1	AI440261	AI440261	tj01d06.x
c 139	66	1.8	249	2	AW197139	AW197139	AGENCOURT	C 212	59	1.6	385	1	AI334804	AI334804	qw24n01.x
c 140	65	1.8	236	5	B0732209	B0732209	AGENCOURT	C 213	59	1.6	399	1	AI954200	AI954200	wx9a402.x
c 141	65	1.8	422	1	AI358581	AI358581	qx60d02.x	C 214	59	1.6	469	7	CF874064	CF874064	tr1c035xe
c 142	65	1.8	596	4	BM569567	BM569567	ih96h01.x	C 215	59	1.6	474	7	CN717811	CN717811	E0753B09-
c 143	65	1.8	732	7	C0879622	C0879622	BovGen_07	C 216	59	1.6	612	5	BQ389802	BQ389802	NISC mq09
c 144	64	1.8	618	2	AW324530	AW324530	AB027_Fas	C 217	59	1.6	675	6	CA123657	CA123657	SCSFIR203
c 145	64	1.8	898	5	BQ230783	BQ230783	AGENCOURT	C 218	59	1.6	719	7	C0882395	C0882395	BovGen_10
146	63	1.8	130	4	BG167830	BG167830	602339983	C 219	59	1.6	721	7	C0887461	C0887461	BovGen_15
147	63	1.8	257	1	AI888022	AI888022	wn12b06.x	C 220	59	1.6	726	7	C0877944	C0877944	BovGen_06
c 148	63	1.8	294	4	CN271810	CN271810	170006003	C 221	59	1.6	738	7	C0879400	C0879400	BovGen_07
c 149	63	1.8	374	1	AJ687174	AJ687174	AGENCOURT	C 222	59	1.6	772	4	BG114985	BG114985	602315847
150	63	1.8	490	2	BF191917	BF191917	242931_MA	C 223	59	1.6	785	6	CB903607	CB903607	tr1c035xe
151	63	1.8	493	5	BQ387802	BQ387802	NISC mm25	C 224	59	1.6	822	7	CK193166	CK193166	FGAS00158
c 152	63	1.8	558	7	C0880948	C0880948	BovGen_09	C 225	59	1.6	837	7	CK193117	CK193117	FGAS00153
c 153	63	1.8	659	7	C0875161	C0875161	BovGen_03	C 226	59	1.6	890	7	CK797460	CK797460	AGENCOURT
c 154	63	1.8	660	7	C0896277	C0896277	BovGen_24	C 227	59	1.6	955	7	CK805318	CK805318	AGENCOURT
c 155	62	1.7	189	7	C0881722	C0881722	tr1c085xc	C 228	59	1.6	1071	5	BM907452	BM907452	AGENCOURT
c 156	62	1.7	434	7	C0889127	C0889127	BovGen_17	C 229	59	1.6	1497	2	BF788820	BF788820	602110529
c 157	62	1.7	621	7	C0885415	C0885415	BovGen_13	C 230	58	1.6	63	1	AI371229	AI371229	qw77h05.x
c 158	62	1.7	656	6	CA239050	CA239050	SCBFL507	C 231	58	1.6	65	1	AI282249	AI282249	qv92f06.x
c 159	62	1.7	656	7	C0526531	C0526531	3530_1_17	C 232	58	1.6	65	1	AI698352	AI698352	tx63f09.x
c 160	62	1.7	758	6	CB908372	CB908372	tr1c085xc	C 233	58	1.6	69	1	AI358271	AI358271	qw19g12.x
161	62	1.7	881	5	BQ735806	BQ735806	AGENCOURT	C 234	58	1.6	70	1	AI225248	AI225248	qx12d07.x
162	62	1.7	925	5	BQ945533	BQ945533	AGENCOURT	C 235	58	1.6	71	1	AI867068	AI867068	tz45h12.x
163	62	1.7	955	7	CK805318	CK805318	AGENCOURT	C 236	58	1.6	71	1	AI952433	AI952433	wx73f09.x
164	61	1.7	161	5	BQ800025	BQ800025	EST 7060	C 237	58	1.6	73	1	AI446495	AI446495	tj20b005.x
165	61	1.7	193	7	CN272018	CN272018	170006000	C 238	58	1.6	74	1	AI567953	AI567953	tg86c10.x
c 166	61	1.7	357	4	BM179900	BM179900	dai13b07.	C 239	58	1.6	74	2	AW074057	AW074057	wk72h07.x
c 167	61	1.7	396	4	BM623800	BM623800	170006874	C 240	58	1.6	74	2	AW074057	AW074057	xb06h12.x
c 168	61	1.7	454	7	C0877819	C0877819	BovGen_06	C 241	58	1.6	75	1	AI428446	AI428446	mo19h10.x
c 169	61	1.7	606	7	C0892945	C0892945	BovGen_21	C 242	58	1.6	77	1	AI866581	AI866581	tz55c11.x
170	60	1.7	86	6	CB258216	CB258216	40-E01108	C 243	58	1.6	79	1	AI469775	AI469775	tm20g03.x

244	58	1.6	80	1	AI521571	to64h04.x	317	58	1.6	120	1	AI590043	AI590043	tr75c04.x
245	58	1.6	80	1	AI561168	tq37d07.x	318	58	1.6	120	1	AI872423	AI872423	wm58g09.x
246	58	1.6	80	1	AI828597	wl42g01.x	319	58	1.6	120	1	AI923989	AI923989	wm73a09.x
247	58	1.6	81	1	AI285419	qt83a06.x	320	58	1.6	121	1	AI582932	AI582932	ts07g04.x
248	58	1.6	81	1	AI559957	tq77c07.x	321	58	1.6	122	1	AI887775	AI887775	wm18f04.x
249	58	1.6	81	2	AW089557	xd20b11.x	322	58	1.6	125	1	AI538850	AI538850	tp74e02.x
250	58	1.6	82	1	AI885949	wn06g06.x	323	58	1.6	127	1	AI500523	AI500523	tn92g08.x
251	58	1.6	83	1	AI878201	fc58f08.y	324	58	1.6	128	1	AI801325	AI801325	tn97g09.x
252	58	1.6	83	7	CF643428	D90_C09_F	325	58	1.6	128	1	AI866691	AI866691	wn10c06.x
253	58	1.6	85	1	AI539707	tp77b02.x	326	58	1.6	129	1	AI815232	AI815232	wk7f110.x
254	58	1.6	85	1	AI702065	tq20h10.x	327	58	1.6	130	7	CF641137	CF641137	D38_E07_F
255	58	1.6	87	1	AI431238	ar56a12.x	328	58	1.6	132	1	AI866465	AI866465	tz48a12.x
256	58	1.6	87	1	AI539781	cp77f12.x	329	58	1.6	133	2	BE883591	BE883591	601508064
257	58	1.6	87	5	BQ392175	NISC_mq23	330	58	1.6	134	1	AI045724	AI045724	DKF2p434D
258	58	1.6	88	2	AW151979	xf71c01.x	331	58	1.6	135	4	BM639526	BM639526	170006875
259	58	1.6	89	1	AI887499	wn06c05.x	332	58	1.6	137	1	AI500659	AI500659	tn93g08.x
260	58	1.6	90	1	AI539260	tp64d08.x	333	58	1.6	137	1	AI815239	AI815239	wk72g07.x
261	58	1.6	90	1	AI828574	wl43d08.x	334	58	1.6	138	1	AI804505	AI804505	tp60b03.x
262	58	1.6	92	1	AI242736	qt86d12.x	335	58	1.6	138	5	BQ392169	BQ392169	NISC_mq23
263	58	1.6	93	1	AI431316	AI431316	336	58	1.6	140	1	AA087985	AA087985	mo39e12.x
264	58	1.6	93	1	AI610557	AI610557	337	58	1.6	142	4	BM628708	BM628708	170006874
265	58	1.6	93	1	AI860003	wm22f10.x	338	58	1.6	143	1	AI494201	AI494201	t109e06.x
266	58	1.6	94	1	AI567971	AI567971	339	58	1.6	144	1	AI537677	AI537677	tp34d01.x
267	58	1.6	94	1	AI866786	AI866786	340	58	1.6	144	5	BQ638107	BQ638107	hd18e10.y
268	58	1.6	96	1	AI440238	AI440238	341	58	1.6	145	1	AI440260	AI440260	tj01d05.x
269	58	1.6	98	1	AI431307	ar55a11.x	342	58	1.6	145	7	CN414669	CN414669	170006004
270	58	1.6	98	1	AI440252	tj01c03.x	343	58	1.6	149	1	AI432644	AI432644	t122a02.x
271	58	1.6	99	1	AI491710	tn94d05.x	344	58	1.6	151	2	BE897632	BE897632	601432481
272	58	1.6	99	1	AI371228	qv77h03.x	345	58	1.6	152	2	BF301996	BF301996	602032834
273	58	1.6	99	1	AI581033	AI581033	346	58	1.6	152	2	AW151132	AW151132	xg33g07.x
274	58	1.6	100	1	AI355779	AI355779	347	58	1.6	152	4	BM612283	BM612283	170006871
275	58	1.6	100	1	AI623736	ts83f07.x	348	58	1.6	154	1	AI539771	AI539771	tp77e11.x
276	58	1.6	101	1	AI889147	AI889147	349	58	1.6	159	2	AI511136	AI511136	xg33h03.x
277	58	1.6	101	1	AI436429	AI436429	350	58	1.6	162	4	BQ252929	BQ252929	602365530
278	58	1.6	101	1	AI859591	AI859591	351	58	1.6	163	4	BQ289279	BQ289279	602384287
279	58	1.6	102	1	AI285439	AI285439	352	58	1.6	163	5	BQ387472	BQ387472	NISC_mn24
280	58	1.6	102	1	AI877953	AI877953	353	58	1.6	163	5	BQ637071	BQ637071	he05c09.y
281	58	1.6	102	7	CO373230	CO373230	354	58	1.6	164	1	AI554821	AI554821	tp73g04.x
282	58	1.6	103	5	BU167500	BU167500	355	58	1.6	164	1	AI561170	AI561170	tq37d10.x
283	58	1.6	103	5	BU167500	AGENCOURT	356	58	1.6	165	1	AI690946	AI690946	tq02e09.x
284	58	1.6	104	1	AI284513	AI284513	357	58	1.6	166	1	AI648567	AI648567	tz54g06.x
285	58	1.6	104	1	AI434248	AI434248	358	58	1.6	166	5	BQ639348	BQ639348	he14d05.y
286	58	1.6	104	1	AI500714	AI500714	359	58	1.6	167	1	AI433157	AI433157	t132b12.x
287	58	1.6	105	1	AI888661	AI888661	360	58	1.6	173	4	BM620920	BM620920	170006874
288	58	1.6	106	1	AI434242	AI434242	361	58	1.6	176	7	CO890294	CO890294	BovGen_18
289	58	1.6	106	1	AI805769	AI805769	362	58	1.6	177	4	BQ294490	BQ294490	602391813
290	58	1.6	107	1	AI866469	AI866469	363	58	1.6	178	4	BM494829	BM494829	IpC8Br1_4
291	58	1.6	108	1	AI434256	AI434256	364	58	1.6	178	5	BQ391656	BQ391656	NISC_mq20
292	58	1.6	109	1	AI633493	AI633493	365	58	1.6	179	4	BQ029667	BQ029667	602296662
293	58	1.6	110	1	AI866573	AI866573	366	58	1.6	179	5	BQ390838	BQ390838	NISC_mq15
294	58	1.6	111	1	AI927233	AI927233	367	58	1.6	179	6	CB216118	CB216118	NISC_mq01
295	58	1.6	112	1	AI440263	AI440263	368	58	1.6	182	4	BQ403110	BQ403110	602418930
296	58	1.6	112	1	AI538885	AI538885	369	58	1.6	182	6	CA340216	CA340216	NISC_ly12
297	58	1.6	112	1	AI889168	AI889168	370	58	1.6	183	4	BG113493	BG113493	602283943
298	58	1.6	112	5	BQ387826	BQ387826	371	58	1.6	183	7	CO893077	CO893077	BovGen_21
299	58	1.6	113	1	AI284509	AI284509	372	58	1.6	184	4	BM594107	BM594107	170006874
300	58	1.6	113	1	AI539800	AI539800	373	58	1.6	185	4	BG110517	BG110517	602378945
301	58	1.6	113	1	AI582912	AI582912	374	58	1.6	185	7	CF319467	CF319467	HD--09-P1
302	58	1.6	113	2	AW172723	AW172723	375	58	1.6	186	1	AI371243	AI371243	qv78h02.x
303	58	1.6	114	1	AI285417	AI285417	376	58	1.6	186	4	BM631584	BM631584	170006875
304	58	1.6	114	1	AI500662	AI500662	377	58	1.6	186	5	BQ239222	BQ239222	TaE05035F
305	58	1.6	114	2	AW151974	AW151974	378	58	1.6	189	5	BQ400307	BQ400307	NISC_mq08
306	58	1.6	115	1	AI521560	AI521560	379	58	1.6	190	4	BQ292880	BQ292880	602389512
307	58	1.6	115	1	AI889189	AI889189	380	58	1.6	191	4	BQ294808	BQ294808	602391631
308	58	1.6	115	7	CO883195	CO883195	381	58	1.6	191	7	CO892085	CO892085	BovGen_20
309	58	1.6	117	1	AI289791	AI289791	382	58	1.6	192	5	BQ761011	BQ761011	EBr004_SQ
310	58	1.6	117	1	AI926593	AI926593	383	58	1.6	193	1	AI031194	AI031194	8D4M_Xeno
311	58	1.6	117	2	BF811804	BF811804	384	58	1.6	194	4	BG257535	BG257535	602377685
312	58	1.6	117	2	AW151138	AW151138	385	58	1.6	195	1	AU060359	AU060359	AU060359
313	58	1.6	118	1	AI445237	AI445237	386	58	1.6	195	5	BQ389262	BQ389262	NISC_mq06
314	58	1.6	118	1	AI491776	AI491776	387	58	1.6	196	1	AL039390	AL039390	DKF2p434J
315	58	1.6	119	1	AI500706	AI500706	388	58	1.6	196	2	BF795712	BF795712	602259590
316	58	1.6	120	1	AI284517	AI284517	389	58	1.6	196	7	CO893749	CO893749	BovGen_22

330	58	1.6	197	2	BF796402	BF796402	602260040	463	58	1.6	319	5	BQ525547	BQ525547	NISC_nol1
331	58	1.6	200	1	A1274759	A1274759	qv66e09.x	464	58	1.6	323	4	AM116311	AM116311	L0834B04-
332	58	1.6	200	1	AW858522	AW858522	CM3-CT034	465	58	1.6	324	4	AI521589	AI521589	LO85B08.x
333	58	1.6	201	5	BQ523741	BQ523741	NISC_n123	466	58	1.6	324	4	BM117156	BM117156	L0847A02-
334	58	1.6	202	4	BQ391612	BQ391612	602417868	467	58	1.6	325	5	BQ525099	BQ525099	NISC_n008
335	58	1.6	202	4	BM641556	BM641556	170006873	468	58	1.6	326	4	BM117385	BM117385	L085OE11-
336	58	1.6	203	5	BQ391918	BQ391918	NISC_m02	c 469	58	1.6	326	7	CF874010	CF874010	tr1c0035xc
337	58	1.6	206	4	BI437582	BI437582	ic81a01.y	470	58	1.6	328	7	AI866503	AI866503	tz49e02.x
338	58	1.6	207	1	AI433976	AI433976	tl12c12.x	471	58	1.6	328	7	CF722703	CF722703	B04_LKF00
339	58	1.6	207	4	BM579757	BM579757	170006872	472	58	1.6	330	7	BM116472	BM116472	L0836G09-
340	58	1.6	207	5	BQ399361	BQ399361	NISC_m002	c 473	58	1.6	330	7	CF639408	CF639408	D15_C12_F
341	58	1.6	209	7	CK420226	CK420226	AUF_IpTrk	c 474	58	1.6	333	7	CF866168	CF866168	tr1c0050xe
342	58	1.6	214	4	BM636166	BM636166	170006875	475	58	1.6	334	1	AI537273	AI537273	tp07a04.x
343	58	1.6	217	6	CD678870	CD678870	hq01d06.x	476	58	1.6	335	5	BQ388737	BQ388737	NISC_mq03
344	58	1.6	217	7	CK622030	CK622030	ml31g04.y	477	58	1.6	336	1	AI537191	AI537191	tp01d05.x
345	58	1.6	218	5	BQ392177	BQ392177	NISC_mq23	478	58	1.6	336	5	BQ400952	BQ400952	NISC_mpl2
346	58	1.6	220	4	BM506521	BM506521	1144f08.y	479	58	1.6	337	2	CF722741	CF722741	F04_LKF00
347	58	1.6	223	4	BM610799	BM610799	170006871	480	58	1.6	337	2	AM151970	AM151970	xf17a07.x
348	58	1.6	224	1	AI539863	AI539863	tp65h06.x	481	58	1.6	338	5	BQ392456	BQ392456	NISC_mq24
349	58	1.6	224	1	AI582910	AI582910	ts07e04.x	482	58	1.6	338	7	CF645623	CF645623	K38_E12_F
350	58	1.6	225	1	AI366900	AI366900	qv94f07.x	c 483	58	1.6	338	7	CF872097	CF872097	tr1c0290xc
351	58	1.6	227	1	AJ770217	AJ770217	AJ770217	484	58	1.6	340	1	AI371265	AI371265	qv79h09.x
352	58	1.6	231	7	CK429584	CK429584	oj38e11.y	485	58	1.6	340	1	AI436456	AI436456	ti08c12.x
353	58	1.6	234	1	AI366910	AI366910	qv94g09.x	486	58	1.6	341	1	AL046681	AL046681	DKFp434B
354	58	1.6	239	5	BQ390209	BQ390209	NISC_mq11	487	58	1.6	343	1	AL039287	AL039287	DKFp434B
355	58	1.6	240	5	BQ265962	BQ265962	NISC_ff10	c 488	58	1.6	346	4	BQ059804	BQ059804	naf44a04.x
356	58	1.6	241	1	AI561177	AI561177	tg37e11.x	489	58	1.6	347	1	AI963846	AI963846	wr67g08.x
357	58	1.6	244	5	BQ392210	BQ392210	NISC_mq23	490	58	1.6	347	5	BQ392745	BQ392745	NISC_mq26
358	58	1.6	249	4	BM593925	BM593925	170006874	c 491	58	1.6	347	7	CK113356	CK113356	213b14.p1
359	58	1.6	253	4	BM637390	BM637390	170006875	492	58	1.6	349	1	AI567940	AI567940	q86a12.x
360	58	1.6	253	7	CF722747	CF722747	F10_LKF00	493	58	1.6	349	5	BQ520314	BQ520314	NISC_n104
361	58	1.6	255	1	AL047611	AL047611	DKFp586H	494	58	1.6	349	6	CD723632	CD723632	oj24f02.y
362	58	1.6	257	4	BG113712	BG113712	602284230	495	58	1.6	350	5	BQ390727	BQ390727	NISC_mq14
363	58	1.6	259	1	AI582926	AI582926	ts07f10.x	496	58	1.6	350	5	BQ397046	BQ397046	NISC_mq25
364	58	1.6	264	7	CO881096	CO881096	BovGen_09	497	58	1.6	351	1	AI610357	AI610357	tp18g10.x
365	58	1.6	265	7	CK275140	CK275140	170006000	498	58	1.6	351	5	BQ526633	BQ526633	NISC_nol7
366	58	1.6	265	7	CO889401	CO889401	BovGen_17	499	58	1.6	353	4	BG178532	BG178532	602328358
367	58	1.6	269	5	BQ392506	BQ392506	NISC_mq24	500	58	1.6	354	1	AI817244	AI817244	wk21e09.x
368	58	1.6	273	7	CF651927	CF651927	23-L02052	501	58	1.6	357	4	BG180295	BG180295	602331131
369	58	1.6	276	5	BQ389379	BQ389379	NISC_mq07	502	58	1.6	358	4	BF968504	BF968504	602271283
370	58	1.6	277	4	BM644186	BM644186	170006873	c 503	58	1.6	360	7	CF640472	CF640472	D27_G03_F
371	58	1.6	278	1	AI521566	AI521566	to64g10.x	c 504	58	1.6	361	1	AI612913	AI612913	tx07g06.x
372	58	1.6	278	4	BG785787	BG785787	SEAUMC005	c 505	58	1.6	361	7	CF874123	CF874123	tr1c035x1
373	58	1.6	279	5	BQ392248	BQ392248	NISC_mq23	506	58	1.6	367	5	BQ525045	BQ525045	NISC_n008
374	58	1.6	281	1	AI499463	AI499463	tn95f08.x	507	58	1.6	368	5	BQ520417	BQ520417	NISC_n104
375	58	1.6	283	4	BG163646	BG163646	602338823	508	58	1.6	368	7	CK273721	CK273721	170006000
376	58	1.6	283	5	BQ391743	BQ391743	NISC_mq20	509	58	1.6	371	1	AI476694	AI476694	tm18b06.x
377	58	1.6	284	5	BQ392194	BQ392194	NISC_mq23	c 510	58	1.6	371	7	CK286273	CK286273	170005999
378	58	1.6	285	1	AL047152	AL047152	DKFp586E	511	58	1.6	372	1	AI285826	AI285826	qu81n06.x
379	58	1.6	286	1	AI355126	AI355126	qr75c04.x	512	58	1.6	375	5	BQ391608	BQ391608	NISC_mq19
380	58	1.6	290	4	BI119510	BI119510	AI18A_Po	c 513	58	1.6	376	4	BG780328	BG780328	SEAUMC000
381	58	1.6	291	1	AL045166	AL045166	DKFp434A	514	58	1.6	377	1	AI863014	AI863014	wm45c09.x
382	58	1.6	291	4	BI186556	BI186556	AR041D09P	515	58	1.6	377	5	BQ390108	BQ390108	NISC_mq11
383	58	1.6	294	7	CF640192	CF640192	D24_E03_F	c 516	58	1.6	377	7	CF881912	CF881912	tr1c0085xn
384	58	1.6	295	1	AI354981	AI354981	qt78c12.x	517	58	1.6	378	5	BQ392652	BQ392652	NISC_mq25
385	58	1.6	296	1	AI610362	AI610362	tp18h07.x	518	58	1.6	378	5	BQ395906	BQ395906	NISC_mq17
386	58	1.6	297	2	BF720448	BF720448	mab54d10	519	58	1.6	380	1	AI355765	AI355765	qt94f06.x
387	58	1.6	297	7	CO892856	CO892856	NISC_mq23	520	58	1.6	380	1	AI521594	AI521594	to65c12.x
388	58	1.6	297	7	CO879901	CO879901	BovGen_08	521	58	1.6	382	1	AI499512	AI499512	tc02d06.x
389	58	1.6	304	5	BQ265956	BQ265956	L0526C06-	522	58	1.6	382	5	BQ524726	BQ524726	NISC_m006
390	58	1.6	304	5	BQ265956	BQ265956	NISC_ff10	523	58	1.6	385	5	BQ520372	BQ520372	NISC_n104
391	58	1.6	305	5	BQ265996	BQ265996	NISC_ff10	524	58	1.6	388	6	CB259870	CB259870	16-B9603-
392	58	1.6	305	5	BQ377746	BQ377746	AGENGOURT	525	58	1.6	389	1	AI588360	AI588360	fb99g09.x
393	58	1.6	309	5	EX517975	EX517975	EX517975	526	58	1.6	390	5	BQ386279	BQ386279	NISC_mn17
394	58	1.6	310	1	AI440239	AI440239	tj01a06.x	527	58	1.6	391	1	AI889133	AI889133	wm45e03.x
395	58	1.6	310	1	AI567961	AI567961	tg86d08.x	528	58	1.6	391	5	BQ520378	BQ520378	NISC_n104
396	58	1.6	310	1	AA285478	AA285478	vc33f02.r	529	58	1.6	392	1	AI538881	AI538881	tp74n05.x
397	58	1.6	311	1	AI521596	AI521596	to65d02.x	530	58	1.6	393	1	AI805774	AI805774	tx89h10.x
398	58	1.6	311	7	CO893754	CO893754	BovGen_22	531	58	1.6	393	5	BQ389292	BQ389292	NISC_mq06
399	58	1.6	312	1	AI436438	AI436438	ti09b04.x	532	58	1.6	393	5	BQ524850	BQ524850	NISC_n007
400	58	1.6	312	2	BF727352	BF727352	by20c12.y	533	58	1.6	393	5	BQ525032	BQ525032	NISC_n008
401	58	1.6	317	5	BQ400927	BQ400927	NISC_mpl2	534	58	1.6	396	5	BQ519847	BQ519847	NISC_nol1
402	58	1.6	318	5	BQ389767	BQ389767	NISC_mq09	c 535	58	1.6	397	4	BG924268	BG924268	HNC26-1-B

536	58	1.6	398	5	BQ524540	NISC no05	BQ524540	NISC no05	609	58	1.6	449	5	BQ390822	NISC mq15
537	58	1.6	398	5	BX847873	BX847873	BX847873	BX847873	610	58	1.6	449	7	CO885887	Bovden_14
538	58	1.6	399	5	BQ520127	NISC nl03	BQ520127	NISC nl03	611	58	1.6	450	5	BQ389233	NISC mq06
539	58	1.6	401	5	BQ524751	NISC no06	BQ524751	NISC no06	612	58	1.6	450	5	BQ399241	NISC mp02
540	58	1.6	401	7	CK120781	206c02.p1	CK120781	206c02.p1	613	58	1.6	450	5	BQ522595	NISC nl17
541	58	1.6	402	1	A1927252	wn24c09.x	A1927252	wn24c09.x	614	58	1.6	451	5	BQ525103	NISC no08
542	58	1.6	402	5	BQ526842	NISC no18	BQ526842	NISC no18	615	58	1.6	451	1	AI355017	qt97a06.x
543	58	1.6	403	1	AI499508	to02d01.x	AI499508	to02d01.x	616	58	1.6	454	1	AL079910	DKFzp586A
544	58	1.6	403	1	AI4885920	wm76c04.x	AI4885920	wm76c04.x	617	58	1.6	456	5	BQ524518	NISC no05
545	58	1.6	403	5	BQ383743	NISC nm02	BQ383743	NISC nm02	618	58	1.6	457	1	AI955441	wt14e10.x
546	58	1.6	405	7	CK620773	ml16d03.y	CK620773	ml16d03.y	619	58	1.6	457	5	BQ400416	NISC mp09
547	58	1.6	406	5	BQ390779	NISC mq15	BQ390779	NISC mq15	620	58	1.6	457	7	CO896683	Bovgen_25
548	58	1.6	408	4	BQ928925	HNC10-1-F	BQ928925	HNC10-1-F	621	58	1.6	458	5	BQ389693	NISC mq09
549	58	1.6	409	1	AI499483	to02a08.x	AI499483	to02a08.x	622	58	1.6	459	1	AI431321	ar55c04.x
550	58	1.6	410	5	BQ387607	NISC nm24	BQ387607	NISC nm24	623	58	1.6	459	1	AI434255	t133d08.x
551	58	1.6	410	5	BQ523105	NISC nl20	BQ523105	NISC nl20	624	58	1.6	459	4	BM117975	L085H01-
552	58	1.6	410	7	CF577499	AGENCOURT	CF577499	AGENCOURT	625	58	1.6	459	5	BQ392701	NISC mq26
553	58	1.6	411	7	CF641990	D46_E08_F	CF641990	D46_E08_F	626	58	1.6	459	5	BQ393509	NISC ng03
554	58	1.6	413	1	AI500658	tn9307.x	AI500658	tn9307.x	627	58	1.6	459	5	BQ520846	NISC nl07
555	58	1.6	413	5	BQ389879	NISC mq10	BQ389879	NISC mq10	628	58	1.6	461	4	BM117198	L0847F03-
556	58	1.6	413	5	BQ524857	NISC no07	BQ524857	NISC no07	629	58	1.6	462	5	BQ389446	NISC mq07
557	58	1.6	414	4	BQ898312	HOA39-1-A	BQ898312	HOA39-1-A	630	58	1.6	463	5	BQ525578	NISC ng11
558	58	1.6	414	5	BQ399519	NISC mp04	BQ399519	NISC mp04	631	58	1.6	463	6	CD721864	oJ2d12.y
559	58	1.6	415	5	BX844259	BX844259	BX844259	BX844259	632	58	1.6	465	1	AI610402	tp18a10.x
560	58	1.6	417	1	AI432653	t122b04.x	AI432653	t122b04.x	633	58	1.6	465	6	CB044392	NISC gc04
561	58	1.6	417	4	BQ924847	HNC4-1-F8	BQ924847	HNC4-1-F8	634	58	1.6	466	5	BQ388149	NISC mn27
562	58	1.6	417	5	BQ400532	NISC mp09	BQ400532	NISC mp09	635	58	1.6	468	4	BM115559	L0831H09-
563	58	1.6	417	5	BQ519962	NISC nl02	BQ519962	NISC nl02	636	58	1.6	468	5	BQ392544	NISC mq25
564	58	1.6	418	5	BQ391548	NISC mq19	BQ391548	NISC mq19	637	58	1.6	468	5	BQ395820	NISC ng17
565	58	1.6	418	5	BQ400406	NISC mp09	BQ400406	NISC mp09	638	58	1.6	468	5	BQ399226	NISC mp02
566	58	1.6	418	5	BQ520326	NISC nl04	BQ520326	NISC nl04	639	58	1.6	469	4	BQ286991	NISC mg01
567	58	1.6	419	2	AW229306	uo09a03.y	AW229306	uo09a03.y	640	58	1.6	469	6	CA334673	NISC l1a1
568	58	1.6	419	5	BQ525525	NISC ng11	BQ525525	NISC ng11	641	58	1.6	470	1	AI521551	to64e12.x
569	58	1.6	420	5	BQ397024	NISC ng25	BQ397024	NISC ng25	642	58	1.6	470	5	BQ521062	NISC nl08
570	58	1.6	422	1	A1537925	tp26g12.x	A1537925	tp26g12.x	643	58	1.6	472	5	BQ391529	NISC mg19
571	58	1.6	425	5	BQ520586	NISC nl05	BQ520586	NISC nl05	644	58	1.6	472	5	BQ522890	NISC nl19
572	58	1.6	425	5	BQ520785	NISC nl07	BQ520785	NISC nl07	645	58	1.6	474	5	BQ523196	NISC nl20
573	58	1.6	426	1	A1282268	qu92h08.x	A1282268	qu92h08.x	646	58	1.6	476	5	BQ397256	NISC pg26
574	58	1.6	427	5	BQ336287	NISC ng03	BQ336287	NISC ng03	647	58	1.6	476	5	BQ399811	NISC mp05
575	58	1.6	427	5	BQ388757	NISC mg03	BQ388757	NISC mg03	648	58	1.6	476	5	BQ522205	NISC nl15
576	58	1.6	427	5	BQ395904	NISC ng17	BQ395904	NISC ng17	649	58	1.6	478	5	BQ389285	NISC mq06
577	58	1.6	429	1	AL042787	DKFzp434E	AL042787	DKFzp434E	650	58	1.6	478	5	BQ521567	NISC nl11
578	58	1.6	429	5	BQ389497	NISC mg07	BQ389497	NISC mg07	651	58	1.6	478	5	BQ524478	NISC no05
579	58	1.6	429	5	BQ393388	NISC ng03	BQ393388	NISC ng03	652	58	1.6	478	5	BX525322	BX525322
580	58	1.6	429	5	BQ522980	NISC nl19	BQ522980	NISC nl19	653	58	1.6	480	5	BQ383958	NISC mn04
581	58	1.6	431	1	A1923061	wn24h02.x	AI923061	wn24h02.x	654	58	1.6	480	5	BQ526773	NISC no18
582	58	1.6	431	5	BQ525081	NISC no08	BQ525081	NISC no08	655	58	1.6	481	4	BQ606034	L0908G01-
583	58	1.6	432	1	AI431323	ar55c08.x	AI431323	ar55c08.x	656	58	1.6	481	5	BQ523936	NISC no01
584	58	1.6	432	5	BQ520532	NISC nl05	BQ520532	NISC nl05	657	58	1.6	484	1	AI434223	t133a04.x
585	58	1.6	432	7	CO885766	Bovgen_14	CO885766	Bovgen_14	658	58	1.6	484	5	BQ389902	NISC mq10
586	58	1.6	433	7	CK620902	ml17h06.y	CK620902	ml17h06.y	659	58	1.6	485	5	BQ520997	NISC nl08
587	58	1.6	434	1	A1357672	qu21b04.x	A1357672	qu21b04.x	660	58	1.6	486	5	BQ387780	NISC mn25
588	58	1.6	435	5	BQ529392	NISC nl19	BQ529392	NISC nl19	661	58	1.6	487	1	AI285432	qt83c04.x
589	58	1.6	436	4	BG114865	602315646	BG114865	602315646	662	58	1.6	487	5	BQ388940	NISC mq04
590	58	1.6	436	5	BQ401004	NISC mp12	BQ401004	NISC mp12	663	58	1.6	488	5	BQ388916	NISC mq04
591	58	1.6	437	1	A1923446	wn85f11.x	AI923446	wn85f11.x	664	58	1.6	489	5	BQ522509	NISC nl17
592	58	1.6	437	5	BQ395916	NISC ng17	BQ395916	NISC ng17	665	58	1.6	490	5	BQ522780	NISC nl18
593	58	1.6	438	5	BQ389812	NISC mg09	BQ389812	NISC mg09	666	58	1.6	490	5	BQ524514	NISC no05
594	58	1.6	438	5	BX515080	NISC nl15	BX515080	NISC nl15	667	58	1.6	491	5	BQ520528	NISC nl05
595	58	1.6	439	5	BQ522280	NISC nl15	BQ522280	NISC nl15	668	58	1.6	491	5	BQ520964	NISC nl08
596	58	1.6	440	5	BQ391695	NISC mq20	BQ391695	NISC mq20	669	58	1.6	492	5	BQ387653	NISC mn25
597	58	1.6	440	5	BQ522645	NISC nl17	BQ522645	NISC nl17	670	58	1.6	492	5	BQ396967	NISC ng25
598	58	1.6	441	5	BQ391237	NISC mg17	BQ391237	NISC mg17	671	58	1.6	493	1	AI697243	qt17f09.x
599	58	1.6	441	5	BQ392753	NISC mq26	BQ392753	NISC mq26	672	58	1.6	493	5	BQ521529	NISC nl11
600	58	1.6	442	5	BQ525620	NISC nl01	BQ525620	NISC nl01	673	58	1.6	493	5	BQ522519	NISC nl17
601	58	1.6	443	5	BQ520151	NISC nl03	BQ520151	NISC nl03	674	58	1.6	493	7	GN485082	hx22f03.y
602	58	1.6	443	5	BQ522776	NISC nl18	BQ522776	NISC nl18	675	58	1.6	494	5	BQ256801	NISC ko06
603	58	1.6	444	5	BQ391745	NISC mq20	BQ391745	NISC mq20	676	58	1.6	494	5	BQ388095	NISC mn27
604	58	1.6	447	1	AL042572	DKFzp434J	AL042572	DKFzp434J	677	58	1.6	494	6	BQ522717	NISC nl18
605	58	1.6	447	2	AW081133	xc29f04.x	AW081133	xc29f04.x	678	58	1.6	494	6	CD677131	ho11f03.y
606	58	1.6	447	4	BQ897194	HOA46-1-A	BQ897194	HOA46-1-A	679	58	1.6	495	5	BQ400644	NISC mq10
607	58	1.6	448	2	AW087954	xb45c10.x	AW087954	xb45c10.x	680	58	1.6	496	4	BQ965898	60282962
608	58	1.6	448	6	CD723606	oJ24c08.y	CD723606	oJ24c08.y	681	58	1.6	497	1	AI610429	tp18d10.x

682	58	1.6	497	5	BQ525592	NISC no11	BQ525592	NISC no11	755	58	1.6	530	1	AL042944	AL042944
683	58	1.6	498	5	BQ526857	NISC no18	BQ526857	NISC no18	756	58	1.6	530	5	BQ396970	BQ396970
684	58	1.6	499	1	AI434222	t133a02.x	AI434222	t133a02.x	757	58	1.6	531	4	BM013859	BM013859
685	58	1.6	499	5	BQ522756	NISC nl18	BQ522756	NISC nl18	758	58	1.6	531	5	BQ522393	BQ522393
686	58	1.6	500	1	AI284515	qt8905.x	AI284515	qt8905.x	759	58	1.6	533	1	AL042451	AL042451
687	58	1.6	500	1	AI628850	ty17c08.x	AI628850	ty17c08.x	760	58	1.6	533	5	BQ387422	BQ387422
688	58	1.6	500	5	BQ388671	NISC mg03	BQ388671	NISC mg03	761	58	1.6	533	1	AL042416	AL042416
689	58	1.6	500	5	BQ521021	NISC nl08	BQ521021	NISC nl08	762	58	1.6	535	5	BQ400600	BQ400600
690	58	1.6	500	6	CD724212	oj31509.y	CD724212	oj31509.y	763	58	1.6	535	5	CA390852	CA390852
691	58	1.6	501	5	BQ520834	NISC nl07	BQ520834	NISC nl07	764	58	1.6	536	7	CF884415	CF884415
692	58	1.6	501	5	BQ521575	NISC nl11	BQ521575	NISC nl11	765	58	1.6	537	5	BQ389732	BQ389732
693	58	1.6	501	7	CK414590	AUF_IpG11	CK414590	AUF_IpG11	766	58	1.6	537	5	BQ399474	BQ399474
694	58	1.6	502	5	BQ400913	NISC mp12	BQ400913	NISC mp12	767	58	1.6	537	5	BQ525297	BQ525297
695	58	1.6	503	6	CD723592	oj24b04.y	CD723592	oj24b04.y	768	58	1.6	538	5	BQ522633	BQ522633
696	58	1.6	503	6	CD723592	oj24b04.y	CD723592	oj24b04.y	769	58	1.6	538	5	BQ389913	BQ389913
697	58	1.6	505	1	AI434240	t133c01.x	AI434240	t133c01.x	770	58	1.6	539	5	BQ526582	BQ526582
698	58	1.6	505	1	AI804515	tp60c04.x	AI804515	tp60c04.x	771	58	1.6	539	5	BQ528904	BQ528904
699	58	1.6	505	5	BQ389788	NISC mg09	BQ389788	NISC mg09	772	58	1.6	540	4	BQ520137	BQ520137
700	58	1.6	505	5	BQ520026	NISC nl02	BQ520026	NISC nl02	773	58	1.6	541	5	BQ520137	BQ520137
701	58	1.6	505	5	BQ522647	NISC nl17	BQ522647	NISC nl17	774	58	1.6	542	5	BQ390259	BQ390259
702	58	1.6	506	5	BQ522850	NISC nl18	BQ522850	NISC nl18	775	58	1.6	544	4	BQ3927920	BQ3927920
703	58	1.6	506	5	BQ388704	NISC mg02	BQ388704	NISC mg02	776	58	1.6	544	5	BQ391651	BQ391651
704	58	1.6	507	5	BQ391912	NISC mp02	BQ391912	NISC mp02	777	58	1.6	544	5	BQ399337	BQ399337
705	58	1.6	507	5	BQ388655	NISC mg03	BQ388655	NISC mg03	778	58	1.6	545	1	AI687614	AI687614
706	58	1.6	507	5	BQ390068	NISC mg11	BQ390068	NISC mg11	779	58	1.6	545	5	BQ390214	BQ390214
707	58	1.6	508	5	BQ391243	NISC mg17	BQ391243	NISC mg17	780	58	1.6	545	5	BQ393105	BQ393105
708	58	1.6	508	1	AI284516	qt8906.x	AI284516	qt8906.x	781	58	1.6	546	1	AI539632	AI539632
709	58	1.6	509	5	BQ383513	NISC no12	BQ383513	NISC no12	782	58	1.6	547	5	BQ399284	BQ399284
710	58	1.6	510	4	BM123229	LO521D08-	BM123229	LO521D08-	783	58	1.6	547	7	CF873233	CF873233
711	58	1.6	510	5	BQ391681	NISC mg20	BQ391681	NISC mg20	784	58	1.6	548	4	BQ3924789	BQ3924789
712	58	1.6	511	5	BQ389929	NISC mp06	BQ389929	NISC mp06	785	58	1.6	549	4	BG111831	BG111831
713	58	1.6	511	5	BQ399969	NISC mg01	BQ399969	NISC mg01	786	58	1.6	550	1	AL039494	AL039494
714	58	1.6	511	7	CO888164	BovGen.16	CO888164	BovGen.16	787	58	1.6	550	5	BQ391749	BQ391749
715	58	1.6	512	5	BQ390352	NISC mg12	BQ390352	NISC mg12	788	58	1.6	550	5	BQ524488	BQ524488
716	58	1.6	512	5	BQ520038	NISC no18	BQ520038	NISC no18	789	58	1.6	550	5	BQ524570	BQ524570
717	58	1.6	512	5	BQ526846	NISC nl02	BQ526846	NISC nl02	790	58	1.6	551	4	BQ3900028	BQ3900028
718	58	1.6	513	5	BQ521513	NISC nl11	BQ521513	NISC nl11	791	58	1.6	551	5	BQ389493	BQ389493
719	58	1.6	514	5	BQ389814	NISC mg09	BQ389814	NISC mg09	792	58	1.6	551	7	CF883818	CF883818
720	58	1.6	514	5	BQ399119	NISC mp01	BQ399119	NISC mp01	793	58	1.6	553	1	AJ457500	AJ457500
721	58	1.6	515	1	AI436458	ti09d02.x	AI436458	ti09d02.x	794	58	1.6	553	5	BQ520659	BQ520659
722	58	1.6	515	1	AI436458	ti09d02.x	AI436458	ti09d02.x	795	58	1.6	553	7	CF873726	CF873726
723	58	1.6	517	5	BQ389921	NISC mg06	BQ389921	NISC mg06	796	58	1.6	553	7	CF873586	CF873586
724	58	1.6	518	5	BQ387993	NISC mn27	BQ387993	NISC mn27	797	58	1.6	554	1	AI889148	AI889148
725	58	1.6	519	1	AI433968	ti12c03.x	AI433968	ti12c03.x	798	58	1.6	555	5	BQ390179	BQ390179
726	58	1.6	519	5	BQ399021	NISC mp01	BQ399021	NISC mp01	799	58	1.6	555	5	BQ397268	BQ397268
727	58	1.6	521	5	BQ389771	NISC mg09	BQ389771	NISC mg09	800	58	1.6	556	4	BG869433	BG869433
728	58	1.6	521	5	BQ522862	NISC nl18	BQ522862	NISC nl18	801	58	1.6	556	5	BQ520577	BQ520577
729	58	1.6	521	7	CO895616	BovGen.23	CO895616	BovGen.23	802	58	1.6	556	6	CA189203	CA189203
730	58	1.6	522	5	BQ390268	NISC mg12	BQ390268	NISC mg12	803	58	1.6	557	5	BQ389775	BQ389775
731	58	1.6	522	7	CK628408	ip11f09.y	CK628408	ip11f09.y	804	58	1.6	558	5	BQ389894	BQ389894
732	58	1.6	522	7	CK628408	ip11f09.y	CK628408	ip11f09.y	805	58	1.6	558	5	BQ520512	BQ520512
733	58	1.6	523	5	BQ522695	NISC nl18	BQ522695	NISC nl18	806	58	1.6	559	5	BQ389896	BQ389896
734	58	1.6	523	7	CF865361	tr1c004xc	CF865361	tr1c004xc	807	58	1.6	559	7	CF873198	CF873198
735	58	1.6	524	5	BQ390040	NISC mg11	BQ390040	NISC mg11	808	58	1.6	561	1	AL042533	AL042533
736	58	1.6	525	4	BM115871	LO826F09-	BM115871	LO826F09-	809	58	1.6	561	5	BQ587060	BQ587060
737	58	1.6	525	5	BQ522265	NISC nl15	BQ522265	NISC nl15	810	58	1.6	562	1	AL042694	AL042694
738	58	1.6	525	5	BQ524568	NISC no05	BQ524568	NISC no05	811	58	1.6	562	7	CF884490	CF884490
739	58	1.6	525	6	CB938583	IPCGUx13	CB938583	IPCGUx13	812	58	1.6	562	7	CF884490	CF884490
740	58	1.6	526	1	AI469784	tm20n06.x	AI469784	tm20n06.x	813	58	1.6	563	7	CF882666	CF882666
741	58	1.6	526	1	AI476086	tl97g03.x	AI476086	tl97g03.x	814	58	1.6	565	7	CF875106	CF875106
742	58	1.6	526	1	AI537187	tp01d01.x	AI537187	tp01d01.x	815	58	1.6	566	1	AI815233	AI815233
743	58	1.6	527	4	BQ259587	602378722	BQ259587	602378722	816	58	1.6	566	5	BQ390642	BQ390642
744	58	1.6	527	1	AI499581	to22h12.x	AI499581	to22h12.x	817	58	1.6	567	4	BG898583	BG898583
745	58	1.6	527	2	AW151131	xg37g06.x	AW151131	xg37g06.x	818	58	1.6	567	7	CO882737	CO882737
746	58	1.6	527	4	BI380914	BFLGI_002	BI380914	BFLGI_002	819	58	1.6	569	7	CM485219	CM485219
747	58	1.6	527	5	BQ387327	NISC mn23	BQ387327	NISC mn23	820	58	1.6	570	5	BQ389346	BQ389346
748	58	1.6	527	5	BQ389790	NISC mg09	BQ389790	NISC mg09	821	58	1.6	570	5	BQ520814	BQ520814
749	58	1.6	528	4	BQ3924370	HNC26-1-G	BQ3924370	HNC26-1-G	822	58	1.6	570	5	BQ522259	BQ522259
750	58	1.6	528	5	BQ4000410	NISC mp09	BQ4000410	NISC mp09	823	58	1.6	571	1	AI702063	AI702063
751	58	1.6	528	5	BQ519883	NISC nl01	BQ519883	NISC nl01	824	58	1.6	571	4	BG900978	BG900978
752	58	1.6	528	6	CA230442	SCJFLL3C0	CA230442	SCJFLL3C0	825	58	1.6	571	5	BQ524526	BQ524526
753	58	1.6	529	1	BQ390324	NISC mg12	BQ390324	NISC mg12	826	58	1.6	572	5	BQ390373	BQ390373
754	58	1.6	530	1	AI469754	tm20e01.x	AI469754	tm20e01.x	827	58	1.6	573	1	AI538867	AI538867

828	58	1.6	573	2	AW118237	AW118237 xel2b08.x	c 901	58	1.6	633	4	BG899001	BG899001 HOA58-1-B
829	58	1.6	574	1	AI439995	AI439995 t163f08.x	902	58	1.6	633	5	BQ527151	BQ527151 NISC no20
830	58	1.6	575	1	AL042377	AL042377 DKF2p434A	c 903	58	1.6	636	4	BQ526743	BQ526743 HNC63-1-D
c 831	58	1.6	576	7	CF867055	CF867055 tr1c009xh	904	58	1.6	643	5	BQ389933	BQ389933 NISC mq10
832	58	1.6	577	7	CF862708	CF862708 tr1c031xm	905	58	1.6	646	5	BQ389769	BQ389769 NISC mq09
833	58	1.6	578	5	BQ390388	BQ390388 NISC mq12	c 906	58	1.6	646	7	CO893125	CO893125 BovGen_21
834	58	1.6	579	5	BQ390338	BQ390338 NISC mq12	907	58	1.6	648	1	AI872300	AI872300 wms7d05.x
835	58	1.6	580	1	AI687587	AI687587 tp97e07.x	908	58	1.6	648	7	CO884930	CO884930 BovGen_13
836	58	1.6	581	5	BQ384132	BQ384132 NISC mn05	909	58	1.6	650	4	BI855926	BI855926 603383093
837	58	1.6	582	5	BQ390195	BQ390195 NISC mn11	910	58	1.6	650	4	BI889674	BI889674 2F637-2-0
838	58	1.6	583	5	BQ392711	BQ392711 NISC mq26	911	58	1.6	651	1	AI554827	AI554827 tp73h04.x
839	58	1.6	584	5	BQ525020	BQ525020 NISC no08	912	58	1.6	652	5	BQ401053	BQ401053 NISC mp12
c 840	58	1.6	585	4	BQ526540	BQ526540 HNC4-1-A9	c 913	58	1.6	654	4	BQ525161	BQ525161 HNC37-1-C
841	58	1.6	586	5	BQ396558	BQ396558 NISC rg21	914	58	1.6	662	4	BI858668	BI858668 603388946
842	58	1.6	585	1	AI539847	AI539847 tp65e12.x	c 915	58	1.6	662	7	CO887751	CO887751 BovGen_16
843	58	1.6	586	5	BQ389752	BQ389752 NISC mq09	916	58	1.6	664	7	CO872672	CO872672 BovGen_00
844	58	1.6	585	5	BQ400077	BQ400077 NISC mp07	917	58	1.6	664	1	AI863357	AI863357 tz47d01.x
845	58	1.6	585	7	CO875413	CO875413 BovGen_03	c 918	58	1.6	664	4	BQ525347	BQ525347 HNC40-1-B
846	58	1.6	586	1	AI690948	AI690948 tq02e11.x	c 919	58	1.6	667	4	BQ527733	BQ527733 HNC44-1-G
847	58	1.6	587	1	AL042853	AL042853 DKF2p434H	920	58	1.6	669	1	AI872310	AI872310 wms7e07.x
848	58	1.6	586	5	BQ400992	BQ400992 NISC mp12	921	58	1.6	669	2	AW172745	AW172745 xj02h09.x
849	58	1.6	586	5	BQ522485	BQ522485 NISC nl16	c 922	58	1.6	677	4	BQ928514	BQ928514 HNC49-1-A
850	58	1.6	587	5	BQ391116	BQ391116 NISC mq16	923	58	1.6	679	1	AL042981	AL042981 DKF2p434M
851	58	1.6	588	1	AI521634	AI521634 to65h04.x	c 924	58	1.6	680	7	CO881552	CO881552 BovGen_09
852	58	1.6	588	1	AU301568	AU301568 AU301568	925	58	1.6	683	1	AI446536	AI446536 tj05b10.x
853	58	1.6	589	1	AI521465	AI521465 th1c02.x	926	58	1.6	685	9	AG076896	AG076896 Pan trogl
854	58	1.6	589	5	BQ388694	BQ388694 NISC mq03	927	58	1.6	688	1	AL042557	AL042557 DKF2p434J
855	58	1.6	589	5	BQ391645	BQ391645 NISC mq19	928	58	1.6	688	7	CO889662	CO889662 BovGen_17
c 856	58	1.6	589	5	EX846370	EX846370 EX846370	929	58	1.6	691	4	BF965904	BF965904 602277262
857	58	1.6	589	7	CF886069	CF886069 tr1c085xe	930	58	1.6	692	1	AI538878	AI538878 tp74h01.x
858	58	1.6	590	1	AI828583	AI828583 w142e08.x	931	58	1.6	693	1	AI354998	AI354998 qu16b10.x
859	58	1.6	591	5	BQ390621	BQ390621 NISC mq14	932	58	1.6	695	1	AI888575	AI888575 wms3b09.x
c 860	58	1.6	592	4	BQ926032	BQ926032 HNC23-1-B	933	58	1.6	695	4	BG179586	BG179586 602328213
861	58	1.6	592	5	BQ390609	BQ390609 NISC mq14	934	58	1.6	700	4	BG299059	BG299059 602397761
862	58	1.6	593	5	BQ390665	BQ390665 NISC mq11	935	58	1.6	701	4	BG111590	BG111590 602282624
c 863	58	1.6	594	5	BQ391024	BQ391024 NISC mq16	936	58	1.6	703	4	BI087461	BI087461 602851091
c 864	58	1.6	594	4	BQ929418	BQ929418 HNC50-1-B	937	58	1.6	704	1	AI863197	AI863197 tz44e08.x
c 865	58	1.6	594	5	BQ400399	BQ400399 NISC mp09	938	58	1.6	705	7	CK118011	CK118011 207k15.p1
c 866	58	1.6	596	4	BG896174	BG896174 HOA9-1-B1	c 939	58	1.6	705	7	CK120856	CK120856 205m12.p1
867	58	1.6	599	5	BQ384194	BQ384194 NISC mn05	c 940	58	1.6	709	7	CK120856	CK120856 205m12.p1
c 868	58	1.6	599	5	EX847993	EX847993 EX847993	941	58	1.6	710	2	BE306712	BE306712 601104130
869	58	1.6	601	4	BF971261	BF971261 602273289	942	58	1.6	712	1	AI567944	AI567944 tq86b08.x
c 870	58	1.6	602	5	BQ525565	BQ525565 NISC no11	943	58	1.6	713	1	AI888665	AI888665 wms3b08.x
c 871	58	1.6	604	4	BG899723	BG899723 HOA39-1-F	944	58	1.6	721	1	AI567968	AI567968 tq86e05.x
872	58	1.6	604	5	BQ522555	BQ522555 NISC nl17	945	58	1.6	725	4	BF968622	BF968622 602271054
873	58	1.6	606	5	BQ389945	BQ389945 NISC mq10	946	58	1.6	727	1	AI804531	AI804531 tp60d11.x
874	58	1.6	606	5	BQ390348	BQ390348 NISC mq12	c 947	58	1.6	728	7	CO881106	CO881106 BovGen_09
875	58	1.6	606	7	CK619769	CK619769 mk28b09.y	948	58	1.6	731	1	AL042865	AL042865 DKF2p434H
876	58	1.6	608	5	BQ524165	BQ524165 NISC no03	949	58	1.6	732	4	BG114012	BG114012 602284496
c 877	58	1.6	609	1	AI866472	AI866472 tz49b10.x	950	58	1.6	733	7	CF520284	CF520284 AGENCOURT
c 878	58	1.6	609	6	CA175113	CA175113 SCJFST101	951	58	1.6	735	1	AI567935	AI567935 tq86a04.x
c 879	58	1.6	610	1	AL042538	AL042538 DKF2p434I	952	58	1.6	737	1	AL043196	AL043196 DKF2p434H
c 880	58	1.6	610	5	EX849028	EX849028 EX849028	953	58	1.6	739	1	AL042750	AL042750 DKF2p434C
c 881	58	1.6	610	6	CA264570	CA264570 SCBPFLA17	954	58	1.6	741	4	BG251851	BG251851 602364466
882	58	1.6	612	5	BQ391612	BQ391612 NISC mq19	955	58	1.6	744	4	BI888935	BI888935 2F637-2-0
883	58	1.6	613	1	AL040006	AL040006 DKF2p434M	956	58	1.6	745	4	BG284564	BG284564 602408723
884	58	1.6	613	4	BI868792	BI868792 603391947	957	58	1.6	747	7	CK357136	CK357136 AGENCOURT
c 885	58	1.6	614	1	AI888317	AI888317 wms3f11.x	958	58	1.6	748	1	AL042515	AL042515 DKF2p434H
c 886	58	1.6	614	6	CA128240	CA128240 SCJFTR203	c 959	58	1.6	750	6	CB903665	CB903665 tr1c035x1
887	58	1.6	614	7	CF878170	CF878170 tr1c016xm	c 960	58	1.6	753	6	CB903554	CB903554 tr1c035xc
c 888	58	1.6	616	1	AI288281	AI288281 qv84a03.x	961	58	1.6	754	1	AI805762	AI805762 tx89g09.x
c 889	58	1.6	617	4	BG927885	BG927885 HNC7-1-D1	962	58	1.6	756	7	CK195662	CK195662 FGAS00410
c 890	58	1.6	618	4	BG928558	BG928558 HNC68-1-E	963	58	1.6	759	6	CB902325	CB902325 tr1c029x0
c 891	58	1.6	619	4	BQ529420	BQ529420 HNC50-1-A	964	58	1.6	760	2	BF538723	BF538723 602051051
892	58	1.6	620	7	CF873624	CF873624 tr1c005xd	c 965	58	1.6	761	9	CG847811	CG847811 ZMMHBB031
893	58	1.6	621	1	AI887785	AI887785 wms18g07.x	966	58	1.6	763	7	CK198343	CK198343 FGAS00682
c 894	58	1.6	622	2	AW180982	AW180982 MGA0133r	967	58	1.6	770	7	CF284480	CF284480 AGENCOURT
c 895	58	1.6	623	4	BG926630	BG926630 HNC62-1-E	968	58	1.6	776	4	BI871663	BI871663 603395562
c 896	58	1.6	623	7	CF884293	CF884293 tr1c038xg	969	58	1.6	777	4	BI855622	BI855622 603383126
897	58	1.6	629	5	BQ522332	BQ522332 NISC nl16	970	58	1.6	779	4	BG782822	BG782822 SEAUWC002
c 898	58	1.6	630	5	BG927301	BG927301 HNC66-1-B	971	58	1.6	780	4	BG165260	BG165260 602344152
c 899	58	1.6	632	1	AL043021	AL043021 DKF2p434O	972	58	1.6	781	7	CK195756	CK195756 FGAS00419
c 900	58	1.6	632	7	CO879146	CO879146 BovGen_07	973	58	1.6	782	6	CB895899	CB895899 tr1c004xc

974	58	1.6	782	6	CB9898562	1047	58	1.6	826	7	CK196393	CK196393	FGAS00485
c 975	58	1.6	782	4	CB903275	1048	58	1.6	826	7	CK196998	CK196998	FGAS00546
976	58	1.6	785	4	BQ288001	1049	58	1.6	827	7	CK195533	CK195533	FGAS00397
977	58	1.6	786	7	CK479384	1050	58	1.6	827	7	CK196232	CK196232	FGAS00468
c 978	58	1.6	788	7	CF285572	1051	58	1.6	827	7	CK200843	CK200843	FGAS00936
c 979	58	1.6	791	6	CB986126	1052	58	1.6	827	7	CK200927	CK200927	FGAS00944
980	58	1.6	793	1	A1610426	1053	58	1.6	828	7	CK193000	CK193000	FGAS00140
981	58	1.6	794	7	CF147535	1054	58	1.6	828	7	CK193053	CK193053	FGAS00146
982	58	1.6	796	7	CK195721	1055	58	1.6	828	7	CK193648	CK193648	FGAS00206
983	58	1.6	797	7	CO566927	1056	58	1.6	828	7	CK194229	CK194229	FGAS00264
984	58	1.6	800	7	CK196897	1057	58	1.6	828	7	CK194448	CK194448	FGAS00287
c 985	58	1.6	800	7	CK792681	1058	58	1.6	828	7	CK194972	CK194972	FGAS00340
986	58	1.6	801	4	BG782551	1059	58	1.6	828	7	CK196355	CK196355	FGAS00481
987	58	1.6	801	5	BQ434265	1060	58	1.6	828	7	CK196878	CK196878	FGAS00534
988	58	1.6	801	7	CF873386	1061	58	1.6	828	7	CK198145	CK198145	FGAS00662
989	58	1.6	801	7	CF873397	1062	58	1.6	828	7	CK198379	CK198379	FGAS00686
990	58	1.6	801	7	CK200310	1063	58	1.6	828	7	CK199532	CK199532	FGAS00803
c 991	58	1.6	801	7	CK792023	1064	58	1.6	828	7	CK200896	CK200896	FGAS00941
992	58	1.6	802	7	CK196378	1065	58	1.6	829	7	CK195739	CK195739	FGAS00418
993	58	1.6	805	7	CK200304	1066	58	1.6	829	7	CK196423	CK196423	FGAS00488
994	58	1.6	807	1	A1432656	1067	58	1.6	829	7	CK196646	CK196646	FGAS00510
995	58	1.6	807	4	BG393344	1068	58	1.6	829	7	CK199037	CK199037	FGAS00752
996	58	1.6	807	7	CK196289	1069	58	1.6	829	7	CK201011	CK201011	FGAS00952
997	58	1.6	807	7	CK197553	1070	58	1.6	830	7	CK193158	CK193158	FGAS00157
c 998	58	1.6	807	7	CK199534	1071	58	1.6	830	7	CK195617	CK195617	FGAS00405
999	58	1.6	809	7	CB997064	1072	58	1.6	830	7	CK196779	CK196779	FGAS00524
1000	58	1.6	811	6	CK194846	1073	58	1.6	830	7	CK196984	CK196984	FGAS00545
1001	58	1.6	812	7	CF872637	1074	58	1.6	830	7	CK198340	CK198340	FGAS00682
1002	58	1.6	812	7	CK195770	1075	58	1.6	831	7	CK196333	CK196333	FGAS00478
c1003	58	1.6	812	9	CG847981	1076	58	1.6	831	7	CK198286	CK198286	FGAS00677
1004	58	1.6	813	7	CK192880	1077	58	1.6	831	7	CK198776	CK198776	FGAS00726
1005	58	1.6	813	7	CK193688	1078	58	1.6	831	7	CK198924	CK198924	FGAS00741
1006	58	1.6	813	7	CK194268	1079	58	1.6	831	7	CK198938	CK198938	FGAS00742
1007	58	1.6	813	7	CK196966	1080	58	1.6	831	7	CK200278	CK200278	FGAS00878
1008	58	1.6	813	7	CK200167	1081	58	1.6	832	7	CK194439	CK194439	FGAS00826
1009	58	1.6	814	5	BQ227852	1082	58	1.6	832	7	CK196953	CK196953	FGAS00542
1010	58	1.6	814	7	CK200261	1083	58	1.6	832	7	CK198323	CK198323	FGAS00680
1011	58	1.6	814	7	CK200263	1084	58	1.6	832	7	CK200757	CK200757	FGAS00927
1012	58	1.6	814	7	CK200329	1085	58	1.6	833	5	BQ233461	BQ233461	AGENCOURT
1013	58	1.6	815	7	CK200375	1086	58	1.6	833	7	CK195815	CK195815	FGAS00426
1014	58	1.6	816	7	CK196242	1087	58	1.6	833	7	CK196827	CK196827	FGAS00529
1015	58	1.6	816	7	CK197263	1088	58	1.6	833	7	CK197043	CK197043	FGAS00551
1016	58	1.6	816	7	CK200360	1089	58	1.6	833	7	CK199653	CK199653	FGAS00815
1017	58	1.6	817	7	CK196872	1090	58	1.6	833	7	CK199679	CK199679	FGAS00818
1018	58	1.6	817	7	CK199307	1091	58	1.6	834	7	CK192938	CK192938	FGAS00134
1019	58	1.6	818	7	CK194869	1092	58	1.6	834	7	CK193106	CK193106	FGAS00151
1020	58	1.6	818	7	CK198899	1093	58	1.6	834	7	CK197725	CK197725	FGAS00620
1021	58	1.6	818	7	CK198929	1094	58	1.6	834	7	CK198335	CK198335	FGAS00682
1022	58	1.6	819	7	CK197025	1095	58	1.6	834	7	CK198390	CK198390	FGAS00687
1023	58	1.6	820	7	CK200974	1096	58	1.6	835	7	CK194334	CK194334	FGAS00275
1024	58	1.6	821	7	CK194961	1097	58	1.6	835	7	CK195582	CK195582	FGAS00402
1025	58	1.6	821	7	CK200359	1098	58	1.6	836	7	CK194202	CK194202	FGAS00262
1026	58	1.6	821	7	CK200794	1099	58	1.6	836	7	CK194248	CK194248	FGAS00266
1027	58	1.6	821	7	CK200879	1100	58	1.6	836	7	CK198202	CK198202	FGAS00668
1028	58	1.6	822	4	BG782371	1101	58	1.6	836	7	CK198244	CK198244	FGAS00672
1029	58	1.6	822	7	CK195026	1102	58	1.6	836	7	CK199507	CK199507	FGAS00800
1030	58	1.6	822	7	CK199583	1103	58	1.6	836	7	CK200220	CK200220	FGAS00872
1031	58	1.6	823	7	CK195025	1104	58	1.6	837	7	CK193585	CK193585	FGAS00159
1032	58	1.6	823	7	CK196405	1105	58	1.6	837	7	CK198005	CK198005	FGAS00648
1033	58	1.6	823	7	CK197545	1106	58	1.6	837	7	CK200849	CK200849	FGAS00936
1034	58	1.6	824	7	CK198388	1107	58	1.6	838	7	CK195428	CK195428	FGAS00386
1035	58	1.6	824	7	CK199020	1108	58	1.6	838	7	CK195643	CK195643	FGAS00408
c1036	58	1.6	825	6	CB908623	1109	58	1.6	838	7	CK196262	CK196262	FGAS00471
1037	58	1.6	825	7	CK192905	1110	58	1.6	838	7	CK196462	CK196462	FGAS00492
1038	58	1.6	825	7	CK193024	1111	58	1.6	838	7	CK196837	CK196837	FGAS00530
1039	58	1.6	825	7	CK194237	1112	58	1.6	838	7	CK197607	CK197607	FGAS00608
1040	58	1.6	825	7	CK196907	1113	58	1.6	838	7	CK198909	CK198909	FGAS00739
1041	58	1.6	825	7	CK197012	1114	58	1.6	839	7	CK193746	CK193746	FGAS00216
1042	58	1.6	825	7	CK199445	1115	58	1.6	839	7	CK194870	CK194870	FGAS00330
1043	58	1.6	825	7	CK200147	1116	58	1.6	839	7	CK196799	CK196799	FGAS00526
1044	58	1.6	825	7	CK200255	1117	58	1.6	839	7	CK197079	CK197079	FGAS00555
1045	58	1.6	826	7	CK193685	1118	58	1.6	840	5	BQ522683	BQ522683	AGENCOURT
1046	58	1.6	826	7	CK195554	1119	58	1.6	840	5	CK192960	CK192960	FGAS00136

1120	58	1.6	840	7	CK196277	FGAS00473	1193	58	1.6	853	7	CK193529	FGAS00194
1121	58	1.6	840	7	CK197060	FGAS00553	1194	58	1.6	853	7	CK194907	FGAS00334
1122	58	1.6	840	7	CK197074	FGAS00554	1195	58	1.6	853	7	CK195119	FGAS00355
1123	58	1.6	840	7	CK197669	FGAS00614	1196	58	1.6	853	7	CK198267	FGAS00675
1124	58	1.6	840	7	CK200853	FGAS00937	1197	58	1.6	853	7	CK199634	FGAS00813
1125	58	1.6	841	7	CF884356	tri6037xn	1198	58	1.6	853	7	CK200279	FGAS00878
1126	58	1.6	841	7	CK193049	FGAS00146	1199	58	1.6	853	7	CK200708	FGAS00922
1127	58	1.6	841	7	CK195765	FGAS00420	c1200	58	1.6	853	7	CO007895	EST79230
1128	58	1.6	841	7	CK196266	FGAS00471	1201	58	1.6	854	7	CK194464	FGAS00289
1129	58	1.6	842	7	CK193110	FGAS00152	1202	58	1.6	854	7	CK195033	FGAS00347
1130	58	1.6	842	7	CK195745	FGAS00418	1203	58	1.6	854	7	CK195063	FGAS00350
1131	58	1.6	842	7	CK196318	FGAS00477	1204	58	1.6	854	7	CK196223	FGAS00467
c1132	58	1.6	843	6	CA127447	SCCCLRC0	1205	58	1.6	854	7	CK196257	FGAS00470
1133	58	1.6	843	7	CK196365	FGAS00482	1206	58	1.6	854	7	CK196456	FGAS00491
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1136	58	1.6	844	7	CK194277	FGAS00269	1209	58	1.6	854	7	CK200848	FGAS00936
1137	58	1.6	844	7	CK194391	FGAS00281	1210	58	1.6	855	7	CK195062	FGAS00350
1138	58	1.6	844	7	CK196422	FGAS00488	1211	58	1.6	855	7	CK195527	FGAS00396
1139	58	1.6	845	7	CK192875	FGAS00128	1212	58	1.6	855	7	CK196217	FGAS00466
1140	58	1.6	845	7	CK193161	FGAS00157	1213	58	1.6	855	7	CK196317	FGAS00477
1141	58	1.6	845	7	CK195076	FGAS00351	1214	58	1.6	855	7	CK196558	FGAS00501
1142	58	1.6	845	7	CK196823	FGAS00528	1215	58	1.6	856	7	CK195138	FGAS00357
1143	58	1.6	845	7	CK199008	FGAS00749	1216	58	1.6	857	4	BG108452	602278402
1144	58	1.6	845	7	CK200777	FGAS00929	1217	58	1.6	857	7	CK198185	FGAS00666
1145	58	1.6	846	7	CK196304	FGAS00475	1218	58	1.6	858	7	CK193712	FGAS00212
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1147	58	1.6	846	7	CK200907	FGAS00942	1220	58	1.6	858	7	CK197083	FGAS00555
1148	58	1.6	846	7	CK200926	FGAS00944	1221	58	1.6	858	7	CK198415	FGAS00650
1149	58	1.6	846	7	CK205064	FGAS01360	1222	58	1.6	859	7	CK196358	FGAS00481
1150	58	1.6	847	7	CK194370	FGAS00279	1223	58	1.6	859	7	CK198166	FGAS00664
1151	58	1.6	847	7	CK196241	FGAS00469	1224	58	1.6	860	7	CK192885	FGAS00129
1152	58	1.6	847	7	CK199544	FGAS00804	1225	58	1.6	860	7	CK194324	FGAS00274
1153	58	1.6	847	7	CK199561	FGAS00806	1226	58	1.6	860	7	CK198177	FGAS00666
1154	58	1.6	847	7	CK199689	FGAS00819	1227	58	1.6	861	2	BE895801	601432727
1155	58	1.6	847	7	CK199697	FGAS00820	1228	58	1.6	861	7	CF885820	tri6083XB
1156	58	1.6	847	7	CK200762	FGAS00927	1229	58	1.6	861	7	CK200203	FGAS000871
1157	58	1.6	847	7	CK204715	FGAS01325	1230	58	1.6	862	7	CK195661	FGAS00410
1158	58	1.6	848	4	BG104735	602311872	1231	58	1.6	862	7	CK197542	FGAS00601
1159	58	1.6	848	7	CK192879	FGAS00128	1232	58	1.6	862	7	CK198129	FGAS00661
1160	58	1.6	848	7	CK193088	FGAS00150	1233	58	1.6	862	7	CK198169	FGAS00665
1161	58	1.6	848	7	CK193796	FGAS00221	1234	58	1.6	862	7	CK200737	FGAS00925
1162	58	1.6	848	7	CK198136	FGAS00661	1235	58	1.6	863	7	CK193790	FGAS00220
1163	58	1.6	848	7	CK199711	FGAS00821	1236	58	1.6	863	7	CK195645	FGAS00408
1164	58	1.6	849	7	CK192884	FGAS00129	1237	58	1.6	863	7	CK196201	FGAS00464
1165	58	1.6	849	7	CK195094	FGAS00353	1238	58	1.6	863	7	CK198188	FGAS00667
1166	58	1.6	849	7	CK196905	FGAS00537	1239	58	1.6	863	7	CK199036	FGAS00752
1167	58	1.6	849	7	CK197700	FGAS00618	1240	58	1.6	864	7	CK193695	FGAS00211
1168	58	1.6	849	7	CK198254	FGAS00673	1241	58	1.6	864	7	CK197565	FGAS00604
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1170	58	1.6	849	7	CK199720	FGAS00822	1243	58	1.6	864	7	CK198412	FGAS00689
1171	58	1.6	849	7	CK200176	FGAS00868	1244	58	1.6	865	7	CK193569	FGAS00198
1172	58	1.6	849	7	CK200363	FGAS00887	1245	58	1.6	865	7	CK196196	FGAS00464
1173	58	1.6	850	7	CK196182	FGAS00462	1246	58	1.6	865	7	CK196364	FGAS00482
1174	58	1.6	850	7	CK196346	FGAS00480	1247	58	1.6	865	7	CK196813	FGAS00527
1175	58	1.6	850	7	CK196881	FGAS00534	1248	58	1.6	865	7	CK197648	FGAS00612
1176	58	1.6	850	7	CK198353	FGAS00683	1249	58	1.6	865	7	CK198814	FGAS00730
1177	58	1.6	851	5	BUI75994	AGENCOURT	1250	58	1.6	866	7	CK198192	FGAS00667
1178	58	1.6	851	7	CK193709	FGAS00212	1251	58	1.6	866	7	CK193452	FGAS00795
1179	58	1.6	851	7	CK195646	FGAS00408	1252	58	1.6	866	7	CK200117	FGAS00862
1180	58	1.6	851	7	CK198407	FGAS00689	1253	58	1.6	867	7	CK192898	FGAS00130
1181	58	1.6	851	7	CK198413	FGAS00689	1254	58	1.6	867	7	CK193007	FGAS00141
1182	58	1.6	851	7	CK199594	FGAS00809	1255	58	1.6	867	7	CK194211	FGAS00263
1183	58	1.6	852	7	CK194319	FGAS00274	1256	58	1.6	867	7	CK194422	FGAS00285
1184	58	1.6	852	7	CK194473	FGAS00290	1257	58	1.6	867	7	CK198339	FGAS00882
1185	58	1.6	852	7	CK195112	FGAS00355	1258	58	1.6	868	7	CK198243	FGAS00672
1186	58	1.6	852	7	CK195558	FGAS00399	1259	58	1.6	868	7	CK198316	FGAS00680
1187	58	1.6	852	7	CK196381	FGAS00483	1260	58	1.6	869	7	CK198922	FGAS00741
1188	58	1.6	852	7	CK198402	FGAS00688	1261	58	1.6	870	4	BM014441	603640204
1189	58	1.6	852	7	CK200159	FGAS00866	1262	58	1.6	870	7	CK195149	FGAS00358
1190	58	1.6	853	7	CK193078	FGAS00149	1263	58	1.6	870	7	CK200739	FGAS00925
1191	58	1.6	853	7	CK193111	FGAS00152	1264	58	1.6	872	7	CK193772	FGAS00218
1192	58	1.6	853	7	CK193528	FGAS00194	1265	58	1.6	873	7	CK199050	FGAS00754

1266	58	1.6	874	7	CK201939	1339	58	1.6	1012	5	BU04623	AGENCY
1267	58	1.6	875	7	CK198221	1340	58	1.6	1013	4	BU180046	AGENCY
1268	58	1.6	876	7	CK193824	1341	58	1.6	1013	4	BU180046	AGENCY
1269	58	1.6	876	7	CK195604	1342	58	1.6	1014	4	BU249858	AGENCY
1270	58	1.6	876	7	CK200933	1343	58	1.6	1014	4	BU249858	AGENCY
1271	58	1.6	877	7	CK193575	1344	58	1.6	1021	4	BU262006	AGENCY
1272	58	1.6	878	7	CK193649	1345	58	1.6	1031	4	BU262006	AGENCY
1273	58	1.6	878	7	CK193649	1346	58	1.6	1032	5	BU262006	AGENCY
1274	58	1.6	880	5	BU0420273	1347	58	1.6	1033	5	BU262006	AGENCY
1275	58	1.6	880	5	BU0420273	1348	58	1.6	1033	5	BU262006	AGENCY
1276	58	1.6	880	7	CK193636	1349	58	1.6	1035	5	BU262006	AGENCY
1277	58	1.6	881	7	CK193636	1350	58	1.6	1040	5	BU262006	AGENCY
1278	58	1.6	881	7	CK193636	1351	58	1.6	1042	5	BU262006	AGENCY
1279	58	1.6	881	7	CK193636	1352	58	1.6	1048	5	BU262006	AGENCY
1280	58	1.6	882	7	CK195123	1353	58	1.6	1049	4	BU262006	AGENCY
1281	58	1.6	882	7	CK195123	1354	58	1.6	1049	4	BU262006	AGENCY
1282	58	1.6	882	7	CK195545	1355	58	1.6	1055	5	BU262006	AGENCY
1283	58	1.6	883	4	BU035330	1356	58	1.6	1055	5	BU262006	AGENCY
1284	58	1.6	883	4	BU035330	1357	58	1.6	1059	4	BU262006	AGENCY
1285	58	1.6	884	7	CK193727	1358	58	1.6	1060	4	BU262006	AGENCY
1286	58	1.6	884	7	CK193727	1359	58	1.6	1063	4	BU262006	AGENCY
1287	58	1.6	885	7	CK193767	1360	58	1.6	1065	7	BU262006	AGENCY
1288	58	1.6	885	7	CK200244	1361	58	1.6	1068	5	BU262006	AGENCY
1289	58	1.6	885	7	CK200244	1362	58	1.6	1074	4	BU262006	AGENCY
1290	58	1.6	887	7	CK194485	1363	58	1.6	1074	4	BU262006	AGENCY
1291	58	1.6	887	7	CK195080	1364	58	1.6	1080	7	BU262006	AGENCY
1292	58	1.6	890	7	CK195659	1365	58	1.6	1080	7	BU262006	AGENCY
1293	58	1.6	891	7	CK195023	1366	58	1.6	1084	4	BU262006	AGENCY
1294	58	1.6	893	5	BU0430100	1367	58	1.6	1098	4	BU262006	AGENCY
1295	58	1.6	893	7	CK194960	1368	58	1.6	1098	4	BU262006	AGENCY
1296	58	1.6	896	7	CK195020	1369	58	1.6	1098	4	BU262006	AGENCY
1297	58	1.6	901	6	BU559551	1370	58	1.6	1105	7	BU262006	AGENCY
1298	58	1.6	903	7	CK193657	1371	58	1.6	1111	4	BU262006	AGENCY
1299	58	1.6	908	7	CK194203	1372	58	1.6	1112	4	BU262006	AGENCY
1300	58	1.6	909	5	BU0911344	1373	58	1.6	1114	5	BU262006	AGENCY
1301	58	1.6	910	5	BU0911344	1374	58	1.6	1121	2	BU262006	AGENCY
1302	58	1.6	911	5	BU0911344	1375	58	1.6	1121	2	BU262006	AGENCY
1303	58	1.6	915	5	BU0911344	1376	58	1.6	1121	2	BU262006	AGENCY
1304	58	1.6	915	5	BU0911344	1377	58	1.6	1121	2	BU262006	AGENCY
1305	58	1.6	921	7	CK194960	1378	58	1.6	1121	2	BU262006	AGENCY
1306	58	1.6	921	7	CK194960	1379	58	1.6	1121	2	BU262006	AGENCY
1307	58	1.6	922	4	BU164752	1380	58	1.6	1121	2	BU262006	AGENCY
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ALIGNMENTS

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RESULT 1
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DEFINITION AGENCOURT_7560030 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055912
5', mRNA sequence.
ACCESSION BQ213573
VERSION BQ213573.1 GI:20394883
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."
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18.5k; Score 663; DB 5; Length 903;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-232;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION 5', mRNA sequence.
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VERSION BU552398.1 GI:22902670
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2774 row: e column: 08
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Qy 1943 TCAAGCCTCATTTGTTATCCAGCATCTCTTAAACCTTTGTAGTCTTGGAAATTCATGACA 2002
Db 661 TCAAGCCTCATTTGTTATCCAGCATCTCTTAAACCTTTGTAGTCTTGGAAATTCATGACA 602
Qy 2003 GAGCAAAATGACTCTCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTA 2062
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Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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RESULT 3
BM469318
LOCUS
DEFINITION BM469318 1014 bp mRNA linear EST 05-FEB-2002
AGENCOURT 644646 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585235
5', mRNA sequence.
ACCESSION BM469318
VERSION BM469318.1 GI:19518360
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1014)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12351 row: d column: 04
High quality sequence stop: 666.
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/notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
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Note: this is a NIH_MGC Library."
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Best Local Similarity 100.0%; Pred. No. 2.6e-228;
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DB 1 AGAGCCCTGCTGGCAGCCTCCACAGCCAGTGGCCAGGAGCTTTGCTGAAGATT 60
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7k29d11.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476804 3',
mRNA sequence.
ACCESSION BF058311
VERSION BF058311.1 GI:10812207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 496.
FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3476804"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/notes="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGACATTTTGTGTTTGT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 15.6%; Score 559; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 3.8e-194;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3022 GAGGATGGGTGGGTGTGGGGACTCATGGGGAATGGCCTGAGGAGTACGTGTGAAGAG 3081

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Db 567 GAGGATGGGTGGGTGGGACTCATGGGAAATGGCTGAGGAGCTACGTGTGAAGAG 508
Qy 3082 GCGCGCGTGTGGCTGACAGCGCTGGAGCGCTCTCTCTGAGCTCAGTTTCCT 3141
Db 507 GCGCGCGTGTGGCTGACAGCGCTGGAGCGCTCTCTCTGAGCTCAGTTTCCT 448
Qy 3142 TTCCTCTAATGAAGAAATGCGCTCGGTGTCTCAGGGCTATTAGACTTGGCCCTCAG 3201
Db 447 TTCCTCTAATGAAGAAATGCGCTCGGTGTCTCAGGGCTATTAGACTTGGCCCTCAG 388
Qy 3202 GAAGTGGCTTGGACAGCGCTCATGTTATTTTCAACAATGCTCTCGCAGCTTGGCTGGG 3261
Db 387 GAAGTGGCTTGGACAGCGCTCATGTTATTTTCAACAATGCTCTCGCAGCTTGGCTGGG 328
Qy 3262 CACGTCTGAATGAGCGCTCATGCTCTCTCTGCTGAGCGCTCGGCTGGAGTGGCAG 3321
Db 337 CACGTCTGAATGAGCGCTCATGCTCTCTCTGCTGAGCGCTCGGCTGGAGTGGCAG 268
Qy 3322 CCAGAGCGGGCCAGACAGCTGCGCTCGGGGTGAGGGAGCGCGCCCGGAGGCGCTCAC 3381
Db 267 CCAGAGCGGGCCAGACAGCTGCGCTCGGGGTGAGGGAGCGCGCCCGGAGGCGCTCAC 208
Qy 3382 AGGAAGTTGGCTCCCGCACACACAGGAGCGCGGCTCCCGCCCGCCCGCGCCACCA 3441
Db 207 AGGAAGTTGGCTCCCGCACACACAGGAGCGCGGCTCCCGCCCGCCCGCGCCACCA 148
Qy 3442 CCGTCCAGGGCGGTAGACAAAGTGAAGTGGCGCTTGGGCTGCGCTCGGACGAGGTAG 3501
Db 147 CCGTCCAGGGCGGTAGACAAAGTGAAGTGGCGCTTGGGCTGCGCTCGGACGAGGTAG 88
Qy 3502 CCCTTGATGACGTGGCGGAGCGCTGCTCCGCGAGCTGGAAGCGCGCCCGTCCACACAGC 3561
Db 87 CCCTTGATGACGTGGCGGAGCGCTGCTCCGCGAGCTGGAAGCGCGCCCGTCCACACAGC 28
Qy 3562 ACGAACACCGGTGCGCT 3580
Db 27 ACGAACACCGGTGCGCT 9

RESULT 5
BU688759
LOCUS
DEFINITION
UI-CF-EC1-adv-c-23-0-UI.s1 UI-CF-EC1 Homo sapiens cdna clone
UI-CF-EC1-adv-c-23-0-UI 3', mRNA sequence.
ACCESSION
BU688759
VERSION
BU688759.1 GI:23545844
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 692)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).

Seq primer: M13 FORWARD
POLVA=Yes.
FEATURES
Location/Qualifiers
1..692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-adv-c-23-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DHI0B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EC1 is a normalized cdna library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGCCTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCCTAC"

ORIGIN
Query Match 15.4%; Score 550; DB 5; Length 692;
Best Local Similarity 99.7%; Pred. No. 7.2e-191;
Matches 650; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2659 AAATTCTCCACACAGATGGCTCTGCAATCTGCCACAGCTCTGGGGCGGTGCTGTAGG 2718
Db 41 AAATTCTCCACACAGATGGCTCTGCAATCTGCCACAGCTCTGGGGCGGTGCTGTAGG 100
Qy 2719 GAAAGGCGCTGTTTTCCTGAGGGCGGCTGGGCTGTTCATGGTCCCGGAGCTGACC 2778
Db 101 GAAAGGCGCTGTTTTCCTGAGGGCGGCTGGGCTGTTCATGGTCCCGGAGCTGACC 160
Qy 2779 GTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGGCGGCGACAGAGCTGCGGGGCT 2838
Db 161 GTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGGCGGCGACAGAGCTGCGGGGCT 220
Qy 2839 GGGGCGACCGGGAGCTAAGACAGAGCTCTGTGTGAGGGGTGAGGCTGTCTCTTAAACG 2898
Db 221 GGGGCGACCGGGAGCTAAGACAGAGCTCTGTGTGAGGGGTGAGGCTGTCTCTTAAACG 280
Qy 2899 ACACCTTGAGTGTCTCTGAGATGCTGGGTCCACCTGAGTGGCACGCGGAGCAGCTGTG 2958
Db 281 ACACCTTGAGTGTCTCTGAGATGCTGGGTCCACCTGAGTGGCACGCGGAGCAGCTGTG 340
Qy 2959 GCGGCTGCTCTCTCTTAGGCCAGTCTGGGGAATAAGCTCGGCGCCCTTCTTTGCAAG 3018
Db 341 GCGGCTGCTCTCTCTTAGGCCAGTCTGGGGAATAAGCTCGGCGCCCTTCTTTGCAAG 400
Qy 3019 ACCGAGGATGGGTGGGTGGGAGCTCATGGGAATAGGCTGAGGAGCTACGTGTGAA 3078
Db 401 ACCGAGGATGGGTGGGTGGGAGCTCATGGGAATAGGCTGAGGAGCTACGTGTGAA 460
Qy 3079 GAGGCGCGGTTTGTGGCTGCGAGCGGCTCTCTCTGAGGCTCAGTTTC 3138
Db 461 AAGGCGCGGTTTGTGGCTGCGAGCGGCTCTCTCTGAGGCTCAGTTTC 520
Qy 3139 CTTTTCGCTTAATGAAGAAATGCGCTCGGTGTCTCAGGGCTATTAGACTTGGCCT 3198
Db 521 CTTTTCGCTTAATGAAGAAATGCGCTCGGTGTCTCAGGGCTATTAGACTTGGCCT 580

Qy	3199	CAGGAAGTGGCTTGGACGAGCGTCATGTTATTTTTCACAACTGCTCTCGACAGCTTGGCCT	3255
Db	581	CAGGAAGTGGCTTGGACGAGCGTCATGTTATTTTTCACAACTGCTCTCGACAGCTTGGCCT	640
Qy	3259	GGGCACGTCATGGAATGCCCATGCTCCCTCTGCTGCGTGACGTCGCGGTCG	3310
Db	641	GGGCACGTCATGGAATGCCCATGCTCCCTCTGCTGCGTGACGTCGCGGTCG	692
RESULT 6			
AQ472645/c			
LOCUS			
DEFINITION	AQ472645	646 bp	DNA linear GSS 23-APR-1999
ACCESSION	CITBI-EI-2585H18.TF CITBI-EI Homo sapiens genomic clone 2585H18,		
VERSION	genomic survey sequence.		
KEYWORDS	AQ472645		
SOURCE	AQ472645.1	GI:4651600	
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 (bases 1 to 646)		
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and		
	Venter,J.C.		
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready		
JOURNAL	Map Building		
	Unpublished (1997)		
	Other GSSs: CITBI-EI-2585H18.TR		
	Contact: Shaying Zhao, William Nierman, Mark Adams		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: hbe@tigr.org		
FEATURES	Clones are available from Research Genetics (info@resgen.com). BAC		
	end search page:		
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.		
	Seq primer: M13-21		
ORIGIN	Class: BAC ends.		
	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="2585H18"		
	/sex="male"		
	/cell_type="sperm"		
	/clone_lib="CITBI-EI"		
ORIGIN	/notes="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;		
	CalTech Human BAC Library D"		
	Query Match 15.1%; Score 540; DB 8; Length 646;		
	Best Local Similarity 99.7%; Pred. No. 3.4e-187;		
	Matches 640; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	1556	AGCCCCACCTGCCAAGACCCGACCTAGAGCGCTGTGAGTTGGTGACGCAAAACCGGGGCA	1615
Db	645	AGCCCCACCTGCCAAGACCCGACCTAGAGCGCTGTGAGTTGGTGACGCAAAACCGGGGCA	586
Qy	1616	CTGTGCTGGCCACAGAGCTAGGGCTGACAAGTGGCCCTCGCTTGGGCATTTCACCAAGAAC	1675
Db	585	CTGTGCTGGCCACAGAGCTAGGGCTGATAGTGGCCCTCGCTTGGGCATTTCACCAAGAAC	526
Qy	1676	CTGACACCCCGCCTCACGAGGAGGCCCAAGTGCCCAATGACAGACCCCTCACTGGTTGGGGT	1735
Db	525	CTGACACCCCGCCTCACGAGGAGGCCCAAGTGCCCAATGACAGACCCCTCACTGGTTGGGGT	466
Qy	1736	GTAGCTGGGTCTACAGTCAGACTTCCTGCTCTTAAGGGTGTCACTGCTGTCATCCACCA	1795
Db	465	GTAGCTGGGTCTACAGTCAGACTTCCTGCTCTTAAGGGTGTCACTGCTGTCATCCACCA	406

ORIGIN	Query Match Best Local Similarity 15.0%; Score 536; DB 5; Length 927; Matches 686; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1892 ATCTTTGGATATCTAAATGAATAGAGTGTGTGGGCTTGTCAACACAGAAATTCAGGCTC 1951
Db	712 ATCTTTGGATATCTAAATGAATAGAGTGTGTGGGCTTGTCAACACAGAAATTCAGGCTC 653
Qy	1952 ATTTGTCTATCCAGCATCTTAAACATTTGTAGTCTTGGATTCATGACAGGCAAT 2011
Db	652 ATTTGTCTATCCAGCATCTTAAACATTTGTAGTCTTGGATTCATGACAGGCAAT 593
Qy	2012 GACTCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTT 2071
Db	592 GACTCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTT 533
Qy	2072 ATCAGGAGCTGAGTGCCTATCTCTTATTAATATGCTTAACACAGGCGGGTCTGGTG 2131
Db	532 ATCAGGAGCTGAGTGCCTATCTCTTATTAATATGCTTAACACAGGCGGGTCTGGTG 473
Qy	2132 CTATGCTGTATCCAGCATCTTGAAGGCTGAGTGTGGCGGACTGCTGAGTCTAG 2191
Db	472 CTATGCTGTATCCAGCATCTTGAAGGCTGAGTGTGGCGGACTGCTGAGTCTAG 413
Qy	2192 GAATTCAGACAGCTGCTGCAACATGGCAAAACCCCATCTCTACTTAAATAATAAAAAAT 2251
Db	412 GAATTCAGACAGCTGCTGCAACATGGCAAAACCCCATCTCTACTTAAATAATAAAAAAT 353
Qy	2252 TATTAGCTGGCATGTGTGTGTGTATCCAGCTACTCAGGAGGATGAGGAGG 2311
Db	352 TATTAGCTGGCATGTGTGTGTGTATCCAGCTACTCAGGAGGATGAGGAGG 293
Qy	2312 AGACCTGCTTGAACCTGGAGTGGAGTGTGAGTGGCGGAGTGTGCACTGCTGCTC 2371
Db	292 AGACCTGCTTGAACCTGGAGTGGAGTGTGAGTGGCGGAGTGTGCACTGCTGCTC 233
Qy	2372 AGTCTGGTAAACAGAGCGAGACTTTCTAGAAAAAGCCTTAAACACAGATAGGTAGACT 2431
Db	232 AGTCTGGTAAACAGAGCGAGACTTTCTAGAAAAAGCCTTAAACACAGATAGGTAGACT 173
Qy	2432 CAACCAACTGAAACCTGACTTTTCCCTGTGTACCTTTCAGCCCTGTGCAAGTGTGAACTC 2491
Db	172 CAACCAACTGAAACCTGACTTTTCCCTGTGTACCTTTCAGCCCTGTGCAAGTGTGAACTC 113
Qy	2492 TTGAGACCTCTCCCTGACAGGACCAAGCAGCAGGCAATTTAGAGCTTTTAGAATAAAC 2551
Db	112 TTGAGACCTCTCCCTGACAGGACCAAGCAGCAGGCAATTTAGAGCTTTTAGAATAAAC 53
Qy	2552 TGGTTTCTTTTAAAAAATAAAAAA 2580
Db	52 TGGTTTCTTTTAAAAAATAAAAAA 24
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LOCUS	AWB15410 527 bp mRNA linear EST 17-MAY-2000
DEFINITION	QV0-ST0215-140200-100-c05 ST0215 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AWB15410
VERSION	AWB15410.1 GI:7908404
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 527) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

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Db      47 AGGTGTGGGGCTTGTCAACAGAAATTCAGCCCTCATTTGCTATCC 1
RESULT 9
BF940697/c      527 bp      mRNA      linear      EST 30-MAR-2001
LOCUS      na224805.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3435945 3',
DEFINITION      mRNA sequence.
ACCESSION      BF940697
VERSION      BF940697.1 GI:12358017
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 527)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 505.
Location/Qualifiers
FEATURES      source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3435945"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Ov18"
/notes="Organ: ovary; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTCGAGCGCGCGACATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      14.5%; Score 519; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.8e-179; Mismatches 0; Indels 0; Gaps 0;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      3062 GAGGAGCTACGTGTGAAGAGGCGCGCGTTTGTGGCTGACGCGCCCTGGAGCGCCTCTC 3121
Db      527 GAGGAGCTACGTGTGAAGAGGCGCGCGTTTGTGGCTGACGCGCCCTGGAGCGCCTCTC 468
Qy      3122 TCCTGAGCCTCAGTTTCCCTTCCGTCTAATGAAGAACATCGCGTCTCGGTGTCTCAGGG 3181
Db      467 TCCTGAGCCTCAGTTTCCCTTCCGTCTAATGAAGAACATCGCGTCTCGGTGTCTCAGGG 408
Qy      3182 CTATTAGACTTGGCCTCAGAGTGGCCTTGGAGCGGTCATGTTATTTTCAACTG 3241
Db      407 CTATTAGACTTGGCCTCAGAGTGGCCTTGGAGCGGTCATGTTATTTTCAACTG 348
Qy      3242 TCCTGCGACGTTGGCCTGGGACGCTCATGGAATGGCCCATCTCCCTCTGCTGCGTGGACG 3301
Db      347 TCCTGCGACGTTGGCCTGGGACGCTCATGGAATGGCCCATCTCCCTCTGCTGCGTGGACG 288
Qy      3302 TCGCGGTGGGAGTGGCGAGCCAGAGGCGGGGCCAGAGCGTGGCCTGGGGGTGAGGGGAG 3361

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Db      287 TCGCGGTGGGAGTGGCGCAGCAGAGGCGGGGCCAGACGTGCGCTGGGGGTGAGGGGAG 228
Qy      3362 GCGCCCGGGGAGGCGCTCACAGGAAGTTGGGCTCCCGCACACACAGGCGAGGCGGGCTCC 3421
Db      227 GCGCCCGGGGAGGCGCTCACAGGAAGTTGGGCTCCCGCACACACAGGCGAGGCGGGCTCC 168
Qy      3422 GCGCCCGCCCGCCCGCCACACCGTCCAGGGGCGCGGTAGACAAAGTGGAGTTCGCGCTTTGG 3481
Db      167 GCGCCCGCGCGCGCCACACCGTCCAGGGGCGCGGTAGACAAAGTGGAGTTCGCGCTTTGG 108
Qy      3482 GCTGCTGGCGCAGCAGGTAGCTTCTGATGCTGAGTGGCGAGCGCGTCTCGCCACCTGGA 3541
Db      107 GCTGCTGGCGCAGCAGGTAGCTTCTGATGCTGAGTGGCGAGCGCGTCTCGCCACCTGGA 48
Qy      3542 AGCAGCGCCCGTCCACACGACGACGAACCGCGTGGCGCT 3580
Db      47 AGCAGCGCCCGTCCACGACGACGAACCGCGTGGCGCT 9
RESULT 10
BM459709
LOCUS      BM459709
DEFINITION      AGENCOURT 6417932 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534341
5', mRNA sequence.
ACCESSION      BM459709
VERSION      BM459709.1 GI:18508749
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 908)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12220 row: k column: 14
High quality sequence stop: 698.
Location/Qualifiers
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1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534341"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="Organ: uterus; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
ORIGIN
Query Match      14.4%; Score 515; DB 4; Length 908;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1637 GCTGAGAGTGGCCCTCGCTTGGGCATTGACACAGAACCTTGAGCCCGCTCAGAGG 1696
Db      1 GCTGAGAGTGGCCCTCGCTTGGGCATTGACACAGAACCTTGAGCCCGCTCAGAGG 60
Qy      1697 AGGCCCCAAGTGCCCAATGCAGACCTCAGCTGTTGGGGTGTAGCTGGGTCTACAGTCA 1756
Db      61 AGGCCCCAAGTGCCCAATGCAGACCTCAGCTGTTGGGGTGTAGCTGGGTCTACAGTCA 120

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QY 1757 CTTCTGCTCTAAGGTGTCACTGGCTGGCATCCACACGCGAATCCTAGAGGAGGAG 1816
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Db 181 AGTGGCTCTGATTTGGGATTTATGGCAAAAGTCCAGAGATGCCAGTCTCTGGAGTAGAAG 240
QY 1877 AGTGGTGTGTTGTTATCTCTCTGGATATAAATGAAGAGAGTGTGGGCTTTGTCAACA 1936
Db 241 AGTGGTGTGTTGTTATCTCTCTGGATATAAATGAAGAGAGTGTGGGCTTTGTCAACA 300
QY 1937 CAGAAATCAAGCTCATTTGGCTATCCAGCATCTCTTAAAGCTTTGTAGTCTTGAATTC 1996
Db 301 CAGAAATCAAGCTCATTTGGCTATCCAGCATCTCTTAAAGCTTTGTAGTCTTGAATTC 360
QY 1997 ATGACAGAGGCAAAATGACTCTCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGG 2056
Db 361 ATGACAGAGGCAAAATGACTCTCTGCTTAACTTATGAAGAAAGTTAAACATGAATCTTGGG 420
QY 2057 AGTCTACATTTCTTATACACAGGAGCTGGAGTGCATCTCTTATAAATGCCATAACA 2116
Db 421 AGTCTACATTTCTTATACACAGGAGCTGGAGTGCATCTCTTATAAATGCCATAACA 480
QY 2117 GCGCGGGTCTGGTGGCTCATGCTCTGAATCCCGC 2151
Db 481 GCGCGGGTCTGGTGGCTCATGCTCTGAATCCCGC 515
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RESULT 11
BM702052
LOCUS
DEFINITION
  UI-E-Q01-ay-c-15-0-UI r1 UI-E-Q01 Homo sapiens cDNA clone
  UI-E-Q01-ay-c-15-0-UI 5', mRNA sequence.
ACCESSION
  BM702052
VERSION
  BM702052.1 GI:19015310
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 500)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  9704477
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  The following repetitive elements were found in this cDNA
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    /db_xref="taxon:9606"
    /clone="UI-E-Q01-ay-c-15-0-UI"
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    /dev_stage="adult"
    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/clone_lib="UI-E-Q01"
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UI-E-Q01 is a normalized cDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAGTG. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."
```

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ORIGIN
Query Match      14.0%; Score 500; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.7e-172;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2055 GGAGTCTACATTTCTTATACACAGGAGCTGGAGTGCATCTCTTATAAATGCCATAACA 2114
Db 1 GGAGTCTACATTTCTTATACACAGGAGCTGGAGTGCATCTCTTATAAATGCCATAACA 60
QY 2115 CAGGCCGGGTCTGGTGGCTCATGCTCTGAATCCAGCAGCTTTGAGAGGCTTGAGTCGGC 2174
Db 61 CAGGCCGGGTCTGGTGGCTCATGCTCTGAATCCAGCAGCTTTGAGAGGCTTGAGTCGGC 120
QY 2175 GGAGTCTGAGGTTCAGGAATTCAGACAGGCTGGCCCAACATGGCAAAACCCATCTCT 2234
Db 121 GGAGTCTGAGGTTCAGGAATTCAGACAGGCTGGCCCAACATGGCAAAACCCATCTCT 180
QY 2235 ACTAAAAATAAAAAAATTTATAGCTGGGCATGTGTGTGTGCTGTGAATCCAGCTACT 2294
Db 181 ACTAAAAATAAAAAAATTTATAGCTGGGCATGTGTGTGTGCTGTGAATCCAGCTACT 240
QY 2295 CAGAGAGTAGGAGGAGGAGACCTCTGTAACCTGGAGTGGAGTTGAGTGGAGCCGAGG 2354
Db 241 CAGAGAGTAGGAGGAGGAGACCTCTGTAACCTGGAGTGGAGTTGAGTGGAGCCGAGG 300
QY 2355 TCGCACCACTGCACCTCCAGTCTGGTAAACAGAGGAGAGCTTTCTAGAAAAAGCTTAACA 2414
Db 301 TCGCACCACTGCACCTCCAGTCTGGTAAACAGAGGAGAGCTTTCTAGAAAAAGCTTAACA 360
QY 2415 ACAGATAAGGTAGGAGTCAACCAACTGAACTTTCCCTCTGTACCTTCAGCCCCCT 2474
Db 361 ACAGATAAGGTAGGAGTCAACCAACTGAACTTTCCCTCTGTACCTTCAGCCCCCT 420
QY 2475 GTGAGGTAGTAACTCTTGAGACCTCTCCCTGACAGGAGCAAGACAGAGGATTTAG 2534
Db 421 GTGAGGTAGTAACTCTTGAGACCTCTCCCTGACAGGAGCAAGACAGAGGATTTAG 480
QY 2535 AGCTTTTATAGATAAACTGG 2554
Db 481 AGCTTTTATAGATAAACTGG 500
RESULT 12
BU552474/c
LOCUS
DEFINITION
  BU552474
  5', mRNA sequence.
ACCESSION
  BU552474
VERSION
  BU552474.1 GI:22902746
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 996)
  REFERENCE
    1 (bases 1 to 996)
```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LNC2774 row: h column: 19
High quality sequence stop: 546.
Location/Qualifiers
1..996
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6576259"
/tissue type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 13.9%; Score 497; DB 5; Length 996;
Best Local Similarity 99.5%; Pred. No. 1.8e-171;
Matches 547; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1931 TCACACAGAAATTCAGGCTCATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTG 1990
Db 673 TCACACAGAAATTCAGGCTCATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTG 614

Qy 1991 GAATTCATGACAGGCGAATGACCTCTTAACTTATGAGAAAGTAAACATGAAT 2050
Db 613 GAATTCATGACAGGCGAATGACCTCTTAACTTATGAGAAAGTAAACATGAAT 554

Qy 2051 CTGGGAGCTACATTTCTTATACACAGGAGCTGAGCTGCATCTCTTATAATGCT 2110
Db 553 CTGGGAGCTACATTTCTTATACACAGGAGCTGAGCTGCATCTCTTATAATGCT 494

Qy 2111 AACACAGCGCGGCTGCTGGCTCATGCTGTAAATCCAGCACATTTGAGAGCGCTGAGGT 2170
Db 493 AACACAGCGCGGCTGCTGGCTCATGCTGTAAATCCAGCACATTTGAGAGCGCTGAGGT 434

Qy 2171 CGGGAGCTGCTGAGTTCAGAAATTAAGACAGCGCTGGCAATGGCAACATGGCAACCCCAT 2230
Db 433 CGGGAGCTGCTGAGTTCAGAAATTAAGACAGCGCTGGCAATGGCAACATGGCAACCCCAT 374

Qy 2231 CTCTACTAAAAATAAAAAATTTATAGCTGGGCTGCTGTGCTGCTTAATCCACG 2290
Db 373 CTCTACTAAAAATAAAAAATTTATGGCTGGGCTGGTGGTGGCTGCTGCTTAATCCACG 314

Qy 2291 TACTCAGGAGGATGAGGAGGAGACCTGCTTGAACCTGGAGGTGAGGTTGCGAGTGAACC 2350
Db 313 TACTCAGGAGGATGAGGAGGAGACCTGCTTGAACCTGGAGGTGAGGTTGCGAGTGAACC 254

Qy 2351 GAGTTCGACCACTGACCTCCAGTCTGGGTAAACAGAGGAGAGCTTTCTAGAAAAAGCCTA 2410
Db 253 GAGTTCGACCACTGACCTCCAGTCTGGGTAAACAGAGGAGAGCTTTCTAGAAAAAGCCTA 194

Qy 2411 ACAACAGATAGGTGAGGACTCAACCAACTGAACTGAACTTCCCTGCTGACCTTCAGC 2470
Db 193 ACAACAGATAGGTGAGGACTCAACCAACTGAACTGAACTTCCCTGCTGACCTTCAGC 134

Qy 2471 CCCTGTGAGGTAGTAACCTCTTGAGACCTCTCCCTGACGAGGACCAAGCACAGGGCAT 2530
Db 133 CCCTGTGAGGTAGTAACCTCTTGAGACCTCTCCCTGACGAGGACCAAGCACAGGGCAT 74

Qy 2531 TTAGAGCTTTTGAATAAAGTGGTTTCTTTAAAAAAGGAAAAA 2580
Db 73 TTAGAGCTTTTGAATAAAGTGGTTTCTTTAAAAAAGGAAAAA 24

RESULT 13
BE675211/c 527 bp mRNA linear EST 08-SEP-2000
LOCUS 7104e08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3293702 3',
DEFINITION mRNA sequence.
ACCESSION BE675211
VERSION BE675211.1 GI:10035752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 527)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
1..527
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3293702"
/tissue type="B-cell, chronic lymphocytic leukemia"
/lab host="DH10B"
/clone lib="NCI_CGAP CLL1"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Patima Bonaldo."

FEATURES
source

ORIGIN

Query Match 13.1%; Score 468; DB 2; Length 527;
Best Local Similarity 99.8%; Pred. No. 9e-161;
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3062 GAGGAGCTACGTGTGAAGAGGCGCGGTTTGTGGCTGACGCGGCTTGGAGCGCTCTC 3121
Db 527 GAGGAGCTACGTGTGAAGAGGCGCGGTTTGTGGCTGACGCGGCTTGGAGCGCTCTC 468

Qy 3122 TCCTGAGCCTCAGTTTCCCTTTCGTCTAATGAAGAACATCCGCTCTCGGTGCTCAGGG 3181
Db 467 TCNTGAGCCTCAGTTTCCCTTTCGTCTAATGAAGAACATCCGCTCTCGGTGCTCAGGG 408

Qy 3182 CTATTAGACTTGCCTCAGGAGTGGCTTGGAGCGCTCATGCTTATTTTCAACATG 3241
Db 407 CTATTAGACTTGCCTCAGGAGTGGCTTGGAGCGCTCATGCTTATTTTCAACATG 348


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/lab_host="DH10B (phage-resistant)"  
/clone_lib="Soares thymus NHFth"  
(note="Organ: thymus, pooled; Vector: pT7T3D-Pac  
(Pharmacia) with a modified polylinker; Site.1: Not I;  
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCCGCAACGTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo. "
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ORIGIN

Query Match		12.7%;	Score 456;	DB 1;	Length 526;
Best Local Similarity		100.0%;	Pred. No. 2.3e-156;		
Matches	456;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	3125	TGAGCCTCAGTTTCCTTTCCGTTCTAATGAAGAACATGCCGTCTCGGTGTCACGGGCTA	3184		
Db	464	TGAGCCTCAGTTTCCTTTCCGTTCTAATGAAGAACATGCCGTCTCGGTGTCACGGGCTA	405		
QY	3185	TTAGGACTTGCCCTCAGGAGTGGCTTGGACGAGCGTCATGTTATTTTCACAACTGTCC	3244		
Db	404	TTAGGACTTGCCCTCAGGAGTGGCTTGGACGAGCGTCATGTTATTTTCACAACTGTCC	345		
QY	3245	TGCGACGTTGGCTCGGCAACGTCATGGAATGSCCCTATGTCCTCTGCTGCGTGGACGTGG	3304		
Db	344	TGCGACGTTGGCTCGGCAACGTCATGGAATGSCCCTATGTCCTCTGCTGCGTGGACGTGG	285		
QY	3305	CGGTCGGGAGTGCGCAGCCAGAGCGGGGCCAGACGTGCGCTGCGGGGTGAGGGAGGCG	3364		
Db	284	CGGTCGGGAGTGCGCAGCCAGAGCGGGGCCAGACGTGCGCTGCGGGGTGAGGGAGGCG	225		
QY	3365	CCCCGGGAGGGCTCAGAGGAAGTTGGGCTCCCGACACACAGGCGGGCGGGCTCCCGC	3424		
Db	224	CCCCGGGAGGGCTCAGAGGAAGTTGGGCTCCCGACACACAGGCGGGCGGGCTCCCGC	165		
QY	3425	CGCGCGCGCGCCACACCGTCCAGGGCGCGGTAGACAAAGTGGAAAGTCGGCTTTGGGCT	3484		
Db	164	CGCGCGCGCGCCACACCGTCCAGGGCGCGGTAGACAAAGTGGAAAGTCGGCTTTGGGCT	105		
QY	3485	CGCTCGCAGCAGGTAGCCCTTTGATGTCAGTGGCGAGCGCGTCGTCCGCCAGCTGGAAGC	3544		
Db	104	CGCTCGCAGCAGGTAGCCCTTTGATGTCAGTGGCGAGCGCGTCGTCCGCCAGCTGGAAGC	45		
QY	3545	AGCGCCCGTCCACACGACGAAACAGCCCGTGGCGCT	3580		
Db	44	AGCGCCCGTCCACACGACGAAACAGCCCGTGGCGCT	9		

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Job time : 10244 secs

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